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(71) Applicant: HUMAN GENOME SCIENCES, INC.
Rockville, MD 20850-3338 (US)

(72) Inventors:
• Kunsch, Charles A.
Gaithersburg, Maryland 20882 (US)
• Choi, Gil H.
Rockville, Maryland 20850 (US)
• Barash, Steven C.
Rockville, Maryland 20850 (US)
• Dillon, Patrick J.
Gaithersburg, Maryland 20879 (US)
• Fannon, Michael R.
Silver Spring, Maryland 20906 (US)
• Rosen, Craig A.
Laytonsville, Maryland 20882 (US)

(74) Representative: VOSSIUS & PARTNER
Postfach 86 07 67
81634 München (DE)

(54) **Staphylococcus aureus polynucleotides and sequences**

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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Description

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Staphylococcus aureus,* contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

The genus *Staphylococcus* includes at least 20 distinct species. (For a review see Novick, R. P., The *Staphylococcus* as a Molecular Genetic System, Chapter 1, pgs. 1-37 in MOLECULAR BIOLOGY OF THE *STAPHYLOCOCCI,* R. Novick, Ed., VCH Publishers, New York (1990)). Species differ from one another by 80% or more, by hybridization kinetics, whereas strains within a species are at least 90% identical by the same measure.

The species *Staphylococcus aureus,* a gram-positive, facultatively aerobic, clump-forming cocci, is among the most important etiological agents of bacterial infection in humans, as discussed briefly below.

Human Health and *S. Aureus*

Staphylococcus aureus is a ubiquitous pathogen. (See, for instance, Mims *et al.,* MEDICAL MICROBIOLOGY, Mosby-Year Book Europe Limited, London, UK (1993)). It is an etiological agent of a variety of conditions, ranging in severity from mild to fatal. A few of the more common conditions caused by *S. aureus* infection are burns, cellulitis, eyelid infections, food poisoning, joint infections, neonatal conjunctivitis,osteomyelitis, skin infections, surgical wound infection, scalded skin syndrome and toxic shock syndrome. some of which are described further below.

Burns

Burn wounds generally are sterile initially. However, they generally compromise physical and immune barriers to infection, cause loss of fluid and electrolytes and result in local or general physiological dysfunction. After cooling, contact with viable bacteria results in mixed colonization at the injury site. Infection may be restricted to the non-viable debris on the burn surface ("eschar"), it may progress into full skin infection and invade viable tissue below the eschar and it may reach below the skin, enter the lymphatic and blood circulation and develop into septicaemia. *S. aureus* is among the most important pathogens typically found in burn wound infections. It can destroy granulation tissue and produce severe septicaemia.

Cellulitis

Cellulitis, an acute infection of the skin that expands from a typically superficial origin to spread below the cutaneous layer, most commonly is caused by *S. aureus* in conjunction with *S. pyrogenes.* Cellulitis can lead to systemic infection. In fact, cellulitis can be one aspect of synergistic bacterial gangrene. This condition typically is caused by a mixture of *S. aureus* and microaerophilic *streptococci.* It causes necrosis and treatment is limited to excision of the necrotic tissue. The condition often is fatal.

Eyelid infections

S. aureus is the cause of styes and of sticky eye" in neonates, among other eye infections. Typically such infections are limited to the surface of the eye, and may occasionally penetrate the surface with more severe consequences.

Food poisoning

Some strains of *S. aureus* produce one or more of five serologically distinct, heat and acid stable enterotoxins that are not destroyed by digestive process of the stomach and small intestine (enterotoxins A-E). Ingestion of the toxin, in sufficient quantities, typically results in severe vomiting, but not diarrhoea. The effect does not require viable bacteria. Although the toxins are known, their mechanism of action is not understood.

Joint infections

S. aureus infects bone joints causing diseases such as osteomyelitis.

Osteomyelitis

S. aureus is the most common causative agent of haematogenous osteomyelitis. The disease tends to occur in

children and adolescents more than adults and it is associated with non-penetrating injuries to bones. Infection typically occurs in the long end of growing bone, hence its occurrence in physically immature populations. Most often, infection is localized in the vicinity of sprouting capillary loops adjacent to epiphysial growth plates in the end of long, growing bones

Skin infections

S. aureus is the most common pathogen of such minor skin infections as abscesses and boils. Such infections often are resolved by normal host response mechanisms, but they also can develop into severe internal infections. Recurrent infections of the nasal passages plague nasal carriers of *S. aureus*.

Surgical Wound Infections

Surgical wounds often penetrate far into the body. Infection of such wound thus poses a grave risk to the patient. *S. aureus* is the most important causative agent of infections in surgical wounds. *S. aureus* is unusually adept at invading surgical wounds; sutured wounds can be infected by far fewer *S. aureus* cells then are necessary to cause infection in normal skin. Invasion of surgical wound can lead to severe *S. aureus* septicaemia. Invasion of the blood stream by *S. aureus* can lead to seeding and infection of internal organs, particularly heart valves and bone, causing systemic diseases, such as endocarditis and osteomyelitis.

Scalded Skin Syndrome

S. aureus is responsible for "scalded skin syndrome" (also called toxic epidermal necrosis, Ritter's disease and Lyell's disease). This diseases occurs in older children, typically in outbreaks caused by flowering of *S. aureus* strains produce exfoliation(also called scalded skin syndrome toxin). Although the bacteria initially may infect only a minor lesion, the toxin destroys intercellular connections, spreads epidermal layers and allows the infection to penetrate the outer layer of the skin, producing the desquamation that typifies the diseases. Shedding of the outer layer of skin generally reveals normal skin below, but fluid lost in the process can produce severe injury in young children if it is not treated properly.

Toxic Shock Syndrome

Toxic shock syndrome is caused by strains of *S. aureus* that produce the so-called toxic shock syndrome toxin. The disease can be caused by *S. aureus* infection at any site, but it is too often erroneously viewed exclusively as a disease solely of women who use tampons. The disease involves toxaemia and septicaemia, and can be fatal.

Nocosomial Infections

In the 1984 National Nocosomial Infection Surveillance Study ("NNIS") *S. aureus* was the most prevalent agent of surgical wound infections in many hospital services, including medicine. surgery, obstetrics, pediatrics and newborns.

Resistance to drugs of S. aureus strains

Prior to the introduction of penicillin the prognosis for patients seriously infected with *S aureus* was unfavorable Following the introduction of penicillin in the early 1940s even the worst *S. aureus* infections generally could be treated successfully. The emergence of penicillin-resistant strains of *S. aureus* did not take long, however Most strains of *S. aureus* encountered in hospital infections today do not respond to penicillin; although, fortunately, this is not the case for *S aureus* encountered in community infections.

It is well known now that penicillin-resistant strains of *S. aureus* produce a lactamase which converts penicillin to penicillinoic acid, and thereby destroys antibiotic activity. Furthermore, the lactamase gene often is propagated episomally typically on a plasmid, and often is only one of several genes on an episomal element that, together, confer

. . . . good substrate for inactivating lactamases. However the methicillin resistance is as important . . . . along with resistance to many other antibiotics effective against this organism including aminoglycosides. tetracycline. chloramphenicol macrolides and lincosamides. In fact methicillin-resistant strains of *S aureus* generally are multiply drug resistant

The molecular genetics of most types of drug resistance in *S. aureus* has been elucidated (See Lyon *et al.*, *Microbiology Reviews* 51: 88-134 (1987)). Generally, resistance is mediated by plasmids, as noted above regarding penicillin resistance; however, several stable forms of drug resistance have been observed that apparently involve integration of a resistance element into the *S. aureus* genome itself.

Thus far each new antibiotic gives rise to resistance strains, stains emerge that are resistance to multiple drugs and increasingly persistent forms of resistance begin to emerge. Drug resistance of *S. aureus* infections already poses significant treatment difficulties, which are likely to get much worse unless new therapeutic agents are developed.

Molecular Genetics *of Staphylococcus Aureus*

Despite its importance in, among other things, human disease, relatively little is known about the genome of this organism.

Most genetic studies of *S. aureus* have been carried out using the the strain NCTC8325, which contains prophages psi11 psi12 and psi13, and the UV-cured derivative of this strain, 8325-4 (also referred to as RN450), which is free of the prophages.

These studies revealed that the *S. aureus* genome, like that of other *staphylococci*, consists of one circular, covalently closed, double-stranded DNA and a collection of so-called variable accessory genetic elements, such as prophages, plasmids, transposons and the like.

Physical characterization of the genome has not been carried out in any detail. Pattee *et al.* published a low resolution and incomplete genetic and physical map of the chromosome of *S. aureus* strain NCTC 8325. (Pattee *et al.* Genetic and Physical Mapping of Chromosome of *Staphylococcus aureus* NCTC 8325, Chapter 11, pgs. 163-169 in. MOLECULAR BIOLOGY OF THE *STAPHYLOCOCCI,* R.P. Novick, Ed., VCH Publishers, New York, (1990) The genetic map largely was produced by mapping insertions of Tn551 and Tn4001, which, respectively, confer erythromycin and gentamicin resistance, and by analysis of Smal-digested DNA by Pulsed Field Gel Electrophoresis ("PFGE").

The map was of low resolution; even estimating the physical size of the genome was difficult, according to the investigators. The size of the largest Smal chromosome fragment, for instance, was too large for accurate sizing by PFGE. To estimate its size, additional restriction sites had to be introduced into the chromosome using a transposon containing a Smal recognition sequence.

In sum, most physical characteristics and almost all of the genes of *Staphylococcus aureus* are unknown. Among the few genes that have been identified, most have not been physically mapped or characterized in detail. Only a very few genes of this organism have been sequenced. (See, for instance Thornsberry, J. , *Antimicrobial Chemotherapy* 21 Suppl C: 9-16 (1988), current versions of GENBANK and other nucleic acid databases, and references that relate to the genome of *S. aureus* such as those set out elsewhere herein.)

It is clear that the etiology of diseases mediated or exacerbated by *S. aureus* infection involves the programmed expression of *S. aureus* genes, and that characterizing the genes and their patterns of expression would add dramatically to our understanding of the organism and its host interactions. Knowledge of *S. aureus* genes and genomic organization would dramatically improve understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover. characterized genes and genomic fragments of *S. aureus* would provide reagents for, among other things, detecting, characterizing and controlling *S. aureus* infections There is a need therefore to characterize the genome of *S. aureus* and for polynucleotides and sequences of this organism.

The present invention is based on the sequencing of fragments of the *Staphylococcus aureus* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS: 1-5,191.

The present invention provides the nucleotide sequence of several thousand contigs of the *Staphylococcus aureus* genome, which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS 1-5,191.

The present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9%, identical to the nucleotide sequences of SEQ ID NOS:1-5,191.

The nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence which is at least 95%, preferably 99% and most preferably 99.9%, identical to the nucleotide sequence of SEQ ID NOS:1-5,191 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment. the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence

information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Staphylococcus aureus* genome.

Another embodiment of the present invention is directed to fragments, preferably isolated fragments, of the *Staphylococcus aureus* genome having particular structural or functional attributes. Such fragments of the *Staphylococcus aureus* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs," fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression modulating fragments or EMFs," and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in a sample, hereinafter referred to as diagnostic fragments or "DFs."

Each of the ORFs in fragments of the *Staphylococcus aureus* genome disclosed in Tables 1-3, and the EMFs found 5' to the ORFs, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Staphylococcus aureus* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Staphylococcus aureus* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Staphylococcus aureus* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to polypeptides and proteins, preferably isolated polypeptides and proteins, encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention can from cells which have been altered to express them.

The invention further provides polypeptides, preferably isolated polypeptides, comprising *Staphylococcus aureus* epitopes and vaccine compositions comprising such polypeptides. Also provided are methods for vacciniating an individual against *Staphylococcus aureus* infection.

The invention further provides methods of obtaining homologs of the fragments of the *Staphylococcus aureus* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the Dfs or antigens of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, antigens, or one of the DFs of the present invention: and (b) one or more other containers comprising one or more of the following:wash reagents, reagents capable of detecting presence of bound antibodies, antigens or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a)contacting an agent with an isolated protein encoded by one of the ORFs of the present invention: and (b)determining whether the agent binds to said protein.

Staphylococcus aureus researchers and for immediate commercial value for the production of proteins or to control gene expression

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes

has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Staphylococcus aureus* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al., Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences,* 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Staphylococcus aureus* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed by seq_filter to trim portions of the sequences with more than 2% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR") for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with zorf. The ORFs are searched against *S. aureus* sequences from Genbank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al., J. Mol. Biol.* 215: 403-410 (1990)). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3..

The present invention is based on the sequencing of fragments of the *Staphylococcus aureus* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS:1-5,191. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Staphylococcus aureus* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS:1-5,191, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-5,191" refers to any portion of the SEQ ID NOS:1-5,191 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Staphylococcus aureus* open reading frames (ORFs"), expression modulating fragment (EMFs") and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in sample ("DFs"). A non-limiting identification of preferred representative fragments is provided in Tables 1-3.

As discussed in detail below, the information provided in SEQ ID NOS:1-5,191 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Staphylococcus aureus* proteins.

While the presently disclosed sequences of SEQ ID NOS:1-5,191 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-5,191. However, once the present invention is made available (*i.e.,* once the information in SEQ ID NOS:1-5,191 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS:1-5,191 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS:1-5,191 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191.

As discussed elsewhere hererin, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining

libraries and for sequencing are provided below, for instance. A wide variety of *Staphylococcus aureus* strains that can be used to prepare *S aureus* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC").

The nucleotide sequences of the genomes from different strains of *Staphylococcus aureus* differ somewhat. However, the nucleotide sequences of the genomes of all *Staphylococcus aureus* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS:1-5,191. Nearly all will be at least 99% identical and the great majority will be 99 9% identical.

Thus, the present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191, in a form which can be readily used, analyzed and interpreted by the skilled artisan.

Methods for determining whether a nucleotide sequence is at least 95%, at least 99% or at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191 are routine and readily available to the skilled artisan. For example, the well known fasta algorithm described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85: 2444 (1988) can be used to generate the percent identity of nucleotide sequences. The BLASTN program also can be used to generate an identity score of polynucleotides compared to one another.

COMPUTER RELATED EMBODIMENTS

The nucleotide sequences provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS. 1-5,191 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, Òprovided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.*, a nucleotide sequence provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-5,191. Such a manufacture provides a large portion of the *Staphylococcus aureus* genome and parts thereof (*e.g.*, a *Staphylococcus aureus* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *Staphylococcus aureus* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD- ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially- available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS 1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and

system was used to identify open reading frames (ORFs) within the *Staphylococcus aureus* genome which contain homology to ORFs or proteins from both *Staphylococcus aureus* and from other organisms Among the ORFs discussed

herein are protein encoding fragments of the *Staphylococcus aureus* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Staphylococcus aureus* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Staphylococcus aureus* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Staphylococcus aureus* genome. In the present examples, implementing software which implement the BLAST and BLAZE algorithms, described in Altschul *et al., J. Mol. Biol.* 215: 403-410 (1990), was used to identify open reading frames within the *Staphylococcus aureus* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for

accessing and processing the genomic sequence (such as search tools, comparing tools, *etc.*) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to fragments of the *Staphylococcus aureus* genome, preferably to isolated fragments. The fragments of the *Staphylococcus aureus* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Staphylococcus aureus* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-5,191, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generated the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Staphylococcus aureus* DNA can be mechanically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate an *Staphylococcus aureus* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS: 1-5,191. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library of Staphylococcus aureus genomic DNA. Thus, given the availability of SEQ ID NOS:1-5,191, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-5,191 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA.

As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

Tables 1, 2 and 3 list ORFs in the *Staphylococcus aureus* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive or more selective lists.

Table 1 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that are at least 80 amino acids long and over a continuous region of at least 50 bases which are 95% or more identical (by BLAST analysis) to an *S. aureus* nucleotide sequence available through Genbank in November 1996.

Table 2 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through Genbank by September 1996.

Table 3 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through Genbank by September 1996.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the reading frame, taking the first 5' nucleotide of the contig as the start of the +1 frame; the fourth column indicates the first nucleotide of the ORF, counting from the 5' end of the contig strand; and the fifth column indicates the length of each ORF in nucleotides.

In Tables 1 and 2, column six, lists the Reference" for the closest matching sequence available through Genbank. These reference numbers are the databases entry numbers commonly used by those of skill in the art, who will be

Descriptions of the numenclature are available from the National Center for Biotech-

nucleotides of the highest scoring sequence identified by the BLA

In Table 3, the last column, column six, indicates the length of each ORF in amino acid residues.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions

1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.,* possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list per cent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the per cent identity" of the highest scoring segment pair" in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Staphylococcus aureus* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Staphylococcus aureus* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Staphylococcus aureus* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Staphylococcus aureus* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Staphylococcus aureus* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably 99% and most preferably 99.9% identical to SEQ ID NOS:1-5,191, with a sequence from another isolate of the same species.

Furthermore, to accomodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the nucleic acid sequences mentioned above. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment. such as an ORF, in both directions (*i.e.,* sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Staphylococcus aureus* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORFs of the *Staphylococcus aureus* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5' to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particular *Staphylococcus aureus*. Especially preferred in this regard are ORF such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Staphylococcus aureus*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Sta-*

phylococcus aureus, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al., Nucl. Acids Res.* 6 3073 (1979); Cooney *et al., Science* 241: 456 (1988); and Dervan *et al., Science* 251: 1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem.* 56: 560 (1991) and OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION, CRC Press, Boca Raton, FL (1988))

The present invention further provides recombinant constructs comprising one or more fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Staphylococcus aureus* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBluescript SK and KS (+ and -), pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.,* BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.,* an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides

. . . . short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies

. . . . .

. . . . peptide . . . . the skilled . . . . readily employ well known . . . . methods . . . . proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immu-

no-affinity chromatography

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.,* microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.,* yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli,* will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Staphylococcus aureus* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

"Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancers and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.,* MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.,* the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *Staphylococcus aureus, E. coli, B. subtilis, Salmonella typhimurium* and various species within the genera *Pseudomonas, Streptomyces,* and *Staphylococcus.* Others

may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available form Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell* 23: 175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

An additional aspect of the invention includes Staphylococcus aureus polypeptides which are useful as immunodiagnostic antigens and/or immunoprotective vaccines, collectively "immunologically useful polypeptides". Such immunologically useful polypeptides may be selected from the ORFs disclosed herein based on techniques well known in the art and described elsewhere herein. The inventors have used the following criteria to select several immunologically useful polypeptides:

As is known in the art, an amino terminal type I signal sequence directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Such outermembrane polypeptides are expected to be immunologically useful. According to Izard, J. W. et al., Mol. Microbiol. 13, 765-773; (1994), polypeptides containing type I signal sequences contain the following physical attributes: The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus; the central region of the signal sequence must adopt an alpha-helical conformation in a hydrophobic environment; and the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

Also known in the art is the type IV signal sequence which is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory. S.. J. Bacteriol. 174. 7345-7351; 1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, all type IV signal sequences contain a phenylalanine residue at the +1 site relative to the cleavage site.

Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S and Wu. H C Lipoproteins in bacteria. J Bioenerg. Biomembr. 22, 451-471; 1990)

It well known that most anchored proteins found on the surface of gram-positive bacteria possess a highly con

and conductor in schall. D A gram-positive commensal bacteria derive antigens to the mucosal and systemic immunity, ASM News 62 405410 1996) The conserved region is comprised of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins ex-

amined. The amino acid sequence of this region is L-P-X-T-G-X, where X is any amino acid.

Amino acid sequence similarities to proteins of known function by BLAST enables the assignment of putative functions to novel amino acid sequences and allows for the selection of proteins thought to function outside the cell wall. Such proteins are well known in the art and include "lipoprotein", "periplasmic", or "antigen".

An algorithm for selecting antigenic and immunogenic *Staphylococcus aureus* polypeptides including the foregoing criteria was developed by the present inventors. Use of the algorithm by the inventors to select immunologically useful *Staphylococcus aureus* polypeptides resulted in the selection of several ORFs which are predicted to be outermembrane-associated proteins. These proteins are identified in Table 4, below, and shown in the Sequence Listing as SEQ ID NOS:5,192 to 5,255. Thus the amino acid sequence of each of several antigenic *Staphylococcus aureus* polypeptides listed in Table 4 can be determined, for example, by locating the amino acid sequence of the ORF in the Sequence Listing. Likewise the polynucleotide sequence encoding each ORF can be found by locating the corresponding polynucleotide SEQ ID in Tables 1, 2, or 3, and finding the corresponding nucleotide sequence in the sequence listing.

As will be appreciated by those of ordinary skill in the art, although a polypeptide representing an entire ORF may be the closest approximation to a protein found *in vivo,* it is not always technically practical to express a complete ORF *in vitro.* It may be very challenging to express and purify a highly hydrophobic protein by common laboratory methods. As a result, the immunologically useful polypeptides described herein as SEQ ID NOS:5,192-5,255 may have been modified slightly to simplify the production of recombinant protein, and are the preferred embodiments. In general, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, are excluded for enhanced *in vitro* expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus are also excluded. Such truncated polypeptides include for example the mature forms of the polypeptides expected to exist in nature.

Those of ordinary skill in the art can identify soluble portions the polypeptide identified in Table 4, and in the case of truncated polypeptides sequences shown as SEQ ID NOS:5,192-5,255, may obtain the complete predicted amino acid sequence of each polypeptide by translating the corresponding polynucleotides sequences of the corresponding ORF listed in Tables 1,2 and 3 and found in the sequence listing.

Accordingly, polypeptides comprising the complete amino acid of an immunologically useful polypeptide selected from the group of polypeptides encoded by the ORFs identified in Table 4, or an amino acid sequence at least 95% identical thereto, preferably at least 97% identical thereto, and most preferably at least 99% identical thereto form an embodiment of the invention; in addition polypeptides comprising an amino acid sequence selected from the group of amino acid sequences shown in the sequence listing as SEQ ID NOS:5,191-5,255, or an amino acid sequence at least 95% identical thereto, preferably at least 97% identical thereto and most preferably at least 99% identical thereto, form an embodiment of the invention. Polynucleotides encoding the foregoing polypeptides also form part of the present invention.

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention, particularly those epitope-bearing portions (antigenic regions) identified in Table 4. The epitope-bearing portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R. A. (1983) "Antibodies that react with predetermined sites on proteins", Science, 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. See, for instance, Wilson et al., Cell 37:767-778 (1984) at 777.

Antigenic epitope-bearing peptides and polypeptides of the invention preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. Non-limiting examples of antigenic polypeptides or peptides that can be used to generate S. aureus specific antibodies include: a polypeptide comprising peptides shown in Table 4 below. These polypeptide fragments have been determined to bear antigenic epitopes of indicated S. aureus proteins by the analysis of the Jameson-Wolf antigenic index, a representative sample of which is shown in Figure 3.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means. See, e.g., Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides:

specificity of antigen-antibody interaction at the level of individual amino acids. Proc. Natl. Acad. Sci. USA 82: 5131-5135; this "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No 4.631,211 to Houghten et al. (1986). Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., supra; Wilson et al., supra;

5 Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. See, for instance, Geysen et al., supra. Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the

10 epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. et al. (1996) on Per-alkylated Oligopeptide Mixtures discloses linear C1-C7-alkyl peralkylated oligopeptides and sets and libraries of such

15 peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a per-alkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

Table 4 lists immunologically useful polypeptides identified by an algorithm which locates novel *Staphylococcus aureus* outermembrane proteins, as is described above. Also listed are epitopes or "antigenic regions" of each of the

20 identified polypeptides. The antigenic regions, or epitopes, are delineated by two numbers x-y, where x is the number of the first amino acid in the open reading frame included within the epitope and y is the number of the last amino acid in the open reading frame included within the epitope. For example, the first epitope in ORF 168-6 is comprised of amino acids 36 to 45 of SEQ ID NO:5,192, as is described in Table 4. The inventors have identified several epitopes for each of the antigenic polypeptides identified in Table 4. Accordingly, forming part of the present invention are

25 polypeptides comprising an amino acid sequence of one or more antigenic regions identified in Table 4. The invention further provides polynucleotides encoding such polypeptides.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are sub-stantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more

30 substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity be-tween reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Staphylococcus aureus,* of the

35 fragments of the *Staphylococcus aureus* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Staphylococcus aureus* is defined as a homolog of a fragment of the *Staphylococcus aureus* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Staphylococcus aureus* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the

40 sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybrid-ization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which prossess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among

45 especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among those are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-5,191 or from

50 a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS:1-5,191 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have

only a sequence of SEQ ID NOS:1-5,191, one skilled in the art will recognize that by employing high stringency conditions (e.g. annealing at 50-60°C in 6X SSPC and 50% formamide and washing at 50-65°C in 0.5X SSPC) only sequences which are greater than 75% nomologous to the primer will be amplified. By employing lower stringency

conditions (*e.g.,* hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NOS:1-5,191, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-5,191, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.,* hybridizing at 50- 65°C in 5X SSPC and 50% formamide. and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.,* hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacterias which are closely related to *Staphylococcus aureus.*

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Staphylococcus aureus* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., Macmillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESES, Tramper *et al.,* Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function. enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Staphylococcus aureus* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-5,191.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al., Symbiosis* 21: 79 (1986) and Voragen *et al.* in BIOCATALYSTS IN AGRICULTURAL BIOTECHNOLOGY, Whitaker *et al.,* Eds., *American Chemical Society Symposium Series* 389: 93 (1989) .

The metabolism of sugars is an important aspect of the primary metabolism of *Staphylococcus aureus.* Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al., Biotechnology* 6(A), Rhine *et al.,* Eds.. Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al., Biotechnology Letters* 1: 21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical. food, feed and concrete industry, as described, for example, in Bigelis *et al.,* beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.,* Eds.. Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for

quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al., Biochem. et Biophysica. Acta.* 872: 83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, Biotechnology, The Textbook of Industrial Microbiology, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, Starch 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.,* Acid Proteases Structure Function and Biology, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.,* Industrial Enzymes, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.,* Report Industrial Enzymes by 1990, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.,* Philosophical Transactions of the Chiral Society of London 310:227 (1985) and Poserke, Journal of the American Oil Chemist Society 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.,* Recent Advances in the Generation of Chiral Intermediates Using Enzymes, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists:hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination. A variety of commercially important enzymes have previously been isolated from members of *Staphylococcus aureus*. These include Sau3A and Sau96I.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein. Such antibodies can be either monoclonal or polyclonal antibodies, as well fragments of these antibodies, and humanized forms.

The invention further provides antibodies which selectively bind to one of the proteins of the present invention and [illegible] which produce these antibodies. A hybridoma is an immortalized cell line which is capable of secreting a

[illegible] desired antibody are well known [illegible] Campbell [illegible] LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al., J. Immunol. Methods* 35: 1-21 (1980); Kohler and Milstein, *Nature* 256: 495-497 (1975)), the trioma technique, the human B- cell hybridoma technique (Kozbor *et al., Immunology Today*

4: 72 (1983), pgs. 77-96 of Cole *et al.,* in MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss. Inc. (1985)).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with the pseudogene polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or interperitoneal

5 injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection.

The protein which is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but

10 are not limited to coupling the antigen with a heterologous protein (such as globulin or galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells. such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces

15 an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al., Exp. Cell Res.* 175: 109-124 (1988)).

Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, A. M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

20 Techniques described for the production of single chain antibodies (U. S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

The present invention further provides the above-described antibodies in detectably labelled form. Antibodies can

25 be detectably labelled through the use of radioisotopes, affinity labels (such as biotin. avidin, *etc.*), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, *etc.*) fluorescent labels (such as FITC or rhodamine, *etc.*), paramagnetic atoms, *etc.* Procedures for accomplishing such labelling are well-known in the art, for example see Sternberger *et al.,* J. Histochem. Cytochem. 18:315 (1970); Bayer, E. A. *et al.,* Meth. Enzym. 62:308 (1979); Engval, E. *et al.,* Immunol. 109:129 (1972); Goding, J W. J. Immunol. Meth. 13:215 (1976)).

30 The labeled antibodies of the present invention can be used for *in vitro, in vivo,* and in situ assays to identify cells or tissues in which a fragment of the *Staphylococcus aureus* genome is expressed.

The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports

35 are well known in the art (Weir, D. M. *et al.,* "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W. D. *et al.,* Meth. Enzym. 34 Academic Press, N. Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro, in vivo,* and in situ assays as well as for immunoaffinity purification of the proteins of the present invention.

40 **3. Diagnostic Assays and Kits**

The present invention further provides methods to identify the expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using one of the DFs,antigens or antibodies of the present invention.

In detail, such methods comprise incubating a test sample with one or more of the antibodies, or one or more of

45 the DFs, or one or more antigens of the present invention and assaying for binding of the DFs, antigens or antibodies to components within the test sample.

Conditions for incubating a DF, antigen or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the DF or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification

50 or immunological assay formats can readily be adapted to employ the Dfs, antigens or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. *et al.,* Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry; PCT publication WO95/32291, and

55 Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985), all of which are hereby incorporated herein by reference.

The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based

on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed
Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be
adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry
out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers
which comprises:(a) a first container comprising one of the Dfs, antigens or antibodies of the present invention; and
(b) one or more other containers comprising one or more of the following:wash reagents, reagents capable of detecting
presence of a bound DF, antigen or antibody.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such
containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one
to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are
not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one
compartment to another. Such containers will include a container which will accept the test sample, a container which
contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline,
Tris-buffers, *etc.*), and containers which contain the reagents used to detect the bound antibody, antigen or DF.

Types of detection reagents include labelled nucleic acid probes, labelled secondary antibodies, or in the alterna-
tive, if the primary antibody is labelled, the enzymatic, or antibody binding reagents which are capable of reacting with
the labelled antibody. One skilled in the art will readily recognize that the disclosed Dfs, antigens and antibodies of the
present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining
and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the
fragments and the *Staphylococcus aureus* fragment and contigs herein described.

In general, such methods comprise steps of:

(a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated
fragment of the Staphylococcus aureus genome; and
(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives,
or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed
using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected
at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally
selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one
skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the
like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides,
for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's
Guide, W H Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, Biochemistry 28:9230-8 (1989), or pharmaceutical
agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to
control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above,
such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled
artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or
multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by
binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can
be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Such agents and derivatives, Science 20:... Such RNA ...
Neurochem 56 560 (1991) Oligodeoxynucleotides as Antisense inhibitors of Gene Expression, CRC Press, Boca
Raton FL (1988)) Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense
RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated

to be effective in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

5. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or path- ogenicity of *Staphylococcus aureus,* or another related organism, *in vivo* or *in vitro.* As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharma- ceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth or pathogenicity of *Staphylococcus aureus* or a related organism, *in vivo* or *in vitro,*" when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth or path- ogenicity by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of vaccines derived from membrane asso- ciated polypeptides are well known in the art. The inventors have identified particularly preferred immunogenic Sta- phylococcus aureus polypeptides for use as vaccines. Such immunogenic polypeptides are described above and sum- marized in Table 4, below.

As used herein, a "related organism" is a broad term which refers to any organism whose growth or pathogenicity can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient man- ner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or proph- ylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of ad- ministration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half- life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.,* inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeu- tically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can

be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e. g., human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

5

1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, Genomics 2: 231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P_0, that any given base in a sequence of size L, in nucleotides, is not sequenced after
10   a certain amount, n, in nucleotides, of random sequence has been determined can be calculated by the equation $P_0 = e^{-m}$, where m is L/n, the fold coverage." For instance, for a genome of 2.8 Mb, m=1 when 2.8 Mb of sequence has been randomly generated (1X coverage) At that point, $P_0 = e^{-1} = 0.37$. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivilent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage,
15   approximately 37% of a polynucleotide of size L, in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G, is determined by the equation $G = Le^{-m}$, and the average gap size, g, follows the
20   equation, g = L/n. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics 2*: 231 (1988).

2. Random Library Construction

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In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Staphylococcus aureus DNA was prepared by phenol extraction. A mixture containing 600 ug DNA in 3.3 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 30% glycerol was sonicated for 1 min. at 0°C in a Branson
30   Model 450 Sonicator at the lowest energy setting using a 3 mm probe. The sonicated DNA was ethanol precipitated and redissolved in 500 ul TE buffer.

To create blunt-ends, a 100 ul aliquot of the resuspended DNA was digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 ul BAL31 buffer . The digested DNA was phenol-extracted, ethanol-precipitated, redissolved in 100 ul TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting
35   temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size was excised from the gel, and the LGT agarose was melted and the resulting solution was extracted with phenol to separate the agarose from the DNA. DNA was ethanol precipitated and redissolved in 20 ul of TE buffer for ligation to vector.

A two-step ligation procedure was used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 ul) contained 2 ug of DNA fragments, 2 ug pUC18 DNA (Pharmacia) cut with SmaI
40   and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and was incubated at 14°C for 4 hr. The ligation mixture then was phenol extracted and ethanol precipitated, and the precipitated DNA was dissolved in 20 ul TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder were visualized by ethidium bromide-staining and UV illumination and identified by size as insert (i), vector (v), v+i, v+2i, v+3i, *etc.* The portion of the gel containing v+i DNA was excised and the v+i DNA was recovered and resuspended
45   into 20 ul TE. The v+i DNA then was blunt-ended by T4 polymerase treatment for 5 min. at 37° C in a reaction mixture (50 ul) containing the v+i linears, 500 uM each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+i linears were dissolved in 20 ul TE. The final ligation to produce circles was carried out in a 50 ul reaction containing 5 ul of v+i linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture was
50   stored at -20°C.

This two-stage procedure resulted in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, E.coli host cells deficient in all recombination and restriction functions (A. Greener, Strategies 3 (1):5 (1990)) were used to prevent rearrangements,
55   deletions, and loss of clones by restriction. Furthermore, transformed cells were plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating was carried out as follows. A 100 ul aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) was thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 ul aliquot of 1.42 M beta-

mercaptoethanol was added to the aliquot of cells to a final concentration of 25 mM. Cells were incubated on ice for 10 min. A 1 ul aliquot of the final ligation was added to the cells and incubated on ice for 30 min. The cells were heat pulsed for 30 sec. at 42° C and placed back on ice for 2 min. The outgrowth period in liquid culture was eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture was plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml MgCl$_2$ (1 M), and 1 ml MgSO$_4$/100 ml SOB agar. The 15 ml top layer was poured just prior to plating. Our titer was approximately 100 colonies/10 ul aliquot of transformation.

All colonies were picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products would be deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates were prepared using an alkaline lysis method developed in collaboration with 5Prime → 3Prime Inc. (Boulder, CO). Plasmid preparation was performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Average template concentration was determined by running 25% of the samples on an agarose gel. DNA concentrations were not adjusted.

Templates were also prepared from a *Staphylococcus aureus* lambda genomic library. An unamplified library was constructed in Lambda DASH II vector (Stratagene). *Staphylococcus aureus* DNA (> 100 kb) was partially digested in a reaction mixture (200 ul) containing 50 ug DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23 C. The digested DNA was phenol-extracted and centrifuges over a 10-40% sucroce gradient. Fractions containing genomic DNA of 15-25 kb were recovered by precipitation . One ul of fragments was used with 1 ul of DASHII vector (Stratagene) in the recommended ligation reaction. One ul of the ligation mixture was used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract Phage were plated directly without amplification from the packaging mixture (after dilution with 500 ul of recommended SM buffer and chloroform treatment). Yield was about 2.5x10^9 pfu/ul.

An amplified library was prepared from the primary packaging mixture according to the manufactureer's protocol. The amplified library is stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1x10^9 pfu/ml.

Mini-liquid lysates (0.1ul) are prepared from randomly selected plaques and template is prepared by long range PCR. Samples are PCR amplified using modified T3 and T7 primers, and Elongase Supermix (LTI).

Sequencing reactions are carried out on plasmid templates using a combination of two workstations (BIOMEK 1000 and Hamilton Microlab 2200) and the Perkin-Elmer 9600 thermocycler with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers. Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. Modified T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are on a combination of AB 373 DNA Sequencers and ABI 377 DNA sequencers. All of the dye terminator sequencing reactions are analyzed using the 2X 9 hour module on the AB 377. Dye primer reactions are analyzed on a combination of ABI 373 and ABI 377 DNA sequencers. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

4. Protocol for Automated Cycle Sequencing

The sequencing was carried out using Hamilton Microstation 2200, Perkin Elmer 9600 thermocyclers, ABI 373 and ABI 377 Automated DNA Sequencers. The Hamilton combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates were combined in the wells of a 96-well thermocycling plate and transferred to the Perkin Elmer 9600 thermocycler. Thirty consecutive cycles of linear amplification (i.e.., one primer synthesis) steps were performed including denaturation, annealing of primer and template, and extension. ...

... labelled ... The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer was labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 or 377 DNA Sequencer for electrophoresis, detection, and base-

calling. ABI currently supplies premixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR-generated templates with both dye-primers and dye- terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions were loaded per ABI 373 Sequencer each day and 96 samples can be loaded on an ABI 377 per day. Electrophoresis was run overnight (ABI 373) or for 2 1/2 hours (ABI 377) following the manufacturer's protocols. Following electrophoresis and fluorescence detection, the ABI 373 or ABI 377 performs automatic lane tracking and base-calling. The lane-tracking was confirmed visually. Each sequence electropherogram (or fluorescence lane trace) was inspected visually and assessed for quality. Trailing sequences of low quality were removed and the sequence itself was loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence was removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 or ABI 377 were around 400 bp and depend mostly on the quality of the template used for the sequencing reaction.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow whereever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi- user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was enployed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 10^4 fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology* 164: 765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repet-itive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of align-ments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain ranged of base pairs (definable for each clone based on the known clone size range for a given library).

3. Identifying Genes

The predicted coding regions of the *Staphylococcus aureus* genome were initially defined with the program zorf. which finds ORFs of a minimum length. The predicted coding region sequences were used in searches against a database of all *Staphylococcus aureus* nucleotide sequences from GenBank (release 92.0), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and and com-pared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs of at least 80 amino acids that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases.

ORFs of at least 120 amino acids that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Staphylococcus aureus* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E coli*, or can by chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., Nature 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., Meth. Enzymol. 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than other and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, J. Clin. Endocrinol. Metab. 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in Handbook of Experimental Immunology, Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0. 1 to 0. 2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described. for example, by Fisher, D., Chap. 42 in Manual of Clinical Immunology, second edition, Rose and Friedman, eds., Amer Soc. For Microbiology. Washington. D C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples, they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, they are useful in various animal models of Staphylococcal disease known to those of skill in the art as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunothereapeutic reagent

. . . . *Staphylococcus aureus* genome . . . . be used in accordance with the present invention to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases. and more preferably at least 18 bases in length When selecting a primer sequence it is preferred that the primer pairs have approximately the same G/C ratio so that melting temperatures are approxi-

mately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

4. Gene expression from DNA Sequences Corresponding to ORFs

5   A fragment of the *Staphylococcus aureus* genome provided in Tables 1-3 is introduced into an expression vector using conventional technology. Techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate

10   proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U. S. Patent No. 5,082,767, incorporated herein by this reference.
       The following is provided as one exemplary method to generate polypeptide(s) from cloned ORFs of the *Staphylococcus aureus* genome fragment. Bacterial ORFs generally lack a poly A addition signal. The addition signal sequence can be added to the construct by, for example, splicing out the poly A addition sequence from pSG5 (Stratagene) using

15   BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene of Moloney Murine Leukemia Virus. The positions of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *Staphylococcus aureus* DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *Staphylococcus*

20   *aureus* DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *Staphylococcus aureus* DNA 3' primer, taking care to ensure that the *Staphylococcus aureus* DNA is positioned such that its followed with the poly A addition sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A addition sequence and digested BglII.

25   The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface. Since it may be necessary to purify and locate the transfected product,

30   synthetic 15-mer peptides synthesized from the predicted *Staphylococcus aureus* DNA sequence are injected into mice to generate antibody to the polypeptide encoded by the *Staphylococcus aureus* DNA.
       Alternativly and if antibody production is not possible, the *Staphylococcus aureus* DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as, for example, a globin fusion. Antibody to the globin moiety then is used to purify the chimeric protein. Corresponding protease cleavage sites are engineered between the

35   globin moiety and the polypeptide encoded by the *Staphylococcus aureus* DNA so that the latter may be freed from the formed by simple protease digestion. One useful expression vector for generating globin chimerics is pSG5 (Stratagene). This vector encodes a rabbit globin. Intron II of the rabbit globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of molecular biology. Standard methods are published in methods

40   texts such as Davis *et al.*, cited elsewhere herein, and many of the methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides of the invention also may be produced using *in vitro* translation systems such as *in vitro* ExpressTM Translation Kit (Stratagene).
       While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true

45   scope of the invention.
       All patents, patent applications and publications referred to above are hereby incorporated by reference.

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S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name ( )	percent ident	HSP nt length	ORF nt length
1	1	1419	757	emb|X17301|SAHD	S.aureus DNA for hld gene and for part of agr gene	100	663	663
1	2	3273	2452	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	99	809	822
1	5	6418	5651	dbj|D14711|STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	223	768
5	1	807	439	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	81	216	369
5	4	5031	3571	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	95	424	1461
10	1	86	904	gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	98	715	819
16	5	5302	6246	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	94	251	945
16	6	6249	7091	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	99	843	843
16	7	7084	7584	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	99	342	501
20	1	995	549	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	443	447
20	2	1011	841	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	91	137	171
20	3	2010	1798	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	110	213
20	4	5300	3825	gb|M76714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	948	1476
20	5	4788	4282	gb|M76714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	309	507
26	1	2	145	gb|U41072|	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	100	126	144
26	2	84	557	gb|U41072|	Staphylococcur aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	99	430	474
26	3	763	3531	emb|X74219|SAIL	S.aureus gene for isoleucyl-tRNA synthetase	99	2769	2769
29	3	1261	4392	gb|U66665|	Staphylococcus aureus DNA fragment with class II promoter activity	100	117	3132
31	14	14977	13463	emb|X73889|SAP1	S.aureus genes P1 and P2	99	1351	1515
31	15	14241	13855	emb|X73889|SAP1	S.aureus genes P1 and P2	98	258	387
38	17	14284	13112	gb|M12715|	S.aureus geh gene encoding lipase (glycerol ester hydrolase)	100	372	1173
38	19	13434	15518	gb|M27715|	S.aureus geh gene encoding lipase (glycerol ester hydrolase)	100	2085	2085

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
46	2	419	1727	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8D, cap8C, cap8D, cap8E, cap8F, cap8G, cap8J, cap8K, cap8H, cap8N, cap8O, cap8P, complete cds	98	1209	1209
46	3	1720	2295	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	576	576
46	4	2259	3182	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	924	924
46	5	3173	4498	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8J, cap8K, cap8M, cap8N, cap... cap8O, cap8P, complete cds	98	1283	1326
46	6	4536	5720	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8J, cap8K, cap8M, cap8N, cap8O, cap8P, complete cds	98	1185	1185
46	7	6455	6120	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8H, cap8I, cap8J, cap8K, cap8M, cap8N, cap8O, cap8P, complete cds	99	278	336
48	1	2	955	gb|L25893|	Staphylococcus aureus recA gene, complete cds	99	954	954
50	3	4465	2924	emb|X85029|SAAH	S.aureus AhpC gene	100	88	1542
50	4	4108	3515	emb|X85029|SAAH	S.aureus AhpC gene	98	540	594
54	3	5074	3392	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	1668	1683
54	4	4865	4122	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	99	720	744
54	5	5056	4562	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	463	495
54	6	11386	8300	gb|J04151|	S.aureus (fibronectin-binding protein (fnbA) mRNA, complete cds	100	3087	3087
58	3	1743	2819	emb|XA7104|SADN	S.aureus mdr, pbp4 and tagD genes (SG511-55 isolate)	89	68	1077
58	4	2858	3280	emb|X91786|SAPB	S.aureus abcA, pbp4, and tagD genes	99	423	423
58	5	6005	4701	emb|X91786|SAPB	S.aureus abcA, pbp4, and tagD genes	99	1305	1305
58	6	5677	5378	gb|J29478|	Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, partial cds	100	300	300
58	7	5086	6840	emb|X91786|SAPB	S.aureus abcA, pbp4, and tagD genes	99	1755	1755
72	1	888	445	gb|Y21854|	S.aureus agr gene encoding an accessory gene regulator protein, complete cds	100	444	444
72	2	2457	1453	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	99	671	1005

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
82	1	357	3917	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	2396	3561
82	2	4027	7677	emb|X89233|SARP	S.aureus DNA for rpoC gene	99	3171	3651
82	3	7745	8068	gb|U20869|	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	320	324
82	4	8103	8579	gb|U20869|	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	477	477
82	5	8618	8821	gb|U20869|	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	154	204
84	1	18	191	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	164	174
84	2	189	893	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	94	705	705
84	3	887	1660	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	774	774
84	4	1584	3503	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1920	1920
84	5	3394	4521	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	1128	1128
84	6	4519	5643	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	1125	1125
96	2	1245	1896	emb|Z18852|SACF	S.aureus gene for clumping factor	83	660	2652
97	2	625	882	gb|U41072|	Staphylococcus aureus isoleucyl-tRNA synthetase (IleS) gene, partial cds	97	68	258
111	1	3	452	gb|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	100	450	450
111	2	526	1041	gt|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	99	516	516
117	2	1278	1958	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	61	681

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
118	4	3787	4254	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; HSP35; ORF35, complete cds	99	467	468
130	4	2597	3640	emb|X13290|SATN	Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003	78	956	1044
130	5	3813	4265	emb|Z16422|SADI	S.aureus dfrB gene for dihydrofolate reductase	98	416	453
130	6	4309	5172	emb|Z16422|SADI	S.aureus dfrB gene for dihydrofolate reductase	98	607	864
136	4	5296	6207	emb|X71437|SAGY	S.aureus genes gyrB, gyrA and recF (partial)	97	838	912
136	5	11680	8987	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	2694	2694
136	6	12886	10940	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	99	1947	1947
136	7	12592	11765	gb|S77055|	recF cluster: dnaA=replisome assembly protein...gyrB=DNA gyrase beta subunit [Staphylococcus aureus. YB886. Genomic. 5 genes. 3573 nt]	99	822	828
143	3	4171	2867	gb|U36379|	Staphylococcus aureus S-adenosylmethionine synthetase gene, complete cds	99	1305	1305
143	4	3100	4281	gb|L42943|	Staphylococcus aureus (clone KIN50) phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	100	1170	1182
143	5	4254	4718	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	100	449	465
143	9	6977	7261	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	75	285
143	10	9464	8361	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	1104	1104
143	11	11232	9748	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	1485	1485
143	12	10739	10320	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	332	420
152	5	2454	3437	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	305	984
152	6	3511	4820	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	1308	1308
152	7	4818	6230	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	1413	1413
153	1	387	1526	gb|S77055|	recF cluster: dnaA=replisome assembly protein...gyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	99	1140	1140
153	2	1877	2152	gb|S77055|	recF cluster: dnaA=replisome assembly protein...gyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	100	276	276

TABLE 1

S. aureus - Coding regions containing known sequences

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
153	3	2143	2283	gb|S77055|	recF cluster: dnaA~replisome assembly protein...gyrB~DNA gyrase beta subunit (Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt)	99	113	147
154	10	10792	9314	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	91	154	1479
154	11	9935	9615	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	229	321
154	12	9943	10167	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	94	123	225
154	13	10089	11501	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	1326	1413
159	2	2195	1212	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	71	984
161	3	2596	2270	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	92	203	327
162	1	1406	705	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	100	702	702
163	4	1263	1772	gb|U19770|	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	127	510
164	7	4774	9117	dbj|D86727|D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	99	1470	6344
168	7	7448	6447	gb|U21636|	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	100	1002	1002
168	8	9538	7961	gb|U21636|	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	99	1158	1578
173	6	9240	7801	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	1440	1440
173	7	11252	9522	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	1731	1731
173	8	8285	8704	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	420	420
173	9	10168	9839	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	330	330
173	10	11815	10829	emb|X14827|SALA	Staphylococcus aureus lacC and lacD genes	100	987	987
173	11	12721	11774	emb|X14827|SALA	Staphylococcus aureus lacC and lacD genes	100	948	948
173	12	12838	12305	gb|M64724|	S.aureus tagatose 6-phosphate isomerase gene, complete cds	100	534	534
173	13	13243	12773 ,	gb|M32103|	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	471	471
173	14	14633	13866	gb|M32103|	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	768	768

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
178	1	2	655	gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	115	654
178	2	2201	1482	gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	720	720
178	3	2361	1909	gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	453	453
17A	4	1551	1853	gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	303	303
17A	5	3541	2777	gb|L42945|	Staphylococcus aureus lytS and lytR genes, complete cds	99	765	765
178	6	3294	3025	gb|L42945|	Staphylococcus aureus lytS and lytR genes, complete cds	99	270	270
181	1	1114	590	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	99	499	525
182	1	3	341	emb|X61307|SASP	Staphylococcus aureus spa gene for protein A	98	277	339
182	2	690	2312	gb|J01786|	S.aureus spa gene coding for protein A, complete csd	97	1332	1623
182	3	5861	4251	emb|X61307|SASP	Staphylococcus aureus spa gene for protein A	99	119	1611
185	1	3	824	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	90	132	822
191	3	841	2760	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	99	1920	1920
191	4	2967	3143	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	99	177	177
191	5	5768	4566	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	99	250	1203
196	1	1741	872	gb|L36472|	Staphylococcus aureus lysyl-tRNA sythetase gene, complete cds, transfer RNA (tRNA) genes, 5S ribosomal RNA (5S rRNA) gene, 16S ribosomal RNA (16S rRNA) gene, 23S ribosomal RNA (23S rRNA) gene	99	870	870
19A	3	1688	2011	emb|X93205|SAPT	S.aureus ptsH and ptsI genes	99	324	324
19A	4	2005	2110	emb|X93205|SAPT	S.aureus ptsH and ptsI genes	97	304	306
202	1	163	1305	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	99	1143	1143
202	2	1303	2175	emb|X73889|SAP1	S.aureus genes P1 and P2	94	444	873
210	1	3114	1558	dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	1552	1557
210	2	2939	2232	gb|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF1, autolysin (atl) genes, complete cds	99	684	708
214	11	7429	7770	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	96	157	342

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
216	1	198	1118	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidine	88	265	921
219	2	1810	1073	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	100	60	738
219	3	2979	2035	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	99	945	945
219	4	4359	3196	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	99	1164	1164
219	5	7044	5176	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	98	1869	1869
219	6	6557	5883	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	99	675	675
219	7	6580	6114	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	98	466	466
221	8	10816	10034	gb|L19298|	Staphylococcus aureus phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	91	67	783
223	1	2855	1506	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	102	1350
234	1	2	1357	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	100	176	1356
234	2	1694	2485	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	100	792	792
234	3	2648	3148	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	99	501	501
234	4	3120	4604	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	99	1305	1485
236	6	3826	5322	gb|U48826|	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds	96	648	1497
248	1	2	403	emb|X62288|SAPE	S.aureus DNA for penicillin-binding protein 2	100	103	402
248	2	388	852	gb|L25426|	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete	99	465	465
253	2	1539	1093	gb|U46541|	Staphylococcus aureus sarA gene, complete cds	96	447	447
254	2	150	1835	gb|U57060|	Staphylococcus aureus scdA gene, complete cds	94	142	1686
254	3	1973	2728	gb|U57060|	Staphylococcus aureus scdA gene, complete cds	99	756	756
260	1	2	1900	gb|M90693|	Staphylococcus aureus glycerol ester hydrolase (lip) gene, complete cds	99	1213	1899
265	1	1	942	dbj|D21131|STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	99	941	942

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
265	2	688	476	dbj|D21131|STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	99	211	213
265	3	2418	1765	dbj|D21131|STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	98	69	654
266	1	2	1018	dbj|D14711|STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	743	1017
282	1	1	525	gb|S72488|	hemB-porphobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]	100	110	525
282	2	516	1502	gb|S72488|	hemB-porphobilinogen synthase [Staphylococcus aureus, SA1959, Genomic, 1087 nt]	100	952	987
284	1	3	170	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	98	84	168
284	2	282	1034	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	712	753
284	3	1028	2026	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	99	979	999
284	4	1990	2202	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	98	187	213
289	1	1536	1991	gb|M32470|	S.aureus Sau3AI-restriction-enzyme and Sau3AI-modification-enzyme genes, complete cds	99	338	456
303	1	2	868	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	99	867	867
303	2	1409	2343	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	100	975	975
303	3	2367	3161	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	99	793	795
305	1	2707	1355	dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	1343	1353
311	1	2628	1315	gb|L42945|	Staphylococcus aureus lytS and lytR genes, complete cds	98	1314	1314
312	6	7019	7870	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	74	351	852
323	1	1998	1003	gb|U31175|	Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase (ddh) gene, complete cds	98	996	996
326	1	1	237	emb|Y00356|SASP	Staphylococcus aureus V8 serine protease gene	100	108	237
338	1	687	388	emb|X64189|SALE	S.aureus leuF-PB3 gene for F component of leucocidin R	98	259	300
338	2	1824	1048	emb|X64189|SALE	S.aureus leuF-PB3 gene for F component of leucocidin R	97	137	741

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
342	2	579	1754	gb|U06462|	Staphylococcus aureus SA4 FtsZ (ftsZ) gene, complete cds	100	1176	1176
344	2	517	1248	emb|V01281|SANU	S.aureus mRNA for nuclease	98	732	732
349	1	457	230	gb|M20393|	S.aureus bacteriophage phi-11 attachment site (attB)	96	172	228
353	1	1016	516	gb|M43994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	187	501
353	2	1582	1046	gb|M43994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	99	537	537
356	1	3	674	gb|U20503|	Staphylococcus aureus MHC class II analog gene, complete cds	75	671	672
361	1	1	903	gb|L19298|	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	98	747	903
361	2	1103	1507	gb|L19298|	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	97	68	405
373	1	3	1148	emb|X62288|SAPE	S.aureus DNA for penicillin-binding protein 2	99	1146	1146
389	3	1904	1248	emb|X62282|SATS	S.aureus target site DNA for IS431 insertion	97	349	657
400	1	1	540	eml|X61716|SANL	S.aureus hlb gene encoding sphingomyelinase	99	389	540
400	2	1693	1187	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	99	178	507
408	1	1810	1049	gb|S76213|	asp23-alkaline shock protein 23 (methicillin resistant) [Staphylococcus aureus, 912, Genomic, 1360 nt]	99	163	762
414	1	2	217	gb|41499|	Staphylococcus aureus ORF1, partial cds, ORF2, CRF1, autolysin (atl) genes, complete cds	100	216	216
418	2	854	639	dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	100	188	216
421	2	1262	2509	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	1248	1248
422	1	2	325	gb|K02985|	S.aureus (strain RN450) transposon Tn554 insertion site	96	200	324
427	1	865	434	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	432	432
427	2	1829	1122	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	151	708
435	1	2	808	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes.complete cds	100	556	807
435	2	832	999	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes.complete cds	100	134	168
436	1	1341	685	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	97	657	657

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
436	2?	2403	1657	|emb|X17648|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	100	294	747
442	1	347	1300	|emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidin	84	204	954
445	2	1906	2178	|gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	98	187	273
447	1	167	1078	|gb|U19770|	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	100	51'	912
447	2	1176	1784	|gb|U19770|	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	597	609
454	3	7309	4319	|emb|Z18852|SACF	S.aureus gene for clumping factor	75	653	2991
472	4	7896	5479	|gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	2418	2418
472	5	8120	6792	|gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	1328	1329
475	2	566	889	|emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	100	76	324
481	4	1922	1560	|emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	250	363
481	5	1244	1534	|emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	224	291
487	2	1388	1188	|gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	98	72	201
489	1	2737	1370	|gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	99	1368	1368
503	2	1135	653	|gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	108	483
511	3	1613	2242	|gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	323	630
511	4	3122	2700	|gb|S76213|	asp23-alkaline shock protein 23 (methicillin resistant) [Staphylococcus aureus, 912, Genomic, 1360 nt]	96	423	421
520	2	758	1297	|emb|X72014|SAFI	S.aureus fib gene for fibrinogen-binding protein	99	540	540
520	3	1436	1801	|emb|X72013|SAFI	S.aureus fib gene for fibrinogen-binding protein	99	221	366
526	1	2150	1092	|dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	641	1059

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
528	2	58	963	gb|L19100|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	260	906
528	3	1098	2870	gb|L19100|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	866	1773
530	1	3	434	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	99	432	432
530	2	1211	2395	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genus, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	91	1185	1185
530	3	2409	2801	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	88	181	393
530	4	2690	3484	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORFJ, complete cds	100	75	795
530	5	3482	4792	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORFJ, complete cds	99	905	1311
530	6	4790	5380	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORFJ, complete cds	100	196	591
539	1	3	338	emb|X76490|SAGL	S.aureus (bb270) glnA and glnR genes	99	336	336
539	2	336	527	emb|X76490|SAGL	S.aureus (bb270) glnA and glnR genes	100	189	192
554	1	727	365	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	100	54	363
554	2	2175	1252	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	918	924
554	3	1574	1374	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	96	122	201
584	2	1019	705	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	99	306	315
587	3	1475	4288	emb|Z18852|SACF	S.aureus gene for clumping factor	98	2588	2814
598	1	3881	1953	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	99	1873	1929

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
605	1	2	745	dbj|DA6240|DB62	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	98	338	744
609	1	1628	816	emb|X76490|SAGL	S. aureus (bb270) glnA and glnR genes	100	495	813
614	1	1280	642	gb|M32103|	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	99	639	639
626	1	2508	1255	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	225,	1253
626	2	3315	2284	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	99	838	1032
629	1	1999	1001	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	99	990	999
629	2	1407	1195	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	98	194	211
631	2	5126	3228	emb|Z18852|SACF	S.aureus gene for clumping factor	82	489	1899
632	1	3	551	emb|Z30588|SAST	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	99	549	549
632	2	529	1323	emb|Z30588|SAST	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	99	795	795
651	1	1909	1070	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	478	840
657	2	1800	1105	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	456	696
662	1	908	456	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	100	369	453
662	2	230	475	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	100	246	246
662	3	746	1399	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	99	653	654
6A2	1	956	480	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	100	116	477
6A5	1	1182	592	gb|U65000|	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	98	534	591
6A5	2	1716	1153	gb|U65000|	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	96	564	564
697	1	3	527	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	100	195	525
697	2	485	784	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	97	280	300

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
710	1	15	503	|dbj|D86240|DR62	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	99	217	489
733	1	26	205	|gb|M80252|	Staphylococcus aureus norA199 gene (which mediates active efflux of fluoroquinolones), complete cds	97	140	180
741	1	1716	1197	|dbj|D83951|STAL	Staphylococcus aureus DNA for LukM component, LukF-PV like component. complete cds	81	522	540
752	1	4	636	|emb|Y00356|SASP	Staphylococcus aureus V8 serine protease gene	99	618	636
752	2	588	956	|emb|Y00356|SASP	Staphylococcus aureus V8 serine protease gene	99	340	369
756	1	1138	709	|emb|X01645|SATO	Staphylococcus aureus (Wood 46) gene for alpha-toxin	98	567	600
777	1	1582	950	|emb|Z49245|SA42	S.aureus partial sod gene for superoxide dismutase	99	429	633
780	1	1111	557	|gb|U20503|	Staphylococcus aureus MHC class-II analog gene, complete cds	86	550	555
784	1	23	687	|gb|U63529|	Staphylococcus aureus novel antigen gene. complete cds	99	568	615
797	1	182	544	|dbj|D14711|STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	363	363
798	1	532	302	|emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	95	196	231
823	1	3	467	|gb|S77055|	recF cluster: dnaA-replisome assembly protein...gyrB-DNA gyrase beta subunit (Staphylococcus aureus, YB886. Genomic, 5 genes, 3573 nt)	99	156	465
848	1	348	175	|gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	174	174
848	2	476	318	|gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	100	131	159
866	1	792	397	|emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	395	396
883	1	1	285	|dbj|D90119|STAN	S. aureus norA gene	99	131	285
884	1	606	334	|emb|X52543|SAAG	S.aureus agrA, agrB, agrB and hld genes	98	265	273
884	2	716	522	|emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	100	195	195
912	2	517	681	|emb|Z30588|SAST	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	99	163	165
917	1	2	265	|gb|M64724|	S.aureus tagatose 6-phosphate isomerase gene, complete cds	99	247	264
917	2	238	396	|gb|M64724|	S.aureus tagatose 6-phosphate isomerase gene, complete cds	95	147	159
918	1	2426	1215	|emt|X93205|SAPT	S.aureus ptsH and ptsI genes	99	1212	1212

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
967	1	1	411	dbj|D90119|STAN	S. aureus norA gene	97	395	411
991	1	672	337	emb|X52543|SAAG	S. aureus agrA, agrB and hld genes	99	336	336
1000	1	1117	845	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	78	190	273
1001	1	498	265	dbj|D86240|D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	99	234	234
1010	1	1	285	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	99	224	285
1046	1	656	330	emb|X72700|SAPV	S. aureus genes for S and F components of Panton-Valentine leucocidin	85	205	327
1060	1	480	286	emb|X58434|SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	180	195
1073	1	1176	589	gb|K02985|	S. aureus (strain RN450) transposon Tn554 insertion site	100	131	588
1079	1	3	230	dbj|D86240|D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	99	228	228
1079	2	218	484	dbj|D86240|D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	267	267
1079	7	460	645	dbj|D86240|D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	186	186
1092	1	289	146	emb|X58434|SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	124	144
1143	1	1	243	gb|M63171|	S. aureus sigma factor (plaC) gene, complete cds	99	243	243
1157	1	2	136	emb|Z48003|SADN	S. aureus gene for DNA polymerase III	97	127	135
1189	1	720	361	gb|S74011|	norA=NorA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	99	360	360
1190	1	2	283	gb|M21854|	S. aureus agr gene encoding an accessory gene regulator protein, complete cds	100	282	282
1190	2	1127	888	emb|X52543|SAAG	S. aureus agrA, agrB and hld genes	100	240	240
1225	1	2	163	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	97	124	162
1243	1	2	529	dbj|D86240|D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	99	495	528
1244	1	1	210	gb|S74011|	norA=NorA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	100	210	210
1301	1	41	472	emb|X76490|SAGL	S. aureus (bb270) glnA and glnR genes	99	299	432

TABLE 1

S. aureus - coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
1315	1	18	326	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta chains	98	277	309
1519	1	2	175	db|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	98	139	174
1663	1	1346	675	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	98	672	672
1797	1	644	324	gb|U73374|	Staphylococcus aureus type 8 capsule genes, capHA, capB, capBC, capBD, capBE, capBF, capBG, capBI, capBJ, capBK, capBL, capBM, capBN, capBO, capBP, complete cds	99	321	321
1857	1	1	192	gb|M90536|	Staphylococcus aureus alpha-hemolysin gene, 3' end	98	192	192
1923	1	2	181	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	100	180	180
1957	1	2	346	gb|U60589|	Staphylococcus aureus novel antigen gene, complete cds	99	345	345
1988	1	1	402	db|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	402	402
2100	1	414	208	gb|H63177|	S.aureus sigma factor (plaC) gene, complete cds	99	207	207
2109	1	1	402	gb|U66664|	Staphylococcus aureus DNA (fragment with class II promoter activity	95	131	402
2537	1	304	156	emb|X176AA|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	99	153	153
2891	1	2	400	gb|L25426|	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds	99	399	399
2950	1	778	398	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	100	358	381
2971	1	3	398	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	97	272	396
2978	1	618	328	gb|J31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	98	250	291
2985	1	832	464	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	98	347	369
3006	1	2170	1784	gb|U11779|	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RNNV30 16S-23S rRNA spacer region	87	82	387
3008	1	474	238	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	88	178	237
3008	2	451	281	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	97	120	171

TABLE 1

S aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP length	ORF nt length
3011	1	793	398	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	93	72	396
3019	1	2	235	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	234	234
3023	1	81	233	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	87	100	153
3029	1	90	287	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	135	198
3039	1	18	164	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	97	135	147
3039	2	70	327	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	77	183	258
3056	1	3	215	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	213	213
3059	1	1	261	dbj|D30690|STAN	Staphylococcus aureus genes for ORF17; HSP20; HSP40; HSP70; ORF35, complete cds	98	234	261
3073	1	27	284	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	229	258
3074	1	2	397	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	96	250	396
3088	1	3	239	dbj|D86727|D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	95	215	237
3097	1	444	244	emb|Z18003|SAEH	S.aureus gene for DNA polymerase III	97	160	201
3102	1	307	155	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	142	153
3121	1	568	398	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	100	88	171
3125	1	463	233	emb|X89233|SARP	S.aureus DNA for rpoC gene	98	192	231
3133	1	2	175	emb|Z18852|SACF	S.aureus gene for clumping factor	96	154	174
3160	1	420	211	dbj|D10489|STAC	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	89	197	210
3176	1	1	378	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	96	91	378
3192	1	420	211	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	72	210
3210	1	3	143	gb|U76714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	96	141	141

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3232	3	2105	1282	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	71	257	825
3538	1	?	394	emb|X49231|SARP	S. aureus DNA for rpoC gene	99	396	393
3543	1	392	634	gb|L11530|	Staphylococcus aureus transfer RNA sequence with two rRNAs	99	102	243
3555	1	617	320	emb|Z18852|SACF	S. aureus gene for clumping factor	99	307	318
3559	1	3	182	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	100	141	180
3559	2	95	313	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	98	174	219
3563	1	278	141	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	100	79	138
3563	2	527	363	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	98	162	165
3566	1	3	422	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	98	175	420
3588	1	2	262	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	253	261
3591	1	1	350	gb|U03479|	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	145	348
3600	1	758	381	emb|Z18852|SACF	S. aureus gene for clumping factor	72	346	378
3602	1	788	396	emb|Z18852|SACF	S. aureus gene for clumping factor	98	319	393
3656	1	1013	528	emb|Z18852|SACF	S. aureus gene for clumping factor	84	403	486
3682	1	3	236	emb|X64172|SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	231	234
3682	2	224	415	emb|X64172|SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	112	192
3693	1	758	423	emb|X62992|SAFN	S. aureus fnbB gene for fibronectin binding protein B	100	229	336
3702	1	593	354	gb|F11530|	Staphylococcus aureus transfer RNA sequence with two rRNAs	94	81	240
3725	1	924	463	emb|Z18852|SACF	S. aureus gene for clumping factor	71	367	462
3761	1	809	450	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	85	333	160
3767	1	1	402	emb|X64172|SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	387	402

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3775	1	2	286	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	227	285
3786	1	456	229	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	204	228
3786	2	542	366	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	95	123	177
3798	1	3	251	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	99	249	249
3811	1	793	398	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	98	396	196
3819	1	184	402	emb|X68425|SA23	S.aureus gene for 23S rRNA	99	161	219
3844	1	932	468	gb|U38826|	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds	87	204	465
3845	1	1	381	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	94	356	381
3856	1	798	400	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	76	192	399
3859	1	1049	573	emb|Z18852|SACF	S.aureus gene for clumping factor	85	347	477
3871	1	650	327	gb|M76714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	299	324
3876	1	2	253	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	217	252
3877	1	572	288	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	209	285
3878	1	1	237	emb|X58434|SAPD	S.aureus pdhA, pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	96	155	237
3888	1	3	173	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	98	171	171
3893	1	1	183	emb|X89233|SARP	S.aureus DNA for rpoC gene	100	170	183
3893	2	181	357	emb|X89233|SARP	S.aureus DNA for rpoC gene	98	79	177
3894	1	3	485	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	450	483
3895	1	836	420	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	95	411	417
3905	1	48	239	gb|L05004|	staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	159	192
3905	2	188	400	gb|L05004|	staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	97	88	213

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3910	1	3	359	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	278	357
3915	1	1	330	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	175	330
3964	1	691	347	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	100	295	345
4007	1	199	390	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	98	163,	192
4036	1	3	371	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	99	339	369
4046	1	692	348	emb|Z18852|SACF	S.aureus gene for clumping factor	87	221	345
4060	1	1	375	emb|Z18852|SACF	S.aureus gene for clumping factor	96	271	375
4061	1	960	432	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	99	429	429
4062	1	606	304	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	198	303
4085	1	58	402	gb|U11786|	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRUV42 16S-23S rRNA spacer region	98	127	345
4088	1	2	301	gb|L43094|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	227	300
4093	1	2	277	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	276	276
4097	1	1	402	emb|Z18852|SACF	S.aureus gene for clumping factor	74	307	402
4116	1	22	402	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroA) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	98	157	341
4125	1	240	401	gb|U73374|	Staphylococcus aureus type 8 capsule genes, capA, capB, capAC, capAD, capAE, capAF, capAG, capBH, capBI, capBJ, capBK, capBL, capBM, capBO, capBP, complete cds	100	86	162
4149	1	35	247	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	200	213
4151	1	629	366	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	87	150	264
4154	1	754	398	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	297	357
4179	1	1	294	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	240	294

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
4203	1	1	255	emb|X89233|SARP	S.aureus DNA for rpoC gene	99	239	255
4206	1	1	303	emb|Z18852|SACF	S.aureus gene for clumping factor	100	216	303
4206	2	195	344	emb|Z18852|SACF	S.aureus gene for clumping factor	95	65	150
4208	1	108	314	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	89	76	207
4216	1	656	330	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	326	327
4226	1	594	298	gb|L11530|	Staphylococcus aureus transfer RNA sequence with two rRNAs	97	132	297
4260	1	216	183	gb|U11784|	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV40 16S-23S rRNA spacer region	83	141	168
4272	1	355	179	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	100	164	177
4276	1	4	177	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	99	150	174
4277	1	1	270	eml|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	265	270
42R2	1	691	377	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	282	315
4291	1	379	191	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	183	189
4295	1	3	329	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	94	144	327
4313	1	435	280	gb|L11530|	Staphylococcus aureus transfer RNA sequence with two rRNAs	100	94	156
4315	1	3	185	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	158	183
4315	2	101	310	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	75	210
4327	1	1	294	gb|L43008|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	98	294	294
4360	1	603	319	gb|U02910|	Staphylococcus aureus ATCC 25923 16S rRNA gene, partial sequence	100	116	285
4364	1	3	146	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	95	140	144
43R8	1	167	310	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	73	119	144

TABLE 1

S. aureus - Coding regions containing known sequences

contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
4401	1	2	313	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	97	243	312
4421	1	36	281	dbj|D12572|STA2	Staphylococcus aureus rrnA gene for 23S ribosomal IUIA	100	112	246
4426	1	3	293	emb|Z18852|SACF	S.aureus gene for clumping factor	85	185	291
4428	1	493	248	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	139	246
4462	1	2	271	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	270	270
4466	1	1	240	emb|Z18852|SACF	S.aureus gene for clumping factor	99	231	240
4469	1	1	312	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	265	312
4485	1	3	261	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	98	259	261
4492	1	74	400	gb|M86227|	Staphylococcus aureus DNA gyrase B subunit (gyrB) RecF homologue (recF) and DNA gyrase A subunit (gyrA) gene, complete cds	85	104	327
4497	1	515	269	emb|Z18852|SACF	S.aureus gene for clumping factor	99	213	267
4529	1	2	172	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	151	171
4547	1	1	300	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	157	300
4554	1	318	160	emb|Z18852|SACF	S.aureus gene for clumping factor	84	126	159
4565	1	9	227	emb|Z18852|SACF	S.aureus gene for clumping factor	84	213	213
4569	1	79	222	emb|Z18852|SACF	S.aureus gene for clumping factor	98	127	144
460R	1	22	216	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acecyltransferase and dihydrolipoamide dehydrogenase	92	168	195
4614	1	464	234	emb|Z18852|SACF	S.aureus gene for clumping factor	86	169	231
4623	1	105	302	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	152	198
4632	1	18	206	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	183	189
4646	1	1	222	emb|Z18852|SACF	S.aureus gene for clumping factor	84	100	222
46R7	1	2	166	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	98	156	165

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
4695	1	313	158	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	155	156
4703	1	1	153	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	103	153

TABLE 1

S. aureus   Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
20	6	5089	4679	gi|511839	ORF1 [Staphylococcus bacteriophage phi 11]	100	100	411
149	3	2032	1577	pir|849703|B497	int gene activator RinA - bacteriophage phi 11	100	100	456
149	5	2209	1912	gi|166161	Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11]	100	100	198
349	2	558	409	gi|166159	integrase (int) [Staphylococcus bacteriophage phi 11]	100	100	150
39A	1	1172	707	gi|166159	integrase (int) [Staphylococcus bacteriophage phi 11]	100	99	666
39A	2	783	1001	gi|455128	excisionase (xis) [Staphylococcus bacteriophage phi 11]	100	100	219
502	4	1914	1744	gi|1204912	H. influenzae predicted coding region HI0660 [Haemophilus influenzae]	100	71	171
R49	1	2	262	gi|1373002	polyprotein [Bean comon mosaic virus]	100	46	261
1149	1	277	140	gi|143359	protein synthesis initiation factor 2 (infB) [Bacillus subtilis] gi|49319 IF2 gene product [Bacillus subtilis]	100	82	138
2880	1	21	108	gi|862933	protein kinase C inhibitor-I [Homo sapiens]	100	98	288
30A5	1	428	216	gi|1354211	PET112-like protein [Bacillus subtilis]	100	100	213
4168	2	571	398	gi|1354211	PET112-like protein [Bacillus subtilis]	100	100	174
331	1	2	247	gi|426473	nusG gene product [Staphylococcus carnosus]	98	95	246
207	2	1272	1463	gi|460259	enolase [Bacillus subtilis]	97	90	192
311	2	395	850	gi|581618	1.11 protein [Staphylococcus carnosus]	97	43	456
366	1	39	215	gi|66161	Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11]	97	95	177
680	3	718	936	gi|426473	nusG gene product [Staphylococcus carnosus]	97	97	219
157A	1	284	144	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	97	79	141
157	1	321	518	gi|1022726	unknown [Staphylococcus haemolyticus]	96	88	198
205	33	16470	16147	gi|1165302	S10 [Bacillus subtilis]	96	91	324
3919	1	48	401	gi|971784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	96	81	354
4133	1	830	417	gi|1022726	unknown [Staphylococcus haemolyticus]	96	84	414
4168	1	708	355	gi|1354211	PET112-like protein [Bacillus subtilis]	96	95	354
4207	1	112	157	gi|602031	similar to trimethylamine DH [Mycoplasma capricolum] pir|S49950|S49950 probable trimethylamine dehydrogenase (EC .5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	96	86	156

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4227	2	152	331	gi|871784	(Clp-like ATP-dependent protease binding subunit [Bos taurus]	96	81	180
4416	1	570	286	gi|1022726	unknown [Staphylococcus haemolyticus]	96	84	285
22	1	858	430	gi|511070	UreG [Staphylococcus xylosus]	95	88	429
22	7	4162	4036	gi|581787	urease gamma subunit [Staphylococcus xylosus]	95	79	327
82	6	8794	9114	pir|JG0008|JG00	ribosomal protein S7 - Bacillus stearothermophilus	95	83	321
154	9	9280	7838	gi|1354211	PET112-like protein [Bacillus subtilis]	95	92	1443
186	3	2798	2055	gi|1514656	serine O-acetyltransferase [Staphylococcus xylosus]	95	87	744
205	3	4406	4014	gi|142462	ribosomal protein S11 [Bacillus subtilis]	95	85	393
205	7	5017	4793	gi|142459	initiation factor 1 [Bacillus subtilis]	95	84	225
205	21	11365	10991	gi|1044974	ribosomal protein L14 [Bacillus subtilis]	95	93	375
259	5	7288	6644	sp|P47995|YSEA_	HYPOTHETICAL PROTEIN IN SECA 5'REGION (ORF1) (FRAGMENT).	95	85	645
302	3	795	1097	gi|40186	homologous to E.coli ribosomal protein L27 [Bacillus subtilis] i|143592 L27 ribosomal protein [Bacillus subtilis] tr|C21895|C21895 ribosomal protein L27 - Bacillus subtilis p|PU5657|RL27_BACSU 50S RIBOSOMAL PROTEIN L27 (BL30) (BL24). i|40175 L24 gene prod	95	89	303
310	1	579	1523	gi|1177684	chorismate mutase [Staphylococcus xylosus]	95	92	945
414	1	2	163	pir|C48396|C483	ribosomal protein L34 - Bacillus stearothermophilus	95	90	162
4185	2	125	277	gi|1276841	glutamate synthase (GOGAT) [Porphyra purpurea]	95	86	153
22	2	1028	723	gi|511069	UreF [Staphylococcus xylosus]	94	91	306
22	5	5046	3310	gi|410516	urease alpha subunit [Staphylococcus xylosus]	94	85	1737
60	4	815	1372	gi|666116	glucose kinase [Staphylococcus xylosus]	94	87	558
205	18	10012	9536	gi|1044978	ribosomal protein S8 [Bacillus subtilis]	94	78	477
326	4	3378	2542	gi|557492	dihydroxynapthoic acid (DHNA) synthetase [Bacillus subtilis] gi|143186 dihydroxynapthoic acid (DHNA) synthetase [Bacillus subtilis]	94	85	837
414	3	737	955	gi|467386	thiophen and furan oxidation [Bacillus subtilis]	94	77	219
426	3	2260	1823	gi|1263908	putative [Staphylococcus epidermidis]	94	87	438
534	1	2	355	gi|633650	enzyme II(mannitol) [Staphylococcus carnosus]	94	84	354
1017	1	2	229	gi|149435	putative [Lactococcus lactis]	94	71	228
1098	1	310	184	g:|411952	lpa-28d gene product [Bacillus subtilis]	94	50	147

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3232	1	610	316	gi|1022725	unknown [Staphylococcus haemolyticus]	94	84	315
42	5	2089	2259	pir|B48396|B483	[ribosomal protein L3] - Bacillus stearothermophilus	93	81	171
101	2	1745	1383	gi|155345	arsenic efflux pump protein (Plasmid pSX267)	93	82	363
205	24	12227	11865	sp|P14577|RL16_	50S RIBOSOMAL PROTEIN L16.	93	83	363
259	4	8291	5673	gi|499335	secA protein [Staphylococcus carnosus]	93	85	2619
275	1	2226	1114	gi|631650	enzyme II(mannitol) [Staphylococcus carnosus]	93	86	1113
444	6	6207	5773	gi|1022726	unknown [Staphylococcus haemolyticus]	93	81	435
491	1	152	622	gi|46912	ribosomal protein L13 [Staphylococcus carnosus]	93	88	471
607	6	1674	2033	gi|1022726	unknown [Staphylococcus haemolyticus]	93	83	360
653	1	973	488	gi|580890	translation initiation factor IF3 (AA 1-172) [Bacillus stearothermophilus]	93	77	486
1864	1	3	194	gi|306553	ribosomal protein small subunit [Homo sapiens]	93	93	192
2997	1	28	300	gi|143390	carbamyl phosphate synthetase [Bacillus subtilis]	93	82	273
3232	2	907	596	gi|1022725	unknown [Staphylococcus haemolyticus]	93	84	312
3761	2	794	621	gi|1022725	unknown [Staphylococcus haemolyticus]	93	88	174
16	1	3	374	gi|142781	putative cytoplasmic protein; putative [Bacillus subtilis] sp|P37954|UVRR_BACSU EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN) FRAGMENT).	92	83	372
11	7	5915	6124	gi|1136430	KIAA0185 protein [Homo sapiens]	92	46	210
56	19	26483	27391	gi|467401	unknown [Bacillus subtilis]	92	80	909
69	6	5882	6110	gi|530200	trophoblastin [Ovis aries]	92	53	249
145	3	2568	2038	gi|1022725	unknown [Staphylococcus haemolyticus]	92	80	531
171	3	2760	2362	gi|517475	D-amino acid transaminase [Staphylococcus haemolyticus]	92	86	399
205	12	7495	6962	gi|49189	secY gene product [Staphylococcus carnosus]	92	85	534
205	19	10812	10255	gi|1044976	ribosomal protein L5 [Bacillus subtilis]	92	82	558
219	1	710	357	gi|1303812	YqeV [Bacillus subtilis]	92	88	354
344	3	1575	1805	gi|1405474	CspC protein [Bacillus cereus]	92	85	231
699	1	20	361	gi|413999	lpa-75d gene product [Bacillus subtilis]	92	81	342
1243	1	2	160	pir|A45434|A454	[ribosomal protein L19 - Bacillus stearothermophilus	92	84	159

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1958	1	524	264	gi|407908	EfIscr (Staphylococcus xylosus)	92	80	261
357R	2	718	386	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	92	78	333
3585	1	644	324	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	92	81	321
1640	1	4	402	gi|1022726	unknown [Staphylococcus haemolyticus]	92	81	399
4362	1	14	178	gi|450688	hadM gene of Ecoprrl gene product (Escherichia coli) pir|S38437|S38437 hadM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	92	78	165
4446	1	358	182	gi|1022725	unknown [Staphylococcus haemolyticus]	92	82	177
4549	1	462	232	gi|1022726	unknown [Staphylococcus haemolyticus]	92	80	231
4626	1	3	224	gi|1022725	unknown [Staphylococcus haemolyticus]	92	84	222
2	4	3980	4531	gi|535349	CodW [Bacillus subtilis]	91	74	552
28	1	2	1126	gi|1001376	hypothetical protein (Synechocystis sp.)	91	78	1125
60	5	1354	1701	gi|1226043	orf2 downstream of glucose kinase [Staphylococcus xylosus]	91	80	348
101	1	1989	1036	gi|150728	arsenic efflux pump protein (Plasmid pI258)	91	80	954
187	2	412	1194	gi|142559	ATP synthase alpha subunit [Bacillus megaterium]	91	79	783
205	22	11579	11298	gi|40149	S17 protein (AA 1-87) [Bacillus subtilis]	91	83	282
206	7	8184	10262	gi|1072418	glcA gene product [Staphylococcus carnosus]	91	83	2079
306	2	3885	2326	gi|143012	GMP synthetase [Bacillus subtilis]	91	78	1560
106	3	5319	3826	gi|467399	IMP dehydrogenase [Bacillus subtilis]	91	79	1494
310	3	2194	3207	gi|1177685	ccpA gene product [Staphylococcus xylosus]	91	81	1014
343	4	2974	3150	gi|949974	sucrose repressor [Staphylococcus xylosus]	91	82	177
480	3	1606	3042	gi|433991	ATP synthase subunit beta [Bacillus subtilis]	91	85	1437
536	3	2026	1280	gi|143366	adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	91	79	747
552	1	1064	615	gi|297874	fructose-bisphosphate aldolase [Staphylococcus carnosus] pir|A49943|A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TM300)	91	79	450
637	1	1	1536	gi|143597	CTP synthetase [Bacillus subtilis]	91	79	1536
859	1	21	359	gi|385178	unknown [Bacillus subtilis]	91	66	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1327	1	333	530	gi|496558	orfX (Bacillus subtilis)	91	71	192
2515	1	466	275	gi|511070	UreG (Staphylococcus xylosus)	91	85	192
2594	1	2	202	gi|146824	beta-cystathionase (Escherichia coli)	91	75	201
3764	1	847	425	gi|1022725	unknown (Staphylococcus haemolyticus)	91	78	423
4011	1	127	495	gi|1022726	unknown (Staphylococcus haemolyticus)	91	75	369
4227	1	1	177	gi|296464	ATPase (Lactococcus lactis)	91	66	177
42	3	815	1033	gi|520401	catalase (Haemophilus influenzae)	90	86	219
51	8	3717	4607	gi|580899	OppF gene product (Bacillus subtilis)	90	74	891
129	3	5317	4001	gi|1146206	glutamate dehydrogenase (Bacillus subtilis)	90	76	1317
164	17	16628	16933	sp|P05766|RS15_	30S RIBOSOMAL PROTEIN S15 (BS18)	90	74	306
171	5	2983	2819	gi|517475	D-amino acid transaminase (Staphylococcus haemolyticus)	90	78	165
205	4	4497	3550	gi|142463	RNA polymerase alpha-core-subunit (Bacillus subtilis)	90	76	948
205	6	4748	4410	gi|104989	ribosomal protein S13 (Bacillus subtilis)	90	73	339
205	10	7165	6404	gi|49189	secY gene product (Staphylococcus carnosus)	90	81	762
205	11	6645	6472	gi|49189	secY gene product (Staphylococcus carnosus)	90	78	174
205	27	13692	13345	gi|7H6157	Ribosomal Protein S19 (Bacillus subtilis)	90	79	348
205	31	15858	15496	gi|1165303	L3 (Bacillus subtilis)	90	79	363
260	5	7023	5773	gi|1161380	IceA (Staphylococcus epidermidis)	90	78	1251
299	6	3178	3947	gi|467440	'phosphoribosylpyrophosphate synthetase (Bacillus subtilis) gi|40218 PRPP synthetase (AA 1-317) [Bacillus subtilis]	90	78	570
320	2	1025	1717	gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) (Bacillus aldolyticus)	90	75	693
330	4	1581	1769	gi|986963	beta-tubulin (Sporidiobolus pararoseus)	90	80	189
369	1	954	523	pir|S14762|S347	L-serine dehydratase beta chain - Clostridium sp.	90	77	432
557	1	)	188	gi|1511589	M. jannaschii predicted coding region MJ1624 (Methanococcus jannaschii)	90	54	186
663	2	657	1200*	gi|143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis] pir|JT0481|YWDS tryptophan-tRNA ligase (EC 6.1.1.2) - Bacillus subtilis	90	71	534
717	1	1	261	gi|143065	hubat (Bacillus stearothermophilus)	90	79	261
745	4	1359	865	g4|1205433	H. influenzae predicted coding region HI1190 (Haemophilus influenzae)	90	81	195

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1007	1	386	565	gi|143366	adenylosuccinate lyase (PUR-8) (Bacillus subtilis) pir[C29326]WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis	90	77	180
1054	1	579	331	gi|1033122	ORF_f729 [Escherichia coli]	90	50	249
1156	1	117	707	gi|1477776	ClpP [Bacillus subtilis]	90	80	591
1180	1	408	205	gi|1377831	unknown [Bacillus subtilis]	90	74	204
1253	1	1	462	gi|40046	phosphoglucose isomerase A (AA 1-449) (Bacillus stearothermophilus) ir[S15936]NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	90	75	462
2951	1	3	269	gi|144816	formyltetrahydrofolate synthetase (FTHFS) (tcg start codon) (EC 3.4.3) [Moorella thermoacetica]	90	76	267
3140	1	327	166	gi|1070014	protein-dependent [Bacillus subtilis]	90	52	162
4594	1	3	231	gi|87184	Clp-like ATP-dependent protease binding subunit (Bos taurus)	90	76	231
87	1	1028	1750	gi|467327	unknown [Bacillus subtilis]	89	75	723
112	1	2	505	gi|153741	ATP-binding protein [Streptococcus mutans]	89	77	504
118	1	120	398	gi|1303804	YqeQ [Bacillus subtilis]	89	75	279
128	4	3545	3757	gi|460257	triose phosphate isomerase (Bacillus subtilis)	89	84	213
164	12	11667	12755	gi|139954	IF2 (aa 1-741) [Bacillus stearothermophilus]	89	80	1089
205	13	7875	7405	ni|216338	ORF for L15 ribosomal protein [Bacillus subtilis]	89	76	471
205	32	16152	15823	gi|1165303	L3 [Bacillus subtilis]	89	80	330
270	3	2407	2207	pir|C41902|C419	arsenate reductase (EC 1.-.-.-) - Staphylococcus xylosus plasmid pSX267	89	81	201
395	2	157	672	gi|520574	glutamate racemase (Staphylococcus haemolyticus)	89	80	516
494	1	3	839	gi|396259	protease [Staphylococcus epidermidis]	89	77	837
510	1	1	444	gi|40046	phosphoglucose isomerase A (AA 1-449) (Bacillus stearothermophilus) ir[S15936]NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	89	74	444
615	1	2124	1210	gi|1103812	YqeV [Bacillus subtilis]	89	74	915
841	1	18	341	gi|1165303	L3 [Bacillus subtilis]	89	80	324
1111	1	352	813	gi|47146	thermonuclease [Staphylococcus intermedius]	89	70	462
1875	1	2	256	gi|1205108	ATP-dependent protease binding subunit (Haemophilus influenzae)	89	82	255
2963	1	11	367	gi|467458	cell division protein [Bacillus subtilis]	89	83	357

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3020	1	90	362	gi|1239988	hypothetical protein [Bacillus subtilis]	89	66	273
3565	1	2	400	gi|1256635	dihydroxy-acid dehydratase [Bacillus subtilis]	89	75	399
3586	1	105	314	gi|580832	ATP synthase subunit gamma [Bacillus subtilis]	89	82	210
3629	1	794	399	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	89	78	396
3688	1	2	400	gi|1146206	glutamate dehydrogenase [Bacillus subtilis]	89	75	399
3699	1	794	399	gi|1139950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	89	75	396
4016	1	42A	216	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	89	71	213
4177	1	471	101	gi|149426	putative [Lactococcus lactis]	89	76	171
4416	1	601	302	gi|1022725	unknown [Staphylococcus haemolyticus]	89	80	300
4635	1	320	162	gi|1022725	unknown [Staphylococcus haemolyticus]	89	73	159
2	2	1330	2676	gi|520754	putative [Bacillus subtilis]	88	76	1347
42	2	468	848	sp|P42321|CATA_	CATALASE (EC 1.11.1.6)	88	76	381
53	5	6389	4722	gi|474177	alpha-D-1,4-glucosidase [Staphylococcus xylosus]	88	80	1668
56	16	18018	18617	gi|467411	recombination protein [Bacillus subtilis]	88	77	600
60	3	376	843	gi|666116	glucose kinase [Staphylococcus xylosus]	88	77	468
70	2	1583	1245	gi|44095	replication initiator protein [Listeria monocytogenes]	88	74	339
82	8	11514	12719	pir|A60661|A606	translation elongation factor Tu - Bacillus subtilis	88	79	1206
103	7	4179	4191	gi|167181	serine/threonine kinase receptor [Brassica napus]	88	77	213
114	8	7732	8232	gi|1022726	unknown [Staphylococcus haemolyticus]	88	72	501
118	2	308	2011	gi|1303804	YqeQ [Bacillus subtilis]	88	77	1704
141	3	657	1136	gi|1405446	transketolase [Bacillus subtilis]	88	72	480
148	7	5871	6116	gi|1118002	dihydropteroate synthase [Staphylococcus haemolyticus]	88	78	246
165	3	1428	2231	gi|40053	phenylalanyl-tRNA synthetase alpha subunit [Bacillus subtilis] tr|S11730|YFBSA phenylalanine--tRNA ligase (EC 6.1.1.20) alpha ein - Bacillus subtilis	88	80	804
205	28	15027	14185	gi|1165306	L2 [Bacillus subtilis]	88	82	843
225	1	1569	898	gi|1301840	Yqfs [Bacillus subtilis]	88	78	672
235	1	2	1975	gi|452309	valyl-tRNA synthetase [Bacillus subtilis]	88	76	1974

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
339	3	2060	1566	gi|1118002	dihydropteroate synthase (Staphylococcus haemolyticus)	88	73	495
443	4	4325	2928	gi|558559	pyrimidine nucleoside phosphorylase (Bacillus subtilis)	88	73	1398
532	1	3	419	gi|143797	valyl-tRNA synthetase (Bacillus stearothermophilus) sp|P19931|SYV_BACST VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--TRNA LIGASE) (VALRS)	88	78	417
534	3	2504	2968	gi|153049	mannitol-specific enzyme-III [Staphylococcus carnosus] pir|JQ0088|JQ0088 phosphotransferase system enzyme II (EC .7.1.69), mannitol-specific factor III - Staphylococcus carnosus sp|P17876|PTMA_STACA PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT EIIA-MTL) (	88	82	465
705	2	584	399	gi|710018	nitrite reductase (nirB) [Bacillus subtilis]	88	70	186
1000	2	1824	1309	gi|1022726	unknown [Staphylococcus haemolyticus]	88	78	516
1299	1	587	324	gi|401786	phosphomannomutase [Mycoplasma pirum]	88	55	264
1341	2	170	400	gi|39963	ribosomal protein L20 (AA 1-119) [Bacillus stearothermophilus] lr|S05348|R5BS20 ribosomal protein L20 - Bacillus serothermophilus	88	82	231
1386	1	41	214	pir|B47154|B471	signal recognition particle 54K chain homolog Fth - Bacillus subtilis	88	71	174
1386	2	183	533	pir|B47154|B471	signal recognition particle 54K chain homolog Fth - Bacillus subtilis	88	73	351
2949	1	704	399	gi|535350	CodX [Bacillus subtilis]	88	73	306
2984	1	5	169	gi|218277	o-acetylserine(thiol) lyase [Spinacia oleracea]	88	70	165
3015	1	1	138	gi|491083	dihydroxyacetone kinase [Citrobacter freundii]	88	67	138
3089	1	3	152	gi|606055	ORF_f746 [Escherichia coli]	88	88	150
3917	1	817	410	gi|143378	pyruvate decarboxylase (E-1) beta subunit (Bacillus subtilis) gi|1377836 pyruvate decarboxylase E-1 beta subunit (Bacillus ubtilis)	88	77	408
4199	1	680	342	gi|1405454	aconitase [Bacillus subtilis]	88	82	339
4201	1	734	369	gi|515938	glutamate synthase (ferredoxin) [Synechocystis sp.] pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	88	84	366
4274	1	1	336	gi|515938	glutamate synthase (ferredoxin) [Synechocystis sp.] pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	88	84	336
4308	1	794	399	gi|1146206	glutamate dehydrogenase [Bacillus subtilis]	88	71	396
2	5	4570	6000	gi|535350	CodX [Bacillus subtilis]	87	70	1431
52	8	6781	6482	gi|1064791	function unknown [Bacillus subtilis]	87	66	300

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
73	3	1584	2480	gi|142992	glycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir|B45868|B45868 glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp|P18157|GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK).	87	72	897
98	12	8813	9100	gi|467433	unknown [Bacillus subtilis]	87	62	288
124	4	4265	2988	gi|556886	serine hydroxymethyltransferase [Bacillus subtilis] pir|S49363|S49363 serine hydroxymethyltransferase - Bacillus ubtilis	87	77	1278
124	6	4457	4012	gi|556883	unknown [Bacillus subtilis]	87	66	426
148	5	3741	4559	gi|467460	unknown [Bacillus subtilis]	87	70	819
164	13	12710	13810	gi|39954	IF2 (aa 1-741) [Bacillus stearothermophilus]	87	72	1101
177	2	1104	2126	gi|467385	unknown [Bacillus subtilis]	87	78	1023
199	1	1982	1158	gi|143527	iron-sulfur protein [Bacillus subtilis]	87	77	825
199	2	4717	2933	pir|A27763|A277	succinate dehydrogenase (EC 1.3.99.1) (flavoprotein - Bacillus subtilis	87	80	1785
205	23	11782	11543	gi|1044972	ribosomal protein L29 [Bacillus subtilis]	87	78	240
205	25	13275	12607	gi|1165309	S3 [Bacillus subtilis]	87	75	669
222	1	2033	1107	gi|177249	rec213 gene product [Bacillus subtilis]	87	70	927
236	3	1635	1333	gi|146198	ferredoxin [Bacillus subtilis]	87	80	303
246	5	2585	2292	gi|467373	ribosomal protein S18 [Bacillus subtilis]	87	77	294
260	2	4189	3422	gi|1161182	icaC [Staphylococcus epidermidis]	87	72	768
320	3	1696	2391	gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aidolyticus]	87	80	696
380	4	1165	1383	gi|142570	ATP synthase c subunit [Bacillus firmus]	87	80	219
414	4	900	1073	gi|467386	thiophen and furan oxidation [Bacillus subtilis]	87	77	174
425	2	1003	794	gi|1046166	pilin repressor [Mycoplasma genitalium]	87	69	210
448	1	1255	722	gi|405134	acetate kinase [Bacillus subtilis]	87	75	534
480	1	1	711	gi|142559	ATP synthase alpha subunit [Bacillus megaterium]	87	79	711
481	1	2	352	sp|Q06797|RL1_B	50S RIBOSOMAL PROTEIN L1 (BL1).	87	72	351
677	2	359	955	gi|460911	fructose-bisphosphate aldolase [Bacillus subtilis]	87	78	597
677	3	934	1284	gi|460911	fructose-bisphosphate aldolase [Bacillus subtilis]	87	78	351
876	1	3	452	gi|1146247	asparaginyl-tRNA synthetase [Bacillus subtilis]	87	79	450

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1376	1	426	214	gi|1065555	F46H6.4 gene product [Caenorhabditis elegans]	87	75	213
2206	1	3	374	gi|215098	excisionase [Bacteriophage L54a]	87	72	372
2938	1	3	290	gi|508979	GTP-binding protein [Bacillus subtilis]	87	69	288
3081	2	126	308	gi|467199	IMP dehydrogenase [Bacillus subtilis]	87	72	183
3515	1	3	401	gi|1405454	aconitase [Bacillus subtilis]	87	80	399
4238	1	547	275	gi|b03769	HutU protein, urocanase [Bacillus subtilis]	87	73	273
4	8	10427	8736	gi|603769	HutU protein, urocanase [Bacillus subtilis]	86	72	1692
22	6	4190	3738	gi|410515	urease beta subunit [Staphylococcus xylosus]	86	73	453
54	2	2480	1572	gi|289287	UDP-glucose pyrophosphorylase [Bacillus subtilis]	86	70	909
124	3	2336	1713	gi|556887	uracil phosphoribosyltransferase [Bacillus subtilis] pir|S49364|S49364 uracil phosphoribosyltransferase - Bacillus subtilis	86	74	624
148	3	1349	3448	gi|467458	cell division protein [Bacillus subtilis]	86	75	2100
148	4	3638	3859	gi|467460	unknown [Bacillus subtilis]	86	73	222
152	3	1340	2086	gi|1377835	pyruvate decarboxylase E-1 alpha subunit (Bacillus subtilis)	86	75	747
164	18	17347	19467	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	86	72	2121
180	2	554	1159	gi|143467	ribosomal protein S4 [Bacillus subtilis]	86	80	606
205	3	2966	2592	gi|142464	ribosomal protein L17 [Bacillus subtilis]	86	77	375
205	26	13364	12990	gi|40107	ribosomal protein L22 [Bacillus stearothermophilus] ir|S10612|S10612 ribosomal protein L22 - Bacillus earothermophilus	86	75	375
246	7	3463	3140	gi|467375	ribosomal protein S6 [Bacillus subtilis]	86	70	324
299	3	1196	1540	gi|39656	spoVG gene product [Bacillus megaterium]	86	70	345
299	7	3884	4345	gi|467440	phosphoribosylpyrophosphate synthetase [Bacillus subtilis] gi|40218 PRPP synthetase (AA 1-317) [Bacillus subtilis]	86	78	462
304	5	2170	2523	gi|666983	putative ATP binding subunit [Bacillus subtilis]	86	65	354
310	2	1487	1678	gi|1177684	chorismate mutase [Staphylococcus xylosus]	86	71	192
337	5	2086	3405	gi|487434	isocitrate dehydrogenase [Bacillus subtilis]	86	78	1320
339	2	1489	1109	gi|1118003	dihydroneopterin aldolase [Staphylococcus haemolyticus]	86	77	381
358	2	2124	3440	gi|1146219	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative [Bacillus subtilis]	86	73	1317

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
404	2	1015	2058	gi|1303817	YqfA [Bacillus subtilis]	86	78	1044
581	2	661	452	gi|40056	phoP gene product [Bacillus subtilis]	86	71	210
642	2	338	1075	gi|1176399	EpiF [Staphylococcus epidermidis]	86	72	738
770	1	622	347	gi|143328	phoP protein [put.]; putative [Bacillus subtilis]	86	69	276
865	1	1777	890	gi|1146247	asparaginyl-tRNA synthetase [Bacillus subtilis]	85	7?	888
868	2	963	1133	gi|1002911	[transmembrane protein [Saccharomyces cerevisiae]	86	69	171
904	1	1	162	gi|1303912	YqhW [Bacillus subtilis]	86	72	162
989	1	35	433	gi|1303993	YqkL [Bacillus subtilis]	85	76	399
1212	1	296	150	gi|141014	ipa-90d gene product [Bacillus subtilis]	86	70	147
1323	1	2	148	gi|40041	pyruvate dehydrogenase (lipoamide) [Bacillus stearothermophilus] ir|S10798|DEBSPF pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) pha chain - Bacillus stearothermophilus	86	75	147
3085	2	540	310	gi|1354211	PET112-like protein [Bacillus subtilis]	86	86	231
1867	1	1	228	gi|296464	ATPase [Lactococcus lactis]	86	63	228
4487	1	476	240	gi|1022726	unknown [Staphylococcus haemolyticus]	86	73	237
4583	1	372	187	gi|1022725	unknown [Staphylococcus haemolyticus]	86	79	186
25	5	4287	5039	gi|1502421	3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis]	85	64	753
56	21	130627	129395	gi|1408507	pyrimidine nucleoside transport protein [Bacillus subtilis]	85	69	1233
68	2	332	1192	gi|467376	unknown [Bacillus subtilis]	85	74	861
73	2	880	1707	gi|142992	glycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir|B45868|B45868 glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp|P18157|GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK).	85	72	828
106	4	1505	3490	gi|143766	(thrSv) (EC 6.1.1.3) [Bacillus subtilis]	85	74	1986
128	2	1153	2202	gi|311924	glyceraldehyda-3-phosphate dehydrogenase [Clostridium pasteurianum] pir|S14254|S14254 glyceraldehyde-3-phosphate dehydrogenase (EC .2.1.12) - Clostridium pasteurianum	85	75	1050
129	4	6466	5252	gi|1064807	ORNITHINE AMINOTRANSFERASE [Bacillus subtilis]	85	73	1215
138	6	3475	5673	gi|1072419	glcB gene product [Staphylococcus carnosus]	85	74	2199
189	1	2	169	gi|467385	unknown [Bacillus subtilis]	85	65	168

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
205	15	8624	8106	gi|1044981	ribosomal protein S5 (Bacillus subtilis)	85	75	519
205	20	10928	10596	pir|A02819|R5BS	ribosomal protein L24 - Bacillus stearothermophilus	85	72	333
220	6	6490	6101	gi|48980	secA gene product (Bacillus subtilis)	85	66	390
231	4	4877	3159	gi|1002520	MutS (Bacillus subtilis)	85	70	1719
243	9	8013	8783	gi|414011	ipa-87r gene product (Bacillus subtilis)	85	72	771
249	2	5894	3186	gi|1405454	aconitase (Bacillus subtilis)	85	73	2709
302	1	140	475	gi|40173	homolog of E.coli ribosomal protein L21 (Bacillus subtilis) ir|S18439|S18439 Ribosomal protein L21 - Bacillus subtilis p|P26908|RL21_BACSU 50S RIBOSOMAL PROTEIN L21 (BL20).	85	72	336
333	1	5445	2968	gi|442360	ClpC adenosine triphosphatase (Bacillus subtilis)	85	69	2478
364	6	6082	8196	gi|871784	Clp-like ATP-dependent protease binding subunit (Bos taurus)	85	68	2115
448	2	1992	1339	gi|405134	acetate kinase (Bacillus subtilis)	85	68	654
747	1	1251	853	gi|1373157	orf-x; hypothetical protein; Method: conceptual translation supplied by author (Bacillus subtilis)	85	73	399
886	2	159	467	gi|541768	hemin permease (Yersinia enterocolitica)	85	55	309
1089	1	1208	606	pir|B47154|B471	signal recognition particle 54K chain homolog Ffh - Bacillus subtilis	85	71	603
1163	1	816	409	gi|304155	diaminopimelate decarboxylase (Bacillus methanolicus) sp|P41023|DCDA_BACMT DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) DAP DECARBOXYLASE).	85	62	408
1924	1	487	251	gi|215098	excisionase (Bacteriophage 154a)	85	73	237
2932	1	776	390	gi|1041099	Pyruvate Kinase (Bacillus licheniformis)	85	71	387
3030	1	3	275	gi|42370	pyruvate formate-lyase (AA 1-760) (Escherichia coli) ir|S01788|S01788 formate C-acetyltransferase (EC 2.3.1.54) - cherichia coli	85	74	273
3111	1	595	299	gi|63568	limb deformity protein (Gallus gallus)	85	85	297
3778	1	630	316	gi|391840	beta-subunit of HDT (Pseudomonas fragi)	85	67	315
3835	1	1	387	gi|1204472	type I restriction enzyme ECOR124/3 I M protein (Haemophilus influenzae)	85	56	387
4042	1	3	386	?|18178	formate acetyltransferase (Chlamydomonas reinhardtii) ir|S24997|S24997 formate C-acetyltransferase (EC 2.3.1.54) - lamydomonas reinhardtii	85	70	384
4053	1	35	340	gi|1204472	type I restriction enzyme ECOR124/3 I M protein (Haemophilus influenzae)	85	56	306
4108	1	2	181	gi|1072418	glcA gene product (Staphylococcus carnosus)	85	61	180
4300	1	575	330	gi|1151932	fructose enzyme II (Rhodobacter capsulatus)	85	59	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4392	1	627	355	gi|1022725	unknown [Staphylococcus haemolyticus]	85	74	273
4408	1	2	235	gi|871784	Clp-like ATP-dependent protease binding subunit (Bos taurus)	85	62	234
4430	1	578	291	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	85	68	288
4555	1	2	253	gi|450688	hadM gene of Ecoprrl gene product [Escherichia coli] pir|S38437|S38437 hadM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	85	52	252
4611	1	481	242	gi|1256635	dihydroxy-acid dehydratase (Bacillus subtilis)	85	65	240
4	10	10061	10591	gi|46982	fosB gene product [Staphylococcus epidermidis]	84	68	531
13	2	1148	1172	gi|162450	ahrC protein (Bacillus subtilis)	84	56	177
16	4	1803	4652	gi|1277198	DNA repair protein (Deinococcus radiodurans)	84	67	2850
22	3	1535	1128	gi|511069	UreF [Staphylococcus xylosus]	84	73	408
23	7	5055	5306	gi|1603320	YerO82p [Saccharomyces cerevisiae]	84	61	252
53	11	11597	11145	gi|1303948	Yqlw (Bacillus subtilis)	84	68	453
53	12	14059	12770	pir|142613	branched chain alpha-keto acid dehydrogenase E2 (Bacillus subtilis) gi|13D3944 BfmB (Bacillus subtilis)	84	71	1290
70	1	1332	982	gi|46647	ORF (repE) [Staphylococcus aureus]	84	68	351
73	4	2512	4311	gi|142993	glycerol-3-phosphate dehydrogenase (glpD) (EC 1.1.99.5) (Bacillus subtilis)	84	74	1800
98	7	4324	6096	gi|467427	methionyl-tRNA synthetase (Bacillus subtilis)	84	66	1773
100	9	9501	8680	gi|1340128	ORF1 [Staphylococcus aureus]	84	78	822
117	3	1934	3208	gi|1237019	Srb (Bacillus subtilis)	84	68	1275
148	6	4720	5670	gi|467462	cysteine synthetase A (Bacillus subtilis)	84	69	951
152	4	2064	2456	pir|141377	pyruvate decarboxylase (E-1) alpha subunit (Bacillus subtilis) pir|B36718|NEBSPA pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) lpha chain - Bacillus subtilis	84	70	393
169	7	3634	3861	gi|1001342	hypothetical protein (Synechocystis sp.)	84	66	228
171	4	2992	2657	gi|517475	D-amino acid transaminase [Staphylococcus haemolyticus]	84	71	336
186	6	6941	6216	gi|467475	unknown [Bacillus subtilis]	84	70	726
205	9	6261	5692	gi|216360	ORF for adenylate kinase (Bacillus subtilis)	84	71	570
224	2	915	1391	gi|288269	beta-fructofuranosidase [Staphylococcus xylosus]	84	70	677

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
251	1	92	388	gi|1303790	YqeI [Bacillus subtilis]	84	65	297
282	1	1526	2836	gi|143040	glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus subtilis] pir|D42728|D42728 glutamate-1-semialdehyde 2,1-aminomutase (EC 4.3.8) - Bacillus subtilis	84	75	1311
307	5	3138	2959	gi|1070014	protein-dependent [Bacillus subtilis]	84	62	180
320	4	2343	4229	gi|143390	carbamyl phosphate synthetase [Bacillus subtilis]	84	70	1887
372	1	3	296	gi|1022725	unknown [Staphylococcus haemolyticus]	84	70	294
413	2	2201	1341	gi|1256146	YbbQ [Bacillus subtilis]	84	65	861
439	1	3	392	gi|1046173	osmotically inducible protein [Mycoplasma genitalium]	84	53	390
461	3	1362	2270	gi|140211	threonine synthase (thrC) (AA 1-352) [Bacillus subtilis] 1r|A25364|A25364 threonine synthase (EC 4.2.99.2) - Bacillus btilis	84	69	909
487	1	3	299	gi|1144531	integrin-like protein alpha Intip [Candida albicans]	84	46	297
491	2	624	905	pir|S08564|R3BS	ribosomal protein S9 - Bacillus stearothermophilus	84	69	282
491	3	816	1033	pir|S08564|R3BS	ribosomal protein S9 - Bacillus stearothermophilus	84	77	198
548	1	3	341	gi|411271	uracil permease [Bacillus caldolyticus]	84	74	339
728	2	2701	1748	gi|912445	DNA polymerase [Bacillus caldotenax]	84	68	954
769	1	3	257	gi|1510953	cobalamin biosynthesis protein N [Methanococcus jannaschii]	84	38	255
954	1	308	156	gi|1405454	aconitase [Bacillus subtilis]	84	57	153
957	1	3	395	gi|143402	recombination protein (ttg start codon) [Bacillus subtilis] gi|1303923 RecN [Bacillus subtilis]	84	68	393
975	1	3	452	gi|885934	ClpB [Synechococcus sp.]	84	70	450
1585	1	3	257	gi|510140	ligoendopeptidase F [Lactococcus lactis]	84	56	255
2954	1	3	323	gi|603769	HutU protein, urocanase [Bacillus subtilis]	84	73	321
2996	1	650	348	gi|18178	formate acetyltransferase [Chlamydomonas reinhardtii] 1r|S24997|S24997 formate C-acetyltransferase (EC 2.3.1.54) - lamydomonas reinhardtii	84	65	303
3766	1	737	375	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	84	72	363
4022	1	2	169	gi|1146206	glutamate dehydrogenase [Bacillus subtilis]	84	54	168
4058	1	620	312	gi|151932	fructose enzyme II [Rhodobacter capsulatus]	84	71	309
4108	2	106	351	gi|1072418	glcA gene product [Staphylococcus carnosus]	84	77	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4183	1	3	308	gi|603769	HutU protein, urocanase [Bacillus subtilis]	84	72	306
4726	1	55	234	gi|146208	glutamate synthase large subunit (EC 2.6.1.53) [Escherichia coli] pir|A29617|A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large chain - Escherichia coli	84	73	180
22	4	2043	1576	gi|393297	urease accessory protein [Bacillus sp.]	83	64	468
53	13	14722	13745	gi|142612	branched chain alpha-keto acid dehydrogenase E1-beta [Bacillus subtilis]	83	68	978
57	16	13357	12872	gi|143132	lactate dehydrogenase (AC 1.1.1.27) [Bacillus -aldolyticus] pir|B29704|B29704 L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus aldolyticus	83	66	486
66	1	1119	2274	gi|1303894	YqhM [Bacillus subtilis]	83	63	846
66	5	6118	4643	gi|1212730	YqhX [Bacillus subtilis]	83	68	1476
70	3	1864	1523	gi|44095	replication initiator protein [Listeria monocytogenes]	83	73	342
90	1	377	1429	gi|155571	alcohol dehydrogenase I (adhA) (EC 1.1.1.1) [Zymomonas mobilis] pir|A35260|A35260 alcohol dehydrogenase (EC 1.1.1.1) I - Zymomonas mobilis	83	70	1053
95	2	708	2162	gi|506381	phospho-beta-glucosidase [Bacillus subtilis]	83	70	1455
137	1	68	694	gi|467391	Initiation protein of replication [Bacillus subtilis]	83	77	627
140	4	3209	2742	gi|634107	kdpB [Escherichia coli]	83	65	468
142	3	3468	2989	gi|1212776	lumazine synthase (b-subunit) [Bacillus amyloliquefaciens]	83	69	480
161	12	5749	6696	gi|903307	ORF75 [Bacillus subtilis]	83	64	948
164	9	9880	11070	gi|49316	ORF2 gene product [Bacillus subtilis]	83	66	1191
164	14	14148	14546	gi|580902	ORF6 gene product [Bacillus subtilis]	83	60	399
170	2	3144	2467	gi|520844	orf4 [Bacillus subtilis]	83	64	678
186	2	2029	1370	gi|289284	cysteinyl-tRNA synthetase [Bacillus subtilis]	83	72	660
205	14	7822	7607	gi|216337	ORF for L30 ribosomal protein [Bacillus subtilis]	83	74	216
237	6	3683	4540	gi|1510488	imidazoleglycerol-phosphate synthase (cyclase) [Methanococcus jannaschii]	83	60	858
301	1	985	638	gi|467419	unknown [Bacillus subtilis]	83	65	348
302	4	1421	2743'	gi|508979	GTP-binding protein [Bacillus subtilis]	83	68	1323
321	4	3933	3571	gi|39884	fumarase (citG) (aa 1-462) [Bacillus subtilis]	83	68	363
367	1	2	352	gi|1039479	ORFU [Lactococcus lactis]	83	54	351

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
387	1	3	662	gi|806281	DNA polymerase I (Bacillus stearothermophilus)	83	70	660
527	2	916	1566	gi|396259	protease (Staphylococcus epidermidis)	83	67	651
533	1	355	179	gi|1142455	alanine dehydrogenase (EC 1.4.1.1) (Bacillus stearothermophilus) pir|B34261|B34261 alanine dehydrogenase (EC 1.4.1.1) - Bacillus tearothermophilus	83	66	177
536	4	1617	1438	gi|1143366	adenylosuccinate lyase (PUR-B) (Bacillus subtilis), lr|C29326|W2BSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis	83	67	180
652	1	2	859	gi|520753	DNA topoisomerase I (Bacillus subtilis)	83	72	858
774	2	200	361	gi|1522665	M. jannaschii predicted coding region MJECL20 (Methanococcus jannaschii)	83	58	162
897	1	120	296	gi|1064807	ORNITHINE AMINOTRANSFERASE (Bacillus subtilis)	83	76	177
1213	1	3	491	gi|289288	lexA (Bacillus subtilis)	83	67	489
2529	1	296	150	gi|1143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Bacillus subtilis) pir|JT0481|YWBS tryptophan-tRNA ligase (EC 6.1.1.2) - Bacillus ubtilis	83	69	147
2973	1	649	326	gi|1109687	ProZ (Bacillus subtilis)	83	58	324
1009	1	1?8	166	i|HR2512	ORF_o294 (Escherichia coli)	83	65	363
3035	2	45	305	gi|950062	hypothetical yeast protein 1 (Mycoplasma capricolum) pir|S48578|S48578 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	83	59	261
3906	1	67	309	gi|1353197	thioredoxin reductase [Eubacterium acidaminophilum]	83	61	241
4458	1	540	271	gi|397526	clumping factor [Staphylococcus aureus]	83	78	270
4570	1	444	223	gi|1022726	unknown [Staphylococcus haemolyticus]	83	74	222
4654	1	97	261	gi|1072419	glcB gene product [Staphylococcus carnosus]	83	79	165
16	2	295	1191	gi|153854	uvs402 protein [Streptococcus pneumoniae]	82	67	897
16	3	1193	1798	gi|153854	uvs402 protein [Streptococcus pneumoniae]	82	70	606
38	12	9644	8724	gi|1204400	N-acetylneuraminate lyase [Haemophilus influenzae]	82	58	921
42	4	988	2019	gi|841192	catalase [Bacteroides fragilis]	82	70	1032
51	6	2590	3489	gi|143607	sporulation protein (Bacillus subtilis)	82	69	900
56	11	12270	13925	gi|39431	oligo-1,6-glucosidase [Bacillus cereus]	82	60	1656
56	15	17673	18014	gi|467410	unknown [Bacillus subtilis]	82	66	342
61	2	881	3313	gi|1?43148	transfer RNA-Leu synthetase [Bacillus subtilis]	82	70	2433

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
82	7	9162	11318	gi|48240	elongation factor G (AA 1-691) (Thermus aquaticus thermophilus] sr|S15928|EFTWG translation elongation factor G - Thermus aquaticus p|P13551|EFG_THETH ELONGATION FACTOR G (EF-G).	82	64	2157
85	2	5470	3260	gi|143369	phosphoribosylformyl glycinamidine synthetase II (PUR-Q) [Bacillus subtilis]	82	66	2211
102	6	3662	5380	gi|256615	dihydroxy-acid dehydratase [Bacillus subtilis]	82	65	1719
117	4	3242	3493	pir|A47154|A471	orf1 5' of Ffh - Bacillus subtilis	82	5?	252
128	6	4377	5933	gi|460258	phosphoglycerate mutase [Bacillus subtilis]	82	66	1557
129	2	1229	2182	gi|403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	82	62	954
170	1	2	1441	gi|1377831	unknown [Bacillus subtilis]	82	67	1440
177	1	3	1094	gi|467386	thiophen and furan oxidation [Bacillus subtilis]	82	65	1092
184	4	3572	4039	gi|153556	ORF (19K protein) [Enterococcus faecalis]	82	59	468
189	8	4455	4225	gi|1001878	CspL protein [Listeria monocytogenes]	82	73	231
206	19	21166	20707	gi|473916	lipopeptide antibiotics Iturin A [Bacillus subtilis] sp|P39144|LP14_BACSU LIPOPEPTIDE ANTIBIOTICS ITURIN A AND SURFACTIN IOSYNTHESIS PROTEIN.	82	50	660
221	2	805	1722	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	82	63	918
223	4	3866	3651	gi|439619	[Salmonella typhimurium IS200 insertion sequence [from SARA17, artial.]. gene product [Salmonella typhimurium]	82	69	216
260	3	5207	4296	gi|116138	IcaB [Staphylococcus epidermidis]	82	61	912
315	3	4864	2855	gi|143397	quinol oxidase [Bacillus subtilis]	82	67	2010
321	10	8520	7945	gi|1429A1	ORF5: This ORF includes a region (aa23-103) containing a potential ron-sulphur centre homologous to a region of Rhodospirillum rubrum nd Chromatium vinosum: putative [Bacillus stearothermophilus] pir|PO0239|PQ0239 hypothetical protein 5 (glaA 3' region) -	82	62	576
331	3	1055	1342	gi|436574	ribosomal protein L1 [Bacillus subtilis]	82	71	288
370	2	262	618	gi|1303793	YqeL [Bacillus subtilis]	82	59	357
404	4	3053	4024	gi|1303821	YqfE [Bacillus subtilis]	82	68	972
405	4	4440	3073	gi|1303913	YqhX [Bacillus subtilis]	82	67	1368
436	3	4096	2864	gi|149521	tryptophan synthase beta subunit [Lactococcus lactis] pir|S35129|S35129 tryptophan synthase (EC 4.2.1.20) beta chain - actococcus lactis subsp. lactis	82	67	1233

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
441	4	3394	2573	gi|142952	glyceraldehyde-3-phosphate dehydrogenase [Bacillus stearothermophilus]	82	67	822
444	12	10415	11227	gi|1204354	spore germination and vegetative growth protein [Haemophilus influenzae]	82	67	813
446	1	3	191	gi|143387	aspartate transcarbamylase [Bacillus subtilis]	82	66	189
462	3	1007	1210	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] pir|A37192|A37192 uvrB protein - Bacillus subtilis sp|P14951|UVRC_BACSU EXCINUCLEASE ABC SUBUNIT C.	82	64	204
537	1	1560	784	gi|A53767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus ubtilis]	82	61	777
680	2	407	700	gi|426472	sacE gene product (Staphylococcus carnosus)	82	69	294
724	2	565	386	gi|143373	phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-HJ) Bacillus subtilis]	82	68	180
763	1	422	213	gi|467458	cell division protein [Bacillus subtilis]	82	35	210
818	1	564	283	gi|1064787	function unknown [Bacillus subtilis]	82	69	282
858	1	175	1176	gi|143043	uroporphyrinogen decarboxylase [Bacillus subtilis] pir|B47045|B47045 uroporphyrinogen decarboxylase (EC 4.1.1.37) - acillus subtilis	82	71	1002
895	1	3	599	gi|1027507	ATP binding protein [Borrelia burgdorferi]	82	72	597
939	1	10	399	gi|143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	82	60	390
961	1	1	306	gi|577647	gamma-hemolysin [Staphylococcus aureus]	82	69	306
1192	1	107	155	gi|146974	NHJ-dependent NAD synthetase [Escherichia coli]	82	71	153
1317	1	49	375	gi|407908	E1ter [Staphylococcus xylosus]	82	72	327
1341	1	1	150	gi|39962	ribosomal protein L35 (AA 1-66) [Bacillus stearothermophilus] lr|S03347|R58535 ribosomal protein L35 - Bacillus earothermophilus	82	68	150
2990	2	567	349	gi|534855	ATPase subunit epsilon [Bacillus stearothermophilus] sp|P42009|ATPE_BACST ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34).	82	47	219
3024	1	45	224	gi|467402	unknown [Bacillus subtilis]	82	64	180
3045	1	276	139	gi|467335	ribosomal protein L9 [Bacillus subtilis]	82	60	138
3045	2	558	400	gi|467335	ribosomal protein L9 [Bacillus subtilis]	82	82	159
3091	1	474	238	gi|499335	secA protein [Staphylococcus carnosus]	82	78	237
3107	1	416	210	gi|546918	orfY 3' of comK [Bacillus subtilis, E26, Peptide Partial, 140 aa] pir|S43612|S43612 hypothetical protein Y - Bacillus subtilis sp|P40398|YHXD_BACSU HYPOTHETICAL PROTEIN IN COMK 3'REGION (ORFY) FRAGMENT).	82	64	207

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4332	1	2	319	gi|42086	nitrate reductase alpha subunit (Escherichia coli) p|P09152|NARG_ECOLI RESPIRATORY NITRATE REDUCTASE 1 ALPHA CHAIN (EC 7.99.4). (SUB 2-1247)	82	75	318
23	3	3275	2574	gi|1199573	spsB (Sphingomonas sp.)	81	64	702
42	1	618	321	gi|466778	lysine specific permease (Escherichia coli)	81	59	318
48	5	4051	4350	gi|1045937	M. genitalium predicted coding region MG246 (Mycoplasma genitalium)	81	62	300
51	4	1578	2579	pir|S16649|S166	dclAC protein - Bacillus subtilis	81	55	1002
53	2	354	1494	gi|1303961	YqjJ (Bacillus subtilis)	81	67	1131
53	8	9419	7971	gi|146930	6-phosphogluconate dehydrogenase (Escherichia coli)	81	66	1449
54	9	10757	10119	gi|143016	permease (Bacillus subtilis)	81	65	639
54	10	13360	11786	gi|143015	gluconate kinase (Bacillus subtilis)	81	64	1575
57	17	13983	13366	pir|A25805|A258	L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis	81	74	618
81	2	2708	2217	gi|1222302	NifU-related protein (Haemophilus influenzae)	81	54	492
86	1	745	374	gi|414017	1fpa-93d gene product (Bacillus subtilis)	81	70	372
103	6	6438	4861	gi|971342	nitrate reductase beta subunit (Bacillus subtilis) sp|P42176|NARH_BACSU NITRATE REDUCTASE BETA CHAIN (EC 1.7.99.4).	81	64	1578
120	15	10845	12338	gi|1524392	GbsA (Bacillus subtilis)	81	67	1494
128	5	3676	4413	gi|143319	triose phosphate isomerase (Bacillus megaterium)	81	64	738
131	9	10308	9280	gi|299163	alanine dehydrogenase (Bacillus subtilis)	81	68	1029
143	6	6088	5471	gi|439619	[Salmonella typhimurium IS200 insertion sequence from SARA17, artsl.], gene product [Salmonella typhimurium]	81	61	618
169	1	43	825	gi|897795	30S ribosomal protein (Pediococcus acidilactici) sp|P49668|RS2_PEDAC 30S RIBOSOMAL PROTEIN S2.	81	65	783
230	1	450	226	gi|1125826	short region of weak similarity to tyrosine-protein kinase receptors in a fibronectin type III-like domain (Caenorhabditis elegans)	81	54	225
233	5	2000	2677	gi|467404	unknown (Bacillus subtilis)	81	61	678
241	2	3081	2149	gi|16510	succinate--CoA ligase (GDP-forming) (Arabidopsis thaliana) tr|S30579|S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) pha chain - Arabidopsis thaliana (fragment)	81	69	933
256	1	1	981	pir|S09411|S094	spoIIE protein - Bacillus subtilis	81	65	981
259	3	3752	2691	sp|P28367|RF2_B	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) (FRAGMENT).	81	65	1062

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
275	2	1728	3581	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis]	81	68	1854
285	1	1466	735	gi|1204844	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	81	63	732
296	1	99	1406	gi|467328	adenylosuccinate synthetase [Bacillus subtilis]	81	67	1308
302	9	5590	5889	gi|147485	queA [Escherichia coli]	81	64	300
317	2	1137	1376	gi|154961	resolvase [Transposon Tn917]	83	54	240
343	2	1034	1342	gi|405955	yeeD [Escherichia coli]	81	60	309
360	2	1404	2471	gi|1204570	aspartyl-tRNA synthetase [Haemophilus influenzae]	81	67	1068
364	5	6251	5706	gi|1204652	methylated-DNA--protein-cysteine methyltransferase [Haemophilus influenzae]	81	63	546
372	2	1707	1135	gi|467416	unknown [Bacillus subtilis]	81	65	573
392	1	43	603	pir|S09411|S094	spoIIIE protein - Bacillus subtilis	81	65	561
404	9	5252	6154	gi|606745	Bex [Bacillus subtilis]	81	65	903
426	2	1727	1119	gi|39453	Manganese superoxide dismutase [Bacillus caldotenax] ir|S22053|S22053 (Mn) - Bacillus ldotenax superoxide dismutase (EC 1.15.1.1)	81	66	609
480	7	4053	5889	pir|C370HJ|C370	hypothetical protein II (ompII 3' region) - Salmonella typhimurium (fragment)	81	57	237
625	3	1105	2070	gi|1262360	protein kinase PknB [Mycobacterium leprae]	81	56	966
754	2	504	1064	gi|1303902	yqhU [Bacillus subtilis]	81	71	561
842	1	86	430	gi|1405446	transketolase [Bacillus subtilis]	81	68	345
953	1	798	400	gi|1205429	dipeptide transport ATP-binding protein [Haemophilus influenzae]	81	57	399
961	2	252	401	gi|487686	synergohymenotropic toxin [Staphylococcus intermedius] pir|S44944|S44944 synergohymenotropic toxin - Staphylococcus ntermedius	81	72	150
1035	1	1	189	gi|1046138	M. genitalium predicted coding region MG423 [Mycoplasma genitalium]	81	43	189
1280	1	670	449	gi|559164	helicase [Autographa californica nuclear polyhedrosis virus] sp|P24107|V141_NPVAC HELICASE.	81	43	222
3371	1	68	241	gi|1322245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	81	62	174
3715	1	475	239	gi|537137	ORF_f388 [Escherichia coli]	81	58	237
390R	1	2	325	gi|439619	[Salmonella typhimurium IS200 insertion sequence from SARA17, artial.l. gene product [Salmonella typhimurium]	81	68	324
3940	1	3	401	gi|296464	ATPase [Lactococcus lactis]	81	69	399

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3954	1	1	318	gi|1224059	amidase [Moraxella catarrhalis]	81	68	318
4049	1	337	170	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	81	68	168
4209	1	1	324	gi|403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	81	58	324
437?	1	627	322	gi|218677	indolepyruvate decarboxylase [Enterobacter cloacae] pir|S16013|S16013 indolepyruvate decarboxylase (EC 4.1.1.-) - nterobacter cloacae	81	72	306
4387	1	19	228	gi|460689	TVG [Thermoactinomyces vulgaris]	81	59	210
4191	1	581	306	gi|1524193	unknown [Mycobacterium tuberculosis]	81	67	276
4425	1	3	341	gi|143015	gluconate kinase [Bacillus subtilis]	81	66	339
9	1	1593	847	gi|1064786	function unknown [Bacillus subtilis]	80	62	747
17	1	544	311	gi|559164	helicase [Autographa californica nuclear polyhedrosis virus] sp|P24307|V143_NPVAC HELICASE.	80	40	234
45	2	1159	2448	gi|1109684	ProV [Bacillus subtilis]	80	63	1290
45	5	4032	4733	gi|1109687	ProZ [Bacillus subtilis]	80	55	702
54	8	10266	9502	gi|563952	gluconate permease [Bacillus licheniformis]	80	62	765
62	12	8852	7545	gi|854655	Na/H antiporter system [Bacillus alcalophilus]	80	62	1308
62	14	8087	8683	gi|559713	ORF [Homo sapiens]	80	68	597
67	16	13781	14122	gi|305002	ORF_f356 [Escherichia coli]	80	65	342
70	13	11495	10296	gi|1303995	YqkN [Bacillus subtilis]	80	64	1200
98	9	6336	7130	gi|467428	unknown [Bacillus subtilis]	80	68	795
98	10	7294	7833	gi|467430	unknown [Bacillus subtilis]	80	64	540
98	11	7820	8737	gi|467431	high level kasugamycin resistance [Bacillus subtilis]	80	61	918
109	16	14154	14813	gi|580875	ipe-57d gene product [Bacillus subtilis]	80	63	660
112	15	14294	16636	gi|1072361	pyruvate-formate-lyase [Clostridium pasteurianum]	80	65	2343
139	1	1448	726	gi|506699	CapC [Staphylococcus aureus]	80	58	723
139	2	2179	1448	gi|506698	CapB [Staphylococcus aureus]	80	59	732
174	4	3271	2870	gi|1146242	aspartate 1-decarboxylase [Bacillus subtilis]	80	61	402

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
177	3	2102	2842	gi|467385	unknown [Bacillus subtilis]	80	70	741
184	6	6124	5912	gi|161953	85-kDa surface antigen [Trypanosoma cruzi]	80	46	213
186	4	5368	3875	gi|289282	glutamyl-tRNA synthetase [Bacillus subtilis]	80	65	1494
205	10	15796	15140	g:|40103	ribosomal protein L4 [Bacillus stearothermophilus]	80	66	657
207	1	140	1315	gi|460259	enolase [Bacillus subtilis]	80	67	1176
211	3	1078	1590	gi|410131	ORFX7 [Bacillus subtilis]	80	61	513
235	2	1962	2255	gi|143797	valyl-tRNA synthetase (Bacillus stearothermophilus) sp|P11931|SYV_BACST VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--TRNA LIGASE) (VALRS).	80	55	294
239	1	1	1263	gi|143000	proton glutamate symport protein (Bacillus stearothermophilus) pir|S26247|S26247 glutamate/aspartate transport protein - Bacillus stearothermophilus	80	59	1263
272	5	2724	2461	gi|709993	hypothetical protein [Bacillus subtilis]	80	54	264
301	3	1446	1111	gi|467418	unknown [Bacillus subtilis]	80	58	336
310	4	5697	4501	gi|117686	acuC gene product [Staphylococcus xylosus]	80	67	1197
310	6	5258	7006	gi|348053	acetyl-CoA synthetase [Bacillus subtilis]	80	67	1749
310	7	7410	9113	gi|1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	80	67	1704
325	3	1114	1389	gi|310325	outer capsid protein [Rotavirus sp.]	80	40	276
337	1	1268	636	gi|537049	ORF_o470 [Escherichia coli]	80	55	633
374	2	929	1228	gi|1405448	YneF [Bacillus subtilis]	80	70	300
375	5	3062	3331	gi|467448	unknown [Bacillus subtilis]	80	68	270
388	1	267	587	gi|1064791	function unknown [Bacillus subtilis]	80	65	321
394	1	9	659	gi|304976	matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to longation factor G, TetM/TetO tetracycline-resistance proteins Escherichia coli]	80	65	651
456	1	625	1263	c:|1146183	putative [Bacillus subtilis]	80	65	639
475	1	1	654	gi|288269	beta-fructofuranosidase [Staphylococcus xylosus]	80	66	654
544	2	1449	2240	gi|529754	speC [Streptococcus pyogenes]	80	50	792
622	4	1623	1871	gi|1143545	unknown [Mycobacterium tuberculosis]	80	65	249
719	1	1	1257	gi|1064791	function unknown [Bacillus subtilis]	80	68	1257
739	1	107	838	gi|666983	putative ATP binding subunit [Bacillus subtilis]	80	61	732

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
745	2	581	414	gi|1511600	coenzyme PQQ synthesis protein III [Methanococcus jannaschii]	80	61	168
822	1	17	679	gi|410141	ORFX17 [Bacillus subtilis]	80	68	663
827	2	901	836	gi|1205301	leukotoxin secretion ATP-binding protein [Haemophilus influenzae]	80	54	156
1044	1	3	149	gi|60632	vp2 [Marburg virus]	80	55	147
1220	2	571	413	pir|A61072|EPSG	gallidermin precursor - Staphylococcus gallinarum	80	78	159
2519	1	75	275	gi|147556	[dpj] [Escherichia coli]	80	45	201
2847	1	501	279	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	80	62	225
3120	1	2	226	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	80	65	225
3191	1	294	148	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevaloni] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.88) Pseudomonas sp.	80	59	147
3560	2	285	434	gi|217110	photosystem J core protein B [Synechococcus vulcanus]	80	70	150
3655	1	47	166	gi|415855	deoxyribose aldolase [Mycoplasma hominis]	80	56	300
3658	2	324	584	gi|551531	2-nitropropane dioxygenase [Williopsis saturnus]	80	54	261
3769	1	798	400	gi|1139950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	80	68	399
3781	1	692	348	gi|166412	NADH-glutamate synthase [Medicago sativa]	80	62	345
3988	1	48	287	gi|1204696	fructose-permease IIBC component [Haemophilus influenzae]	80	69	240
4030	1	571	287	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	80	60	285
4092	1	547	275	gi|1370207	orf6 [Lactobacillus sake]	80	69	273
4103	1	680	342	gi|139956	IIGlc [Bacillus subtilis]	80	65	339
4231	1	692	348	gi|289287	UDP-glucose pyrophosphorylase [Bacillus subtilis]	80	65	345
4265	1	595	299	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	80	63	297
4504	1	498	250	gi|1139950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	80	68	249
2	6	5998	6798	gi|535351	CodY [Bacillus subtilis]	79	63	801
4	7	8295	7051	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	79	64	1245
25	6	5273	5515	pir|A36728|AJ67	acyl carrier protein - Rhizobium meliloti	79	65	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
59	2	1173	1424	gi|147923	threonine dehydratase 2 (EC 4.2.1.16) (Escherichia coli)	79	75	252
60	1	1	204	gi|666115	orf1 upstream of glucose kinase (Staphylococcus xylosus) pir|SS2351|SS2351 hypothetical protein 1 - Staphylococcus xylosus	79	60	204
81	1	3002	1590	gi|466882	ppsI; B1496_C2_189 (Mycobacterium leprae)	79	64	1413
85	7	7023	6505	gi|143364	phosphoribosyl aminoimidazole carboxylase I (PUR-E) (Bacillus subtilis)	79	60	519
89	6	5660	4554	gi|144906	product homologous to E.coli thioredoxin reductase: J.Biol.Chem. 1988) 263:9015-9019, and to F52a protein of alkyl hydroperoxide eductase (from S.typhimurium: J.Biol.Chem. (1990) 265:10515-10540: pen reading frame A [Clostridium pasteurianum]	79	35	1107
102	11	7489	8571	gi|143093	ketol-acid reductoisomerase (Bacillus subtilis) sp|P37251|ILVC_BACSU KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86) ACETOHYDROXY-ACID ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL EDUCTOISOMERASE)	79	64	1083
102	14	11190	12563	gi|149428	putative (Lactococcus lactis)	79	65	1374
127	9	7792	9372	gi|458688	PrfC/RF3 (Dichelobacter nodosus)	79	68	1581
139	3	2540	1983	gi|506697	CapA (Staphylococcus aureus)	79	55	558
144	2	1644	1156	gi|1498296	peptide methionine sulfoxide reductase (Streptococcus pneumoniae)	79	47	489
14A	2	529	1098	gi|467457	hypoxanthine-guanine phosphoribosyltransferase (Bacillus subtilis) gi|467457 hypoxanthine-guanine phosphoribosyltransferase (Bacillus ubtilis]	79	59	570
150	1	965	591	gi|755602	unknown (Bacillus subtilis)	79	61	375
176	1	1039	587	gi|297874	fructose-bisphosphate aldolase (Staphylococcus carnosus) pir|A49943|A49943 (fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TM300)	79	65	453
186	7	7584	6874	gi|1314298	ORF5; putative Sms protein; similar to Sms proteins from Haemophilus influenzae and Escherichia coli (Listeria monocytogenes)	79	64	711
205	16	8887	8498	gi|1044980	ribosomal protein L1A (Bacillus subtilis)	79	70	390
211	1	1	519	gi|1303994	YqkM (Bacillus subtilis)	79	62	519
223	2	4183	2801	gi|488430	alcohol dehydrogenase 2 (Entamoeba histolytica)	79	60	1381
243	8	8915	7896	gi|580883	lpa-88d gene product (Bacillus subtilis)	79	60	1020
279	4	3721	4329*	gi|413930	lpa-6d gene product (Bacillus subtilis)	79	59	609
300	1	11	1393	gi|403372	glycerol 3-phosphate permease (Bacillus subtilis)	79	62	1383
307	3	2930	1935	gi|1950062	hypothetical yeast protein 1 (Mycoplasma capricolum) pir|S48578|S48578 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	79	60	996

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
352	6	10106	8886	gi|216854	P47K [Pseudomonas chlororaphis]	79	59	1221
412	1	1153	578	gi|143177	putative [Bacillus subtilis]	79	51	576
481	3	621	1124	gi|786163	Ribosomal Protein L10 [Bacillus subtilis]	79	66	504
516	1	702	352	gi|805090	NisF [Lactococcus lactis]	79	48	351
525	2	2457	1426	gi|143371	phosphoribosyl aminoimidazole synthetase (PUR-M) [Bacillus subtilis] pir|H39326|A1BSCL phosphoribosylformylglycinamidine cyclo-ligase EC 6.3.3.1) - Bacillus subtilis	79	61	1032
53R	4	3448	2825	gi|1370207	orf6 [Lactobacillus sake]	79	67	624
570	1	2	421	gi|476160	arginine permease substrate-binding subunit [Listeria monocytogenes]	79	61	420
645	8	2663	3241	gi|153898	transport protein [Salmonella typhimurium]	79	62	579
683	1	75	374	gi|1064795	function unknown [Bacillus subtilis]	79	62	300
R16	3	4700	3987	gi|1407784	orf-1; novel antigen [Staphylococcus aureus]	79	62	714
2929	1	3	401	gi|1524197	glycine betaine transporter OpuD [Bacillus subtilis]	79	61	399
2937	1	357	202	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	79	58	156
2940	1	768	385	gi|149429	putative [Lactococcus lactis]	79	72	384
2946	1	570	286	gi|143267	2-oxoglutarate dehydrogenase (odhA; EC 1.2.4.2) [Bacillus subtilis]	79	61	285
2999	1	3	212	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	79	59	210
3022	1	514	332	gi|450686	3-phosphoglycerate kinase [Thermotoga maritima]	79	61	183
3064	1	3	314	gi|1204436	pyruvate formate-lyase [Haemophilus influenzae]	79	60	312
3083	1	2	220	gi|1149662	hypD gene product [Clostridium perfringens]	79	56	219
3126	1	701	411	g.-|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	79	55	291
3181	1	607	326	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	79	59	282
3345	1	3	476	gi|871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	79	63	474
3718	1	536	270	pir|C36889|C368	leuB protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)	79	71	267
3724	2	159	401	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	79	64	243
3836	1	608	312	gi|1524193	unknown [Mycobacterium tuberculosis]	79	65	297
3941	1	2	334	gi|415855	deoxyribose aldolase [Mycoplasma hominis]	79	54	333
4113	1	3	341	gi|143015	gluconate kinase [Bacillus subtilis]	79	63	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4501	1	406	209	gi|1022726	unknown [Staphylococcus haemolyticus]	79	66	198
4612	1	2	238	gi|460689	TVG [Thermoactinomyces vulgaris]	79	58	237
2	1	2	1213	gi|520753	DNA topoisomerase I [Bacillus subtilis]	78	64	1212
8	2	2266	1220	gi|216151	DNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi|579197 SPO2 DNA polymerase (aa 1-648) [Bacteriophage SPO2] pir|A21498|DJBFPS2 DNA-directed DNA polymerase (EC 1.7.7.7) - phage PO2	78	72	1047
9	2	1340	1089	gi|1064787	function unknown [Bacillus subtilis]	78	57	252
32	8	6803	7702	gi|146974	NH3)-dependent NAD synthetase [Escherichia coli]	78	63	900
36	4	2941	3138	gi|290503	glutamate permease [Escherichia coli]	78	53	198
53	15	17664	16221	gi|1303941	yqiv [Bacillus subtilis]	78	58	1464
57	14	10520	12067	gi|1072418	glcA gene product [Staphylococcus carnosus]	78	65	1548
66	7	6798	5812	gi|1212729	YqhJ [Bacillus subtilis]	78	67	987
67	4	4029	4376	gi|466612	nika [Escherichia coli]	78	71	348
91	9	10058	10942	gi|467380	stage 0 sporulation [Bacillus subtilis]	78	50	885
102	12	8574	10130	gi|149426	putative [Lactococcus lactis]	78	61	1557
112	6	3540	4463	gi|854234	cymG gene product [Klebsiella oxytoca]	78	56	924
124	2	1888	1061	gi|405622	unknown [Bacillus subtilis]	78	60	828
130	3	1805	2260	gi|1256636	putative [Bacillus subtilis]	78	71	456
133	1	751	377	gi|168060	lamB [Emericella nidulans]	78	59	375
166	4	7125	6163	gi|451216	Mannosephosphate Isomerase [Streptococcus mutans]	78	63	963
186	1	1586	795	gi|289284	cysteinyl-tRNA synthetase [Bacillus subtilis]	78	63	792
195	4	2749	2315	gi|1351874	unknown [Rhodobacter capsulatus]	78	58	435
199	3	4279	3623	gi|143525	succinate dehydrogenase cytochrome b-558 subunit [Bacillus subtilis] pir|A29843|DEBSSC succinate dehydrogenase (EC 1.3.99.1) cytochrome 558 - Bacillus subtilis	78	57	657
199	4	7209	5557	gi|142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] pir|A37192|A37192 uvrB protein - Bacillus subtilis sp|P14951|UVRC_BACSU EXCINUCLEASE ABC SUBUNIT C	78	62	1653
223	3	3831	3523	gi|1135596	[Escherichia coli IS200 insertion sequence from ECOR63, partial.], ene product [Escherichia coli]	78	47	309

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
299	4	1865	2149	gi|467439	temperature sensitive cell division (Bacillus subtilis)	78	62	285
321	9	7734	7315	gi|142979	ORF3 is homologous to an ORF downstream of the spot gene of E.coli; RF) (Bacillus stearothermophilus)	78	55	420
352	4	3714	3944	gi|349050	actin 1 (Pneumocystis carinii)	78	42	231
352	5	7592	6093	gi|903587	NADH dehydrogenase subunit 5 (Bacillus subtilis) sp|P19755|NDH5_BACSU NADH DEHYDROGENASE SUBUNIT 5 (EC 1.6.5.3) NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5).	78	58	1500
376	1	2	583	gi|551693	dethiobiotin synthase (Bacillus sphaericus)	78	34	582
424	2	1595	1768	gi|1524417	alpha-acetolactate decarboxylase (Lactococcus lactis)	78	68	174
450	1	1914	988	gi|1030068	NAD(P)H oxidoreductase, isoflavone reductase homologue (Solanum tuberosum)	78	63	927
558	1	762	562	gi|1511588	bifunctional protein (Methanococcus jannaschii)	78	60	201
670	3	1152	1589	gi|1122759	unknown (Bacillus subtilis)	78	64	438
714	1	64	732	gi|1141460	37 kd minor sigma factor (rpoF, sigB; ttg start codon) (Bacillus subtilis)	78	57	669
814	1	3	368	nl|1377813	unknown (Bacillus subtilis)	78	59	366
981	1	1381	692	gi|143802	GerC2 (Bacillus subtilis)	78	64	690
995	2	978	727	gi|296947	uridine kinase (Escherichia coli)	78	64	252
1045	1	3	401	gi|1407784	orf-1; novel antigen (Staphylococcus aureus)	78	61	399
1163	2	168	186	gi|410117	diaminopimelate decarboxylase (Bacillus subtilis)	78	54	183
2191	1	794	399	g|215098	excisionase (Bacteriophage 154a)	78	65	396
2933	1	2	181	gi|1204436	pyruvate formate-lyase (Haemophilus influenzae)	78	73	180
3041	2	179	317	gi|624612	GltL (Escherichia coli)	78	53	189
3581	1	105	401	gi|761186	3-ketoacyl-CoA thiolase (Saccharomyces cerevisiae)	78	55	297
3709	1	3	230	gi|460689	TVG (Thermoactinomyces vulgaris)	78	58	228
3974	1	528	265	g|558839	unknown (Bacillus subtilis)	78	65	264
3980	1	3	401	gi|39956	IIGlc (Bacillus subtilis)	78	62	399
4056	1	647	354	gi|1256635	dihydroxy-acid dehydratase (Bacillus subtilis)	78	55	294
4114	1	630	316	pir|S09372|S093	hypothetical protein - Trypanosoma brucei	78	62	315
4185	1	3	179	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	78	58	177

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4235	1	655	329	gi|558839	unknown (Bacillus subtilis)	78	60	327
4352	1	541	302	gi|603768	HutI protein, imidazolone-5-propionate hydrolase (Bacillus subtilis) gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis	78	63	240
4368	1	612	307	gi|1353678	heavy-metal transporting P-type ATPase (Proteus mirabilis)	78	59	306
4461	1	428	216	gi|1276841	glutamate synthase (GOGAT) (Porphyra purpurea)	78	36	213
4530	1	474	238	gi|39956	IIGlc (Bacillus subtilis)	78	65	237
3	2	2969	2073	gi|1109684	ProV (Bacillus subtilis)	77	56	897
12	2	2426	1965	gi|467335	ribosomal protein L9 (Bacillus subtilis)	77	59	462
27	1	2	388	gi|1212728	yqhI (Bacillus subtilis)	77	63	387
39	2	590	1252	gi|40054	phenylalanyl-tRNA synthetase beta subunit (AA 1-804) (Bacillus btilis)	77	60	663
42	6	2704	2931	gi|606241	30S ribosomal subunit protein S14 (Escherichia coli) sp|P02370|RS14_ECOLI 30S RIBOSOMAL PROTEIN S14. (SUB 2-101)	77	65	228
46	1A	15459	16622	gi|297798	mitochondrial formate dehydrogenase precursor (Solanum tuberosum) pir|JQ2272|JQ2272 formate dehydrogenase (EC 1.2.1.2) procursor. itochondrial - potato	77	55	1164
100	4	4562	4002	gi|1340128	ORF1 (Staphylococcus aureus)	77	54	561
102	8	5378	5713	gi|1311482	acetolactate synthase (Thermus aquaticus)	77	57	336
109	7	4742	5383	gi|710637	Unknown (Bacillus subtilis)	77	56	642
117	1	2	1228	gi|1237015	ORF4 (Bacillus subtilis)	77	53	1227
124	10	8323	7688	gi|405819	thymidine kinase (Bacillus subtilis)	77	63	636
147	3	1146	985	gi|849027	hypothetical 15.9-kDa protein (Bacillus subtilis)	77	37	162
152	10	7354	7953	gi|1205583	spermidine/putrescine transport ATP-binding protein (Haemophilus influenzae)	77	55	600
169	2	1004	1282	gi|473825	elongation factor EF-Ts' (Escherichia coli)	77	58	279
184	2	380	1147	gi|216314	esterase (Bacillus stearothermophilus)	77	60	768
189	7	3296	3868	gi|853809	ORF3 (Clostridium perfringens)	77	48	573
193	1	132	290	gi|1103788	YqeH (Bacillus subtilis)	77	54	159
195	8	8740	8414	gi|1499620	M. jannaschii predicted coding region MJ0798 (Methanococcus jannaschii)	77	44	327
205	8	5428	5204	gi|216340	ORF for adenylate kinase (Bacillus subtilis)	77	61	225

TABLE 2

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
205	29	14795	14502	gi|786155	Ribosomal Protein L23 (Bacillus subtilis)	77	62	294
211	5	1908	2084	gi|410132	ORFX8 (Bacillus subtilis)	77	47	177
217	5	3478	4416	gi|496254	(fibronectin/fibrinogen-binding protein (Streptococcus pyogenes)	77	54	939
232	1	267	998	gi|1407784	orf-1; novel antigen (Staphylococcus aureus)	77	57	732
233	2	1819	1346	gi|467408	unknown (Bacillus subtilis)	77	61	474
243	3	2661	2299	gi|516155	unconventional myosin (Sus scrofa)	77	32	363
299	1	68	769	gi|467436	unknown (Bacillus subtilis)	77	54	702
301	4	1468	1283	gi|950071	ATP-bind. pyrimidine kinase (Mycoplasma capricolum) pir|S48605|S48605 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	77	48	186
302	5	2741	3211	gi|508980	pheB (Bacillus subtilis)	77	57	471
302	7	3835	4863	gi|147783	ruvB protein (Escherichia coli)	77	60	1029
307	9	5402	4797	gi|1070015	protein-dependent (Bacillus subtilis)	77	60	606
312	1	99	1391	gi|143165	malic enzyme (EC 1.1.1.38) (Bacillus stearothermophilus) pir|A33307|DEBSXS malate dehydrogenase oxaloacetate-decarboxylating) (EC 1.1.1.38) - Bacillus stearothermophilus	77	62	1293
312	2	1541	2443	gi|1399855	carboxyltransferase beta subunit (Synechococcus PCC7942)	77	58	903
321	5	5666	4596	gi|39844	fumarase (citG) (aa 1-462) (Bacillus subtilis)	77	65	1071
164	1	47	568	gi|154634	YvmB (Bacillus subtilis)	77	57	522
365	1	2	1021	gi|143374	phosphoribosyl glycinamide synthetase (PUR-D; ytg start codon) Bacillus subtilis	77	62	1020
374	1	1	708	gi|1405446	transketolase (Bacillus subtilis)	77	61	708
385	1	1128	565	gi|533099	endonuclease III (Bacillus subtilis)	77	63	564
392	2	594	1940	gi|555014	UDP-N-acetyl muramate-alanine ligase (Bacillus subtilis) sp|P40778|MURC_BACSU UDP-N-ACETYLMURAMATE-ALANINE LIGASE (EC 6.3.2.8) (UDP-N- ACETYLMURANOYL-L-ALANINE SYNTHETASE)	77	65	1347
405	5	4079	3570	gi|1303912	YqhW (Bacillus subtilis)	77	64	510
487	4	1302	1472	gi|432427	ORF1 gene product (Acinetobacter calcoaceticus)	77	48	171
522	1	2	562	pir|A01179|SYHS	tyrosine--tRNA ligase (EC 6.1.1.1) - Bacillus stearothermophilus	77	61	561

S. aureus   Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
523	2	1587	1351	gi|1387979	44% identity over 302 residues with hypothetical protein from Synechocystis sp. accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subti]	77	48	237
536	2	983	612	gi|143366	adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	77	61	372
548	2	339	872	gi|143387	aspartate transcarbamylase [Bacillus subtilis]	77	56'	514
597	1	2	481	gi|904198	hypothetical protein [Bacillus subtilis]	77	73	480
633	2	1747	1313	gi|387577	ORF1A [Bacillus subti]	77	64	435
642	1	85	360	gi|46971	epiP gene product [Staphylococcus epidermidis]	77	61	276
659	1	125	1219	gi|1072381	glutamyl-aminopeptidase [Lactococcus lactis]	77	62	1095
670	4	1587	1820	gi|1122760	unknown [Bacillus subtilis]	77	58	234
789	1	2	391	gi|1377823	aminopeptidase [Bacillus subtilis]	77	65	390
815	1	10	573	gi|1303861	YqgN [Bacillus subtilis]	77	49	564
990	1	1	225	gi|1201M44	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	77	55	225
1083	1	3	188	gi|460828	B969 [Saccharomyces cerevisiae]	77	66	186
1942	1	415	209	gi|160047	p101/acidic basic repeat antigen [Plasmodium falciparum] pir|A29232|A29232 101k malaria antigen precursor - Plasmodium falciparum (strain Camp)	77	38	207
2559	1	1	171	gi|1499014	M. jannaschii predicted coding region MJ0255 [Methanococcus jannaschii]	77	61	171
2933	2	243	401	gi|42370	pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir|S01788|S01788 formate C-acetyltransferase (EC 2.3.1.54) - charichia coli	77	72	159
2966	1	56	292	gi|1524397	glycine betaine transporter OpuD [Bacillus subtilis]	77	45	237
2976	1	614	309	gi|40003	oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] p|P23129|ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE).	77	60	306
2979	2	678	400	gi|1204354	spore germination and vegetative growth protein [Haemophilus influenzae]	77	61	279
2988	1	601	377	gi|438465	Probable operon with orfF. Possible alternative initiation codon. Aas 2151-2153. Homology with acetyltransferases.; putative Bacillus subtilis]	77	55	225
2990	1	331	167	gi|142562	ATP synthase epsilon subunit [Bacillus megaterium] pir|B28599|PWBSEM H+- transporting ATP synthase (EC 3.6.1.34) psilon chain - Bacillus megaterium	77	63	165
3032	1	3	389	gi|468430	alcohol dehydrogenase 2 [Entamoeba histolytica]	77	56	387
3057	1	1	195	gi|468764	mocR gene product [Rhizobium meliloti]	77	50	195

TABLE 2

S aureus   Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4008	1	726	400	gi|603768	HutI protein, imidazolone-5-propionate hydrolase (Bacillus subtilis) gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis	77	52	327
4048	1	703	386	gi|216278	gramicidin S synthetase 1 (Bacillus brevis)	77	55	318
4110	1	3	368	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	77	61	366
4115	1	1	348	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus yogenes)	77	65	348
4225	1	590	297	gi|1322245	mevalonate pyrophosphate decarboxylase (Rattus norvegicus)	77	60	294
4611	2	494	327	gi|508979	GTP-binding protein (Bacillus subtilis)	77	57	168
466A	1	361	182	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	77	61	180
25	1	2	1627	gi|1150620	HmsA (Streptococcus pneumoniae)	76	58	1626
3A	5	1488	2537	pir|A3577|A435	regulatory protein pfoR - Clostridium perfringens	76	57	1050
52	5	2962	4041	gi|1161061	dioxygenase (Methylobacterium extorquens)	76	62	1080
56	20	27389	27955	gi|467402	unknown (Bacillus subtilis)	76	56	567
57	15	12046	12219	gi|1206040	weak similarity to keratin (Caenorhabditis elegans)	76	40	174
91	2	1062	2261	gi|475715	acetyl coenzyme A acetyltransferase (thiolase) (Clostridium cetobutylicum)	76	57	1200
9A	2	818	1624	gi|467422	unknown (Bacillus subtilis)	76	62	807
9A	5	2965	3228	gi|89793	y98 gene product (Pediococcus acidilactici)	76	52	264
98	8	5922	6326	gi|467427	methionyl-tRNA synthetase (Bacillus subtilis)	76	53	405
104	3	1322	1885	gi|216151	DNA polymerase (gene L; ttg start codon) (Bacteriophage SPO2] gi|579197 SPO2 DNA polymerase (aa 1-648) (Bacteriophage SPO2] pir|A21498|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage F02	76	63	564
124	9	8134	7055	gi|853776	peptide chain release factor 1 (Bacillus subtilis] pir|S55437|S55437 peptide chain release factor 1 - Bacillus subtilis	76	58	1080
164	5	2832	3311	gi|1204976	prolyl-tRNA synthetase (Haemophilus influenzae)	76	53	480
168	2	2617	1841	gi|1177251	putative ATP-binding protein of ABC-type (Bacillus subtilis)	76	58	777
189	2	163	888	gi|467384	unknown (Bacillus subtilis)	76	63	726
235	3	2253	3518	gi|142936	folyl-polyglutamate synthetase (Bacillus subtilis] pir|B40646|B40646 folC - Bacillus subtilis	76	53	1266
236	1	335	925	gi|1146197	putative (Bacillus subtilis)	76	54	591
237	8	5323	5541	gi|1279261	F13G3.6 (Caenorhabditis elegans)	76	47	219

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
263	5	5490	4585	gi|1510348	[dihydrodipicolinate synthase (Methanococcus jannaschii]	76	49	906
304	3	1051	1794	gi|666982	putative membrane spanning subunit [Bacillus subtilis] pir|S52182|S52182 probable membrane spanning protein - Bacillus subtilis	76	60	744
312	4	3611	4624	gi|143312	6-phospho-1-fructokinase (gtg start codon; EC 2.7.1.11) [Bacillus tearothermophilus]	76	56	1014
343	1	2	1016	gi|405956	[yeaE (Escherichia coli]	76	59'	1035
347	1	409	1701	gi|396304	acetylornithine deacetylase [Escherichia coli]	76	72	1293
358	1	672	1907	gi|1146215	39.0% identity to the Escherichia coli S1 ribosomal protein; putative [Bacillus subtilis]	76	58	1236
371	1	1	222	gi|537084	alternate gene name mgt; CG Site No. 497 (Escherichia coli] pir|S56468|S56468 mgtA protein - Escherichia coli	76	61	222
379	4	4331	4858	gi|143268	dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) [Bacillus subtilis]	76	61	528
404	5	4022	4492	gi|303823	[yqfG [Bacillus subtilis]	76	60	471
411	1	2	307	gi|186025	ORF YKL027w [Saccharomyces cerevisiae]	76	55	306
472	3	4356	2854	gi|1405464	AlsT [Bacillus subtilis]	76	57	1503
546	1	273	995	gi|153821	streptococcal pyrogenic exotoxin type C (speC) precursor Streptococcus pyogenes]	76	36	723
588	1	1054	557	gi|1002520	MutS [Bacillus subtilis]	76	61	498
591	1	16	735	gi|885934	ClpB [Synechococcus sp.]	76	44	720
602	2	175	798	gi|1486422	OppD homologue [Rhizobium sp.]	76	52	624
619	2	547	290	gi|330613	major capsid protein [Human cytomegalovirus]	76	47	258
660	4	2568	3302	gi|904199	hypothetical protein [Bacillus subtilis]	76	55	735
677	1	452	228	gi|40177	spoOF gene product [Bacillus subtilis]	76	58	225
962	1	24	206	gi|142443	adenylosuccinate synthetase [Bacillus subtilis] sp|29726|PURA_BACSU ADENYLOSUCCINATE SYNTHETASE (EC 6.3 4.4) IMP-ASPARTATE LIGASE).	76	67	183
978	1	1158	580	gi|1511333	M. jannaschii predicted coding region MJ1322 [Methanococcus jannaschii]	76	56	579
997	1	486	244	gi|1467154	No definition line found [Mycobacterium leprae]	76	38	243
1563	1	529	266	gi|1303984	YqkG [Bacillus subtilis]	76	52	264
2184	1	361	182	gi|506706	CapJ [Staphylococcus aureus]	76	38	180
2572	1	1	387	gi|153898	transport protein [Salmonella typhimurium]	76	65	387

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
2942	1	29	400	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	76	?9	372
2957	1	377	216	gi|511251	hypothetical protein (SP:P42604) [Methanococcus jannaschii]	76	47	162
2980	1	554	279	gi|1405464	AlsT [Bacillus subtilis]	76	53	276
3015	1	649	326	gi|408115	ornithine acetyltransferase [Bacillus subtilis]	76	61	324
3124	1	13	174	gi|882705	ORF_o401 [Escherichia coli]	76	65*	162
3179	1	3	161	gi|164477	ferredoxin-dependent glutamate synthase [Zea mays] pir|A38596|A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - alze	76	53	159
3789	1	2	379	gi|39956	IIGlc [Bacillus subtilis]	76	55	378
3892	1	3	314	gi|1510398	ferripyochelin binding protein [Methanococcus jannaschii]	76	52	312
3928	1	798	400	gi|143016	permease [Bacillus subtilis]	76	59	399
4159	1	757	386	sp|P80544|MRSP_	METHICILLIN-RESISTANT SURFACE PROTEIN (FRAGMENTS)	76	66	372
4204	1	17	331	gi|296464	ATPase [Lactococcus lactis]	76	56	315
4398	1	494	249	gi|987255	Menkes disease gene [Homo sapiens]	76	48	246
4506	1	2	313	gi|216746	D-lactate dehydrogenase [Lactobacillus plantarum]	76	47	312
4546	1	477	247	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	76	61	231
4596	1	379	191	gi|560027	cellulose synthase [Acetobacter xylinum]	76	70	189
4	5	5257	4337	gi|882532	ORF_o294 [Escherichia coli]	75	59	921
6	1	164	952	gi|40960	OTCase [Escherichia coli]	75	56	789
12	3	5935	3944	gi|467336	unknown [Bacillus subtilis]	75	57	1992
23	1A	18272	17310	gi|1296433	O-acetylserine sulfhydrylase B [Alcaligenes eutrophus]	75	55	963
25	3	2356	3393	gi|1502419	PlsX [Bacillus subtilis]	75	56	1038
36	8	5765	6037	gi|1256517	unknown [Schizosaccharomyces pombe]	75	45	273
46	13	11486	12058	gi|48972	nitrate transporter [Synechococcus sp.]	75	46	873
51	7	3474	3677	gi|143607	sporulation protein [Bacillus subtilis]	75	61	204
53	16	16850	16590	gi|143402	recombination protein (ttg start codon), [Bacillus subtilis] gi|1303923 RecN [Bacillus subtilis]	75	51	261
74	3	3572	2568	gi|1204847	ornithine carbamoyltransferase [Haemophilus influenzae]	75	61	1005

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
85	3	4628	3930	gi|143368	phosphoribosylformyl glycinamidine synthetase I (PUR-L; gtg start codon) [Bacillus subtilis]	75	63	699
85	5	5588	4878	gi|143367	phosphoribosyl aminoidazole succinocarboxamide synthetase (PUR-C; tg start codon) [Bacillus subtilis]	75	55	711
85	8	6625	7530	gi|1303916	YqiA [Bacillus subtilis]	75	53	906
87	3	2340	3590	gi|1064813	homologous to sp:PHOR_BACSU [Bacillus subtilis]	75	56	1251
87	6	6084	6896	gi|1064810	function unknown [Bacillus subtilis]	75	61	813
108	2	1844	1503	gi|1001824	hypothetical protein [Synechocystis sp.]	75	51	342
110	3	1748	3727	gi|1147593	putative ppGpp synthetase [Streptomyces coelicolor]	75	55	1980
110	7	4151	5252	gi|117/251	clwD gene product [Bacillus subtilis]	75	75	900
120	14	11266	10649	gi|1524394	ORF-2 upstream of gbsAB operon [Bacillus subtilis]	75	55	618
121	5	2050	4221	gi|1154632	NrdE [Bacillus subtilis]	75	54	2172
124	1	283	143	gi|405622	unknown [Bacillus subtilis]	75	56	141
128	1	81	1139	gi|143316	[gap] gene products [Bacillus megaterium]	75	48	1059
130	8	5760	5903	gi|1256654	54.8% identity with Neisseria gonorrhoeae regulatory protein PilB; putative [Bacillus subtilis]	75	62	144
136	2	4480	3185	gi|467403	seryl-tRNA synthetase [Bacillus subtilis]	75	54	1296
161	10	5439	5798	gi|1001195	hypothetical protein [Synechocystis sp.]	75	55	360
172	4	3819	2995	gi|755153	ATP-binding protein [Bacillus subtilis]	75	52	825
179	1	2024	1107	gi|143037	porphobilinogen deaminase [Bacillus subtilis]	75	58	918
195	10	9529	9174	sp|P25745|YCFH_	HYPOTHETICAL PROTEIN IN PURB 5'REGION (ORF-15) (FRAGMENT).	75	60	156
200	4	2605	4596	gi|142440	ATP-dependent nuclease [Bacillus subtilis]	75	56	1992
206	3	6900	5620	gi|1256135	YbbF [Bacillus subtilis]	75	53	1281
216	2	159	389	gi|1052600	unknown [Schizosaccharomyces pombe]	75	58	231
229	1	29	847	gi|1205958	branched chain aa transport system II carrier protein [Haemophilus influenzae]	75	49	819
230	2	518	1714	gi|971337	nitrite extrusion protein [Bacillus subtilis]	75	53	1197
231	1	2240	1122	gi|1002521	MutL [Bacillus subtilis]	75	54	1119
233	3	1314	1859	gi|467405	unknown [Bacillus subtilis]	75	59	546

TABLE 2

S. aureus : Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
269	1	325	164	gi|1511246	methyl coenzyme M reductase system, component A2 [Methanococcus jannaschii]	75	50	162
292	1	1369	772	gi|1511604	M. jannaschii predicted coding region MJ1651 [Methanococcus jannaschii]	75	46	618
304	4	1773	2261	gi|1205328	surfactin [Haemophilus influenzae]	75	55	489
312	3	2417	3387	gi|285621	undefined open reading frame [Bacillus stearothermophilus]	75	62	951
312	5	4622	6403	gi|1041097	Pyruvate kinase [Bacillus psychrophilus]	75	57'	1782
319	1	353	877	gi|1212728	Yqhi [Bacillus subtilis]	75	54	525
320	5	4321	5031	gi|1070361	OMP decarboxylase [Lactococcus lactis]	75	56	711
320	6	5010	5642	gi|143394	OMP-PRPP transferase [Bacillus subtilis]	75	60	633
337	4	1519	2088	gi|487433	citrate synthase II [Bacillus subtilis]	75	58	570
394	2	669	1271	gi|304976	matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to longation factor G, TetM/TetO tetracycline-resistance proteins Escherichia coli]	75	51	603
423	1	127	570	gi|1183839	unknown [Pseudomonas aeruginosa]	75	59	444
433	2	1603	1929	gi|149211	acetolactate synthase [Klebsiella pneumoniae]	75	63	327
446	2	176	1540	gi|312241	dihydroorotase [Bacillus caldolyticus]	75	62	1365
446	1	494	249	gi|1149682	potF gene product [Clostridium perfringens]	75	55	246
496	1	3	794	gi|143582	spoIIIEA protein [Bacillus subtilis]	75	59	792
498	2	824	1504	gi|143324	phoP protein (put.); putative [Bacillus subtilis]	75	47	681
499	2	1061	1624	gi|1387979	44% identity over 302 residues with hypothetical protein from Synechocystis sp. accession D64006.CD: expression induced by environmental stress: some similarity to glycosyl transferases: two potential membrane-spanning helices [Bacillus subtil]	75	51	564
568	1	641	453	ptr|JC4110|JC41	triacylglycerol lipase (EC 3.1.1.3) 2 - Mycoplasma mycoides subsp. mycoides (SGC3)	75	50	189
613	2	430	233	gi|330993	tegument protein [Saimiriine herpesvirus 2]	75	75	198
621	1	1	525	gi|529754	speC [Streptococcus pyogenes]	75	43	525
642	5	1809	2474	gi|1176401	EpiG [Staphylococcus epidermidis]	75	51	666
646	2	454	657	gi|172442	ribonuclease P [Saccharomyces cerevisiae]	75	37	204
657	1	3	347	gi|882561	ORF_o236 [Escherichia coli]	75	47	345
750	1	1662	832	gi|46971	epiP gene product [Staphylococcus epidermidis]	75	57	831

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
754	1	2	481	gi|1103901	YqhT [Bacillus subtilis]	75	57	480
763	2	563	393	gi|1205145	multidrug resistance protein [Haemophilus influenzae]	75	51	171
775	1	961	482	pir|B36889|B36B	leuA protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)	75	63	480
793	1	1	180	gi|143316	[gap] gene products [Bacillus megaterium]	75	57	180
800	1	318	160	gi|509411	NFRA protein [Azorhizobium caulinodans]	75	34'	159
811	1	1117	560	gi|143434	Rho Factor [Bacillus subtilis]	75	60	558
940	1	493	329	gi|1276985	arginase [Bacillus caldovelox]	75	50	165
971	2	37	252	gi|1001373	hypothetical protein [Synechocystis sp.]	75	58	216
1059	1	384	232	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis]	75	67	153
1109	2	219	374	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	75	53	156
126R	1	271	137	gi|304135	ornithine acetyltransferase [Bacillus stearothermophilus] sp|Q07908|ARGJ_BACST GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) ORNITHINE ACETYLTRANSFERASE) (ORNITHINE TRANSACETYLASE) (OATASE) / MINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1) (N-ACETYLGLUTAMATE YNTHA	75	63	135
1500	1	324	163	gi|1205488	excinuclease ABC subunit B [Haemophilus influenzae]	75	57	162
1529	1	798	400	gi|1002521	MutL [Bacillus subtilis]	75	54	399
3010	1	770	387	gi|1204435	pyruvate formate-lyase activating enzyme [Haemophilus influenzae]	75	54	384
3105	1	1	180	gi|1041097	Pyruvate kinase [Bacillus psychrophilus]	75	57	180
3117	2	45	212	gi|899117	peptide synthetase module [Microcystis aeruginosa] pir|S49111|S49111 probable amino acid activating domain - icrocystis aeruginosa (fragment) (SUB 144-528)	75	42	168
3139	2	139	345	gi|145294	adenine phosphoribosyl-transferase [Escherichia coli]	75	66	207
3880	1	618	310	gi|1009366	[Respiratory nitrate reductase [Bacillus subtilis]	75	58	309
3911	1	48	401	gi|433991	ATP synthase subunit beta [Bacillus subtilis]	75	68	354
3957	1	2	379	pir|D36889|D36R	3-isopropylmalate dehydratase (EC 4.2.1.33) chain leuC - Lactococcus lactis subsp. lactis (strain IL1403)	75	65	378
4005	1	5	259	gi|216746	D-lactate dehydrogenase [Lactobacillus plantarum]	75	48	255
4080	1	73	333	gi|415855	deoxyribose aldolase [Mycoplasma hominis]	75	59	261

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4111	1	1	339	gi|49435	putative (Lactococcus lactis)	75	57	339
4136	1	602	301	gi|430688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	75	56	300
4144	1	658	336	gi|48972	nitrate transporter (Synechococcus sp.)	75	49	333
4237	1	664	374	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	75	55'	291
4306	2	73	318	gi|294260	major surface glycoprotein (Pneumocystis carinii)	75	6A	246
4343	1	715	359	gi|1204652	methylated-DNA - protein-cysteine methyltransferase (Haemophilus influenzae)	75	52	357
4552	1	620	312	gi|296464	ATPase (Lactococcus lactis)	75	55	309
38	9	5776	6126	gi|441793	NupC (Escherichia coli)	74	50	351
50	8	6910	6221	gi|1239988	hypothetical protein (Bacillus subtilis)	74	55	690
56	9	10770	12221	gi|1000451	TreP (Bacillus subtilis)	74	57	1452
64	2	2266	1622	gi|41015	aspartate-tRNA ligase (Escherichia coli)	74	57	645
66	6	5063	4848	gi|1212729	YqhJ (Bacillus subtilis)	74	47	216
67	18	14334	14897	gi|1510631	endoglucanase (Methanococcus jannaschii)	74	52	564
102	15	12561	13136	gi|149429	putative (Lactococcus lactis)	74	67	576
102	16	13121	14419	gi|149435	putative (Lactococcus lactis)	74	57	1299
108	4	4873	3902	gi|39478	ATP binding protein of transport ATPases (Bacillus firmus) lr|S15406|S15406 ATP-binding protein - Bacillus firmus p|P26946|YATR_BACFI HYPOTHETICAL ATP-BINDING TRANSPORT PROTEIN.	74	59	972
116	5	8574	7093	gi|1205430	dipeptide transport system permease protein (Haemophilus influenzae)	74	49	1482
120	7	4342	4803	gi|146970	ribonucleoside triphosphate reductase (Escherichia coli) pir|A67331|A67331 anaerobic ribonucleotide reductase - Escherichia oli	74	58	462
121	7	5961	6581	gi|1107528	ttg start (Campylobacter coli)	74	51	621
128	3	2320	3531	gi|143318	phosphoglycerate kinase (Bacillus megaterium)	74	57	1212
130	7	5237	5791	gi|1256653	DNA-binding protein (Bacillus subtilis)	74	60	555
136	3	6745	5150	gi|143076	histidase (Bacillus subtilis)	74	58	1596
145	2	664	1368	gi|407773	devA gene product (Anabaena sp.)	74	45	705
152	1	552	277	gi|1377833	unknown (Bacillus subtilis)	74	54	276

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
164	10	11064	11375	gi|580900	ORF3 gene product [Bacillus subtilis]	74	52	312
175	2	3109	2624	gi|642656	unknown [Rhizobium meliloti]	74	34	486
175	9	6064	5612	gi|854656	Na/H antiporter system ORF2 [Bacillus alcalophilus]	74	46	453
195	11	11346	10339	gi|1204430	hypothetical protein (SP:P25745) [Haemophilus influenzae]	74	55	1008
205	17	9619	9059	gi|1044979	ribosomal protein L6 [Bacillus subtilis]	74	64	561
216	7	5574	6710	gi|1146207	putative [Bacillus subtilis]	74	63	1137
241	3	4521	3334	gi|694121	malate thiokinase [Methylobacterium extorquens]	74	52	1188
246	6	3305	2799	gi|467374	single strand DNA binding protein [Bacillus subtilis]	74	64	507
249	4	6551	5313	gi|1524397	glycine betaine transporter OpuD [Bacillus subtilis]	74	55	1239
261	7	4389	4081	gi|809542	CbrB protein [Erwinia chrysanthemi]	74	42	309
278	6	5714	4665	gi|1204872	ATP-binding protein [Haemophilus influenzae]	74	54	1050
309	1	1220	666	gi|1205579	hypothetical protein (GB:U14003_102) [Haemophilus influenzae]	74	53	555
315	2	1473	862	gi|143398	quinol oxidase [Bacillus subtilis]	74	57	612
320	1	1	1065	gi|143389	glutaminase of carbamyl phosphate synthetase [Bacillus subtilis] pir|E39845|E39845 carbamoyl-phosphate synthase glutamine-hydrolyzing) (EC 6.3.5.5), pyrimidine-repressible, small hain - Bacillus subtilis	74	60	1065
380	2	382	1128	gi|534657	ATPase subunit a [Bacillus stearothermophilus]	74	56	747
405	2	1742	1311	gi|1303915	YqhZ [Bacillus subtilis]	74	65	432
433	5	2503	3270	gi|473902	alpha-acetolactate synthase [Lactococcus lactis]	74	56	768
452	1	1	942	gi|411982	ipa-58r gene product [Bacillus subtilis]	74	52	942
461	1	3	1193	gi|558494	homoserine dehydrogenase [Bacillus subtilis]	74	51	1191
461	2	1174	1407	gi|40211	threonine synthase (thrC) (AA 1-352) [Bacillus subtilis] ir|A25364|A25364 threonine synthase (EC 4.2.99.2) - Bacillus btilis	74	56	234
462	2	402	734	gi|142520	thioredoxin [Bacillus subtilis]	74	62	333
478	1	574	320	gi|1499005	glycyl-tRNA synthetase [Methanococcus jannaschii]	74	52	255
501	2	739	1740	gi|217040	acid glycoprotein [Streptococcus pyogenes]	74	58	1002
551	2	4083	2791	gi|143040	glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus subtilis] pir|D42728|D42728 glutamate-1-semialdehyde 2,1-aminomutase (EC .4.3.8) - Bacillus subtilis	74	51	1293

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
571	1	1	477	gi|1006605	hypothetical protein (Synechocystis sp.)	74	45	477
596	2	1780	1298	gi|1301853	YqgF (Bacillus subtilis)	74	55	483
618	2	2924	1758	gi|1146237	21.4% of identity to trans-acting transcription factor of Sacharomyces ceraviaie; 25% of identity to sucrose synthase of Zea mays; putative (Bacillus subtilis)	74	55	1167
659	2	1269	1595	gi|1072380	ORF3 (Lactococcus lactis)	74	62	327
724	1	373	188	gi|143374	phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) Bacillus subtilis)	74	58	186
743	2	604	1209	gi|153833	ORF1; putative (Streptococcus parasanguis)	74	50	606
836	1	2	259	gi|143458	ORF V (Bacillus subtilis)	74	47	258
989	2	443	724	gi|1303994	YqkM (Bacillus subtilis)	74	46	282
1106	1	1	492	gi|46970	epiD gene product (Staphylococcus epidermidis)	74	54	492
1135	2	373	528	gi|41948	ipa-24d gene product (Bacillus subtilis)	74	48	156
1234	1	417	352	gi|495245	recJ gene product (Erwinia chrysanthemi)	74	36	366
2586	1	2	238	gi|1149701	abcC gene product (Clostridium perfringens)	74	62	237
2959	1	798	400	gi|1405454	aconitase (Bacillus subtilis)	74	60	399
2962	1	650	363	gi|450686	3-phosphoglycerate kinase (Thermotoga maritima)	74	58	288
2983	1	3	191	gi|1303893	YqhL (Bacillus subtilis)	74	56	189
3018	1	2	223	gi|143040	glutamate-1-semialdehyde 2.1-aminotransferase (Bacillus subtilis) pir|D42728|D42728 glutamate-1-semialdehyde 2,1-aminomutase (EC 4.3.8) - Bacillus subtilis	74	56	222
3038	1	510	256	pir|SS2915|SS29	nitrate reductase alpha chain - Bacillus subtilis (fragment)	74	57	255
3062	1	374	189	gi|1107528	ttg start (Campylobacter coli)	74	51	186
4035	1	184	360	gi|1022725	unknown (Staphylococcus haemolyticus)	74	64	177
4045	1	607	305	gi|1510977	M. jannaschii predicted coding region MJ0938 (Methanococcus jannaschii)	74	41	303
42A3	1	471	304	gi|520844	orf4 (Bacillus subtilis)	74	58	168
4449	1	3	221	gi|580910	peptide-synthetase ORF1 (Bacillus subtilis)	74	54	219
4587	1	458	231	gi|1170207	orf6 (Lactobacillus sake)	74	59	228

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4603	1	29	214	gi|146208	glutamate synthase large subunit (EC 2.6.1.53) (Escherichia coli) pir|A29617|A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large hain - Escherichia coli	74	60	186
4670	1	366	184	gi|256115	YbbF [Bacillus subtilis]	74	61	183
5	10	7953	7162	gi|143727	putative [Bacillus subtilis]	73	42	792
11	2	2454	1372	gi|166338	dihydroorotate dehydrogenase [Agrocybe aegerita]	73	55	1083
14	1	2024	1020	gi|143373	phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H[J] Bacillus subtilis]	73	54	1005
21	5	5426	4635	gi|1468939	meso-2,3-butanediol dehydrogenase (D-acetoin forming) [Klebsiella pneumoniae]	73	58	792
23	17	17379	16360	gi|297060	ornithine cyclodeaminase [Rhizobium meliloti]	73	37	1020
29	2	692	1273	gi|467442	stage V sporulation [Bacillus subtilis]	73	54	582
31	5	6467	4914	gi|414000	ipa-76d gene product [Bacillus subtilis]	73	55	1554
37	8	8658	7402	gi|429259	pepT gene product [Bacillus subtilis]	73	59	1257
37	9	7738	7562	gi|168367	alpha-isopropylmalate isomerase (put.); putative [Rhizomucor ircinelloides]	73	52	177
38	7	3931	4896	gi|405885	yeiN [Escherichia coli]	73	58	966
44	6	5041	4238	gi|5H0895	unknown [Bacillus subtilis]	73	53	804
44	11	7767	8306	gi|42009	moaB gene product [Escherichia coli]	73	50	540
45	3	2439	3080	gi|1109685	ProW [Bacillus subtilis]	73	47	642
54	13	14036	13794	gi|413931	ipa-7d gene product [Bacillus subtilis]	73	61	243
59	4	1430	2248	gi|147921	threonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]	73	53	819
65	1	1458	730	gi|677944	AppF [Bacillus subtilis]	73	56	729
80	2	1375	860	gi|580932	murD gene product [Bacillus subtilis]	73	53	516
102	13	10124	11179	gi|580891	3-isopropylmalate dehydrogenase (AA 1 - 365) [Bacillus subtilis] pir|A26522|A26522 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - acillus subtilis	73	55	1056
109	2	3493	2600	gi|1510849	M. jannaschii predicted coding region MJ0775 [Methanococcus jannaschii]	73	40	894
120	8	4782	5756	gi|146970	ribonucleoside triphosphate reductase [Escherichia coli] pir|A47331|A47331 anaerobic ribonucleotide reductase - Escherichia oli	73	56	975
120	9	5726	6223	gi|1204333	anaerobic ribonucleoside-triphosphate reductase [Haemophilus influenzae]	73	62	498

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S aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
132	5	4151	4363	gi|871048	HPSH2 - heavy chain potential motor protein (Giardia intestinalis)	73	43	213
140	6	5952	4324	gi|634107	kdpB (Escherichia coli)	73	59	1629
142	6	7060	5939	gi|410125	rluC gene product (Bacillus subtilis)	73	57	1122
149	4	1866	1717	gi|460892	heparin binding protein-44, HBP-44 [mice, Peptide, 360 aa] pir|JX0281|JX0281 heparin-binding protein-44 precursor - mouse gi|220434 ORF [Mus musculus] (SUB 2-360)	73	53	150
158	1	1	1431	gi|882504	ORF_f560 (Escherichia coli)	73	57	1431
174	6	5352	4525	gi|1146240	ketopantoate hydroxymethyltransferase (Bacillus subtilis)	73	55	828
175	H	5537	5178	gi|854657	Na/H antiporter system ORF3 (Bacillus alcalophilus)	73	56	360
186	5	6593	5493	gi|467477	unknown (Bacillus subtilis)	73	48	1101
249	6	6281	5729	gi|1524397	glycine betaine transporter OpuD (Bacillus subtilis)	73	56	555
265	4	1873	2280	gi|39848	U3 (Bacillus subtilis)	73	41	408
270	1	328	582	gi|780461	220 kDa polyprotein (African swine fever virus)	73	53	255
278	4	4283	3618	gi|1204965	hypothetical 23.3 kd protein (Escherichia coli)	73	49	666
279	3	4984	3593	gi|1185288	isochorismate synthase (Bacillus subtilis)	73	58	1392
291	4	1207	1575	gi|1511440	glutamine-fructose-6-phosphate transaminase (Methanococcus jannaschii)	73	63	369
229	2	735	1166	gi|467437	unknown (Bacillus subtilis)	73	58	432
299	5	2050	3234	gi|467439	temperature sensitive cell division (Bacillus subtilis)	73	53	1185
334	1	1237	728	gi|536655	ORF YBR244w (Saccharomyces cerevisiae)	73	43	510
336	2	1827	1036	gi|790943	urea amidolyase (Bacillus subtilis)	73	51	792
374	3	1389	1874	gi|1405451	YmeJ (Bacillus subtilis)	73	55	486
433	4	1916	2554	gi|473902	alpha-acetolactate synthase (Lactococcus lactis)	73	54	639
509	2	1795	1028	gi|467483	unknown (Bacillus subtilis)	73	56	768
513	1	1709	918	gi|1146220	NAD· dependent glycerol-3-phosphate dehydrogenase (Bacillus subtilis)	73	56	792
533	2	239	733	gi|1510605	hypothetical protein (SP:P42297) (Methanococcus jannaschii)	73	44	495
546	2	1148	2815	gi|41748	hmdM protein (AA 1-520) (Escherichia coli)	73	52	1668
549	1	762	382	gi|1314847	CinA (Bacillus subtilis)	73	57	381
567	1	1346	675	gi|410137	ORFX13 (Bacillus subtilis)	73	58	672

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
716	2	654	1112	gi|1256623	exodeoxyribonuclease [Bacillus subtilis]	73	56	459
772	1	3	677	gi|142010	Shows 70.2% similarity and 48.6% identity to the EnvH protein of almonella typhimurium [Anabaena sp.]	73	57	675
774	1	3	209	gi|409286	bmrU [Bacillus subtilis]	73	52	207
782	1	1	402	gi|143320	|gap| gene products [Bacillus megaterium]	73	56	402
789	2	451	762	gi|1063246	low homology to P14 protein of Heamophilus influenzar and 14.2 kDa protein of Escherichia coli [Bacillus subtilis]	73	56	312
796	1	3	911	gi|853754	ABC transporter [Bacillus subtilis]	73	58	909
806	3	1209	949	gi|143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis] plr|JT0481|WBS tryptophan-tRNA ligase (EC 6.1.1.2) - Bacillus subtilis	73	51	261
816	2	4839	3097	gi|41748	hsdM protein (AA 1-520) [Escherichia coli]	73	52	1743
839	1	798	400	gi|886906	argininosuccinate synthetase [Streptomyces clavuligerus] plr|S57659|S57659 - streptomyces clavuligerus argininosuccinate synthase (EC 6.3.4.5)	73	59	399
857	1	3	290	gi|348052	acetoin utilization protein [Bacillus subtilis]	73	50	288
1008	1	790	398	gi|40100	rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] 1r|S06049|S06049 rodC protein - Bacillus subtilis p|P13485|TAGF_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F.	73	41	393
1018	1	1	213	gi|529357	No definition line found (Caenorhabditis elegans) sp|P46975|STT3_CAEEL OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT OMOLOG.	73	53	213
1011	1	3	491	gi|142706	comG1 gene product [Bacillus subtilis]	73	61	489
1174	1	395	204	gi|1149513	alpha3a subunit of laminin 5 [Homo sapiens]	73	60	192
1175	1	655	329	gi|473817	'ORF' [Escherichia coli]	73	57	327
1187	1	3	209	gi|580870	ipa-37d qoxA gene product [Bacillus subtilis]	73	52	207
1206	1	72	245	gi|144816	formyltetrahydrofolate synthetase (FTHFS) (ttg start codon) (EC .3.4.3) [Neorella thermoacetica]	73	43	174
1454	1	423	241	gi|1213253	unknown [Schizosaccharomyces pombe]	73	53	183
1469	1	517	260	gi|1303787	YqeG [Bacillus subtilis]	73	55	258
1761	1	374	189	gi|9135	Mst26Aa gene product [Drosophila simulans]	73	34	186
1849	1	467	243	gi|162307	DNA topoisomerase II [Trypanosoma cruzi]	73	60	225
2055	1	2	400	gi|559381	P47K protein [Rhodococcus erythropolis]	73	34	199
2556	1	2	244	gi|145925	fecB [Escherichia coli]	73	62	243

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S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
2947	2	549	400	gi|1184680	polynucleotide phosphorylase (Bacillus subtilis)	73	51	150
2956	1	746	375	gi|143397	quinol oxidase (Bacillus subtilis)	73	58	372
3017	1	655	329	gi|143091	acetolactate synthase (Bacillus subtilis)	73	55	327
3115	1	385	194	gi|323866	overlapping out-of-phase protein (Eggplant mosaic virus) sp|P20129|V70K_EMV 70 KD PROTEIN.	73	53	192
3603	2	700	527	gi|1419521	glutaryl-CoA dehydrogenase precursor (Mus musculus)	73	48	174
3743	1	798	400	gi|450688	hsdM gene of Ecoprl gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	73	54	399
3752	1	640	359	gi|1524193	unknown (Mycobacterium tuberculosis)	73	59	282
3852	1	2	181	gi|216746	D-lactate dehydrogenase (Lactobacillus plantarum)	73	68	180
3914	1	475	239	pir|S13490|S134	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Chicken (fragment)	73	53	237
3914	2	570	343	gi|528991	unknown (Bacillus subtilis)	73	38	228
4069	1	2	316	gi|40003	oxoglutarate dehydrogenase (NADP+) (Bacillus subtilis) pir|P23129|ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).	73	55	315
4165	1	715	365	gi|1419521	glutaryl-CoA dehydrogenase precursor (Mus musculus)	73	48	351
4196	1	1	177	gi|809660	deoxyribose-phosphate aldolase (Bacillus subtilis) pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - Bacillus subtilis	73	60	177
4202	1	572	378	gi|528991	unknown (Bacillus subtilis)	73	38	195
4314	1	2	193	gi|435797	N-acyl-L-amino acid amidohydrolase (Bacillus stearothermophilus) sp|P37112|AMA_BACST N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC .5.1.14) (AMINOACYLASE).	73	47	192
4393	1	3	263	gi|216267	ORF2 (Bacillus megaterium)	73	47	261
35	2	903	1973	gi|1146196	phosphoglycerate dehydrogenase (Bacillus subtilis)	72	53	1071
38	22	19094	17877	(c 602031	similar to trimethylamine DH (Mycoplasma capricolum) pir|S49950|S49950 probable trimethylamine dehydrogenase (EC .5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	72	54	1218
38	23	18134	19162	gi|413968	lpa-44d gene product (Bacillus subtilis)	72	54	1029
44	19	11895	12953	gi|516272	unknown (Bacillus subtilis)	72	49	1059
48	7	6240	7117	gi|43459	pyruvate synthase (Halobacterium halobium)	72	49	870
50	7	6563	5691	gi|1205399	proton glutamate symport protein (Haemophilus influenzae)	72	53	873

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
53	9	10521	9259	gi|1303956	YqjE [Bacillus subtilis]	72	52	1263
56	21	29549	29995	gi|467471	unknown [Bacillus subtilis]	72	47	447
69	4	5298	4123	gi|1354775	pfoS/R [Treponema pallidum]	72	46	1176
69	5	4377	4982	gi|904198	hypothetical protein [Bacillus subtilis]	72	43	606
73	1	2	856	gi|142997	glycerol uptake facilitator [Bacillus subtilis]	72	59	855
98	13	9371	10258	gi|467435	unknown [Bacillus subtilis]	72	50	888
127	1	1	1593	gi|217144	alanine carrier protein (thermophilic bacterium PS3) pir|A45111|A45111 alanine transport protein - thermophilic acterium PS-3	72	56	1593
131	1	5197	2600	gi|153952	polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] pir|A45915|A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III lpha chain - Salmonella typhimurium	72	53	2598
141	4	1040	1978	gi|1405446	transketolase [Bacillus subtilis]	72	54	939
149	8	2819	2535	gi|606234	secY [Escherichia coli]	72	44	285
149	17	5472	5245	gi|1304472	DNA polymerase [Unidentified phycodnavirus clone OTU6]	72	55	228
154	1	1	210	gi|1205620	ferritin like protein [Haemophilus influenzae]	72	40	210
155	1	2207	1320	gi|391610	farnesyl diphosphate synthase [Bacillus stearothermophilus] pir|JX0257|JX0257 geranyltranstransferase (EC 2.5.1.10) - Bacillus taarothermophilus	72	57	888
180	1	2	328	gi|133630	A18O (Saccharomyces cerevisiae)	72	62	327
184	3	1145	3553	gi|1205110	virulence associated protein homolog [Haemophilus influenzae]	72	49	2409
195	2	1923	1279	gi|1001730	hypothetical protein [Synechocystis sp.]	72	45	645
206	13	14646	15869	gi|1064807	ORNITHINE AMINOTRANSFERASE [Bacillus subtilis]	72	50	1224
209	2	462	932	gi|1204666	hypothetical protein (GB:X73124_53) [Haemophilus influenzae]	72	60	471
215	2	764	522	gi|881513	insulin receptor homolog [Drosophila melanogaster] pir|SS7245|SS7245 insulin receptor homolog - fruit fly (Drosophila elanogaster) (SUB 46-2146)	72	63	243
224	1	2	790	gi|949974	sucrose repressor [Staphylococcus xylosus]	72	54	789
233	1	1526	765	gi|1408493	homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	72	52	762
240	1	220	1485	gi|537049	ORF_o470 [Escherichia coli]	72	52	1266
245	1	3	1340	gi|1204578	hypothetical protein (GB:U06949_1) [Haemophilus influenzae]	72	46	1338

TABLE 2

S aureus : Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
259	2	2108	1245	gi|1340128	ORF1 [Staphylococcus aureus]	72	59	864
104	2	285	1094	gi|1205330	glutamine-binding periplasmic protein [Haemophilus influenzae]	72	52	810
107	10	5326	5039	gi|1070015	protein-dependent [Bacillus subtilis]	72	53	288
315	1	517	260	gi|143399	quinol oxidase [Bacillus subtilis]	72	55	258
116	11	9622	9308	gi|1204445	hypothetical protein (SP:P27857) [Haemophilus influenzae]	72	52	315
337	3	926	1609	gi|467433	citrate synthase II [Bacillus subtilis]	72	55	684
164	7	12538	10493	gi|1510643	ferrous iron transport protein B [Methanococcus jannaschii]	72	53	2046
409	2	340	1263	gi|1402944	orfRM1 gene product [Bacillus subtilis]	72	49	924
441	3	2177	1590	gi|312379	highly conserved among eubacteria [Clostridium acetobutylicum] pir|S34312|S34312 hypothetical protein v - Clostridium cetobutylicum	72	48	588
453	6	2654	2505	pir|S00601|BXSA	antibacterial protein 3 - Staphylococcus haemolyticus	72	70	150
460	1	2	625	gi|1016162	ABC transporter subunit [Cyanophora paradoxa]	72	51	624
463	1	3253	1628	gi|666014	The polymorphism (RFLP) of this gene is associated with usceptibility to essential hypertension. The SA gene product has light homology to acetyl-CoA synthetase [Homo sapiens]	72	60	1626
480	4	3047	3466	gi|433992	ATP synthase subunit epsilon [Bacillus subtilis]	72	53	420
502	1	1086	586	gi|1310859	ORF2 [Synechococcus sp.]	72	50	501
519	1	81	1184	gi|1303704	yrkE [Bacillus subtilis]	72	54	1104
559	1	3	746	gi|1107530	ceuD gene product [Camylobacter coli]	72	56	744
575	1	1142	573	gi|1303866	Yqgs [Bacillus subtilis]	72	56	570
671	1	2	592	gi|1204497	protein-export membrane protein [Haemophilus influenzae]	72	44	591
679	2	295	1251	gi|563358	virulence-associated protein E [Dichelobacter nodosus]	72	52	957
687	2	295	957	gi|1144214	44% identical amino acids with the Escherichia coli smba supress; putative [Bacillus subtilis]	72	49	663
837	1	1	435	gi|1146183	putative [Bacillus subtilis]	72	54	435
868	1	150	788	gi|1377842	unknown [Bacillus subtilis]	72	55	639
922	1	130	432	gi|1088269	unknown protein [Azotobacter vinelandii]	72	58	303
941	1	2	238	gi|153929	NADPH-sulfite reductase (levoprotein component [Salmonella yphimurium]	72	49	237
980	1	840	421	gi|853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	72	59	420

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1209	1	383	213	gi|144735	neurotoxin type B (Clostridium botulinum)	72	44	171
1469	2	671	474	gi|1205458	hypothetical protein (GB:D26562_47) (Haemophilus influenzae)	72	63	198
1956	1	727	365	gi|154409	hexosephosphate transport protein [Salmonella typhimurium] pir|B41853|B41853 hexose phosphate transport system regulatory rotein uhpB - Salmonella typhimurium	72	44	363
2101	1	3	401	gi|1303950	YqiY [Bacillus subtilis]	72	50	399
2503	1	569	399	gi|149713	formate dehydrogenase [Methanobacterium formicicum] pir|A42712|A42712 formate dehydrogenase (EC 1.2.1.2) - ethanobacterium formicicum	72	56	171
2967	1	3	155	gi|1212729	YqhJ [Bacillus subtilis]	72	46	153
3004	1	367	185	gi|665999	hypothetical protein [Bacillus subtilis]	72	55	183
3109	1	278	141	gi|413968	Apa-44d gene product [Bacillus subtilis]	72	45	138
3171	1	3	287	gi|515938	glutamate synthase (ferredoxin) [Synechocystis sp.] pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - synechocystis sp.	72	52	285
3771	1	26	367	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	72	63	342
3951	1	1	222	gi|1500409	M. jannaschii predicted coding region MJ1519 [Methanococcus jannaschii]	72	38	222
4190	1	721	362	gi|39956	11Glc [Bacillus subtilis]	72	57	160
4444	1	3	347	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	72	55	345
6	2	911	1200	gi|537095	ornithine carbamoyltransferau [Escherichia coli]	71	5?	270
11	15	11350	10859	gi|532309	25 kDa protein [Escherichia coli]	71	47	492
19	2	1248	2435	gi|1244574	D-alanine:D-alanine ligase [Enterococcus hirae]	71	52	1188
21	2	898	1488	gi|149629	anthranilate synthase component 2 [Leptospira biflexa] pir|C32840|C32840 component II Leptospira biflexa anthranilate synthase (EC 4.1.3.27)	71	45	591
34	1	1	567	gi|1303983	YqkF [Bacillus subtilis]	71	59	567
37	3	3192	2806	gi|1209681	glutamate-rich protein [Bacillus firmus]	71	50	387
38	18	12250	12462	gi|927645	arginyl endopeptidase [Porphyromonas gingivalis]	71	50	213
39	3	1246	4431	pir|S09411|S094	spoIIIE protein - Bacillus subtilis	71	49	3186
53	14	15770	14760	gi|142611	branched chain alpha-keto acid dehydrogenase E1-alpha [Bacillus subtilis]	71	58	1011
54	11	13461	12625	gi|143014	gnt repressor [Bacillus subtilis]	71	46	837

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
57	7	7152	5860	gi|508175	EIIC domain of PTS-dependent Gat transport and phosphorylation Escherichia coli	71	48	1293
57	18	13897	14334	gi|1063247	high homology to (levohemoprotein (Haemoglobin-like protein) of Alcaligenes eutrophus and Saccharomyces cerevisiae (Bacillus subtilis)	71	56	438
62	16	9831	10955	gi|1303926	YqiG (Bacillus subtilis)	71	54	1125
70	12	8505	8966	gi|147198	phnE protein (Escherichia coli)	71	38	462
86	5	2394	2089	gi|904205	hypothetical protein (Bacillus subtilis)	71	51	306
96	7	7601	8269	gi|709991	hypothetical protein (Bacillus subtilis)	71	49	669
100	6	4822	5931	gi|1060848	Opine dehydrogenase (Arthrobacter sp.)	71	45	1110
101	1	1062	532	gi|143089	isp protein (Bacillus subtilis)	71	41	531
109	18	15312	15695	gi|413985	ipa-61d gene product (Bacillus subtilis)	71	57	384
113	1	630	316	gi|661254	probable protein kinase (Saccharomyces cerevisiae)	71	57	315
114	5	6598	5603	gi|143156	membrane bound protein (Bacillus subtilis)	71	40	996
133	2	3087	1723	gi|1303913	YghX (Bacillus subtilis)	71	53	1165
149	19	6335	5895	gi|529650	G40P (Bacteriophage SPP1)	71	51	441
154	5	3635	3087	gi|425488	repressor protein (Streptococcus sobrinus)	71	47	549
164	11	11354	11649	gi|147318	ORF4 gene product (Bacillus subtilis)	71	52	116
169	5	1936	2745	gi|1403403	unknown (Mycobacterium tuberculosis)	71	56	810
193	2	272	1234	gi|1303788	YqeH (Bacillus subtilis)	71	49	963
205	1	1743	895	gi|1215694	GlnQ (Mycoplasma pneumoniae)	71	46	849
233	4	1849	2022	gi|613712	ORF1 (Campylobacter jejuni)	71	50	174
237	7	4501	5169	gi|149384	HisIE (Lactococcus lactis)	71	54	669
272	4	2848	2273	gi|709993	hypothetical protein (Bacillus subtilis)	71	48	576
274	2	618	1496	gi|143035	NAD(P)H:glutamyl-transfer RNA reductase (Bacillus subtilis) pir|A35252|A35252 5-aminolevulinate synthase (EC 2.1.1.37) - acillus subtilis	71	53	879
276	5	3349	2720	gi|303562	ORF210 (Escherichia coli)	71	50	630
287	1	136	660	gi|310634	20 kDa protein (Streptococcus gordonii)	71	53	525
288	6	3322	2771	gi|1256625	putative (Bacillus subtilis)	71	47	552

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
301	6	1492	2461	gi|467417	similar to lysine decarboxylase (Bacillus subtilis)	71	57	1032
306	4	6607	5222	gi|1256618	transport protein (Bacillus subtilis)	71	56	1386
307	2	1536	925	gi|632683	orfc (Mycoplasma capricolum)	71	45	612
310	5	5793	5146	gi|348052	acetoin utilization protein (Bacillus subtilis)	71	51	648
322	1	2	1303	gi|1001819	hypothetical protein (Synechocystis sp.)	71	46	1302
333	4	4171	3995	gi|467473	unknown (Bacillus subtilis)	71	57	177
350	2	548	922	gi|551879	ORF 1 (Lactococcus lactis)	71	55	375
375	4	1860	3071	gi|467447	unknown (Bacillus subtilis)	71	57	1212
380	5	1560	2102	gi|142557	ATP synthase b subunit (Bacillus megaterium)	71	43	543
414	2	251	637	gi|580904	homologous to E.coli rnpA (Bacillus subtilis)	71	49	387
424	1	335	1354	gi|581305	L-lactate dehydrogenase (Lactobacillus plantarum)	71	57	1020
436	4	3701	3270	pir|PN0501|PN05	phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Bacillus subtilis (fragment)	71	66	432
482	1	3	1280	gi|410142	ORFX18 (Bacillus subtilis)	71	49	1278
525	3	2272	1844	gi|143370	phosphoribosylpyrophosphate amidotransferase (PUR-F; EC 2.4.2.14) Bacillus subtilis	71	56	429
529	4	2739	2047	gi|606150	ORF_f309 (Escherichia coli)	71	41	693
563	1	22	969	gi|1237015	ORF4 (Bacillus subtilis)	71	53	948
581	1	506	255	gi|1301730	T25G3.2 (Caenorhabditis elegans)	71	47	252
612	2	1068	913	gi|153968	fimbrias z (Salmonella typhimurium)	71	55	156
613	1	1	654	gi|466778	lysine specific permease (Escherichia coli)	71	50	654
618	1	1243	623	gi|1146238	poly(A) polymerase (Bacillus subtilis)	71	52	621
630	1	1170	586	gi|486243	unknown (Bacillus subtilis)	71	53	585
691	1	1126	641	gi|289260	comE ORF1 (Bacillus subtilis)	71	51	486
694	2	149	427	gi|12971	NADH dehydrogenase subunit V (AA 1-605) (Gallus gallus) ir|S10197|S10197 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain - chicken mitochondrion (SGC1)	71	47	279
715	2	169	777	gi|1303810	YqfL (Bacillus subtilis)	71	53	609
746	2	1473	970	gi|1377843	unknown (Bacillus subtilis)	71	52	504

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Seq ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4	1	1417	802	gi|1405459	YneS [Bacillus subtilis]	71	49	636
5	1	1018	524	gi|1510389	M. jannaschii predicted coding region MJ0296 [Methanococcus jannaschii]	71	53	495
1	1	3	215	gi|475972	pentafunctional enzyme [Pneumocystis carinii]	71	47	213
5	1	1203	703	gi|536655	ORF YBR244w [Saccharomyces cerevisiae]	71	52	501
0	3	1292	987	gi|1204326	tRNA delta(2)-isopentenylpyrophosphate transferase [Haemophilus influenzae]	71	48	306
6	1	116	286	gi|1419075	cblM gene product [Methanobacterium thermoautotrophicum]	71	50	171
1	1	973	488	gi|891358	PgsA [Bacillus subtilis]	71	56	486
41	1	2	262	gi|1408507	pyrimidine nucleoside transport protein [Bacillus subtilis]	71	45	261
70	1	2	172	gi|709993	hypothetical protein [Bacillus subtilis]	71	46	171
76	1	57	365	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	71	49	309
81	1	366	184	gi|46971	eplP gene product [Staphylococcus epidermidis]	71	50	183
81	1	3	290	gi|153016	ORF 419 protein [Staphylococcus aureus]	71	50	288
46	1	456	229	gi|602683	orfC [Mycoplasma capricolum]	71	48	228
02	1	756	379	gi|1008177	ORF YJL046w [Saccharomyces cerevisiae]	71	48	378
19	1	2	217	gi|1046088	arginyl-tRNA synthetase [Mycoplasma genitalium]	71	50	216
18	3	3	320	gi|1499771	M. jannaschii predicted coding region MJ0936 [Methanococcus jannaschii]	71	57	318
61	1	2	187	gi|312243	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolyticus]	71	57	186
99	2	67	306	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	71	43	240
03	1	2	184	gi|262235	YmaA [Bacillus subtilis]	71	57	183
84	1	3	338	gi|401716	beta-isopropylmalate dehydrogenase [Neurospora crassa]	71	55	336
15	2	743	399	gi|563952	gluconate permease [Bacillus licheniformis]	71	59	345
85	1	770	387	gi|47382	acyl-CoA-dehydrogenase [Streptomyces purpurascens]	71	57	384
75	1	541	272	gi|1001541	hypothetical protein [Synechocystis sp.]	71	38	270
35	1	637	320	gi|142695	S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium	71	52	318
49	1	63	239	gi|1205163	deoxyribose aldolase [Haemophilus influenzae]	71	63	177
08	1	530	267	gi|1197667	vitellogenin [Anolis pulchellus]	71	46	264

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
6	3	1237	2721	gi|1321788	arginine ornithine antiporter [Clostridium perfringens]	70	54	1485
11	11	6572	7486	gi|216854	P47K [Pseudomonas chlororaphis]	70	41	915
12	1	2890	1481	vi|467330	replicative DNA helicase [Bacillus subtilis]	70	49	1410
15	1	1756	893	gi|451216	Mannosephosphate isomerase [Streptococcus mutans]	70	46	864
15	2	1277	1050	gi|476092	unknown [Bacillus subtilis]	70	50	228
17	2	2132	1350	gi|145402	choline dehydrogenase [Escherichia coli]	70	52	783
21	1	2	925	gi|149516	anthranilate synthase alpha subunit (Lactococcus lactis) pir|S35124|S35124 anthranilate synthase (EC 4.1.3.27) alpha chain - actococcus lactis subsp. lactis	70	50	924
25	7	5580	6251	gi|1389549	ORF3 [Bacillus subtilis]	70	52	672
33	6	6071	7423	gi|1303875	YqhB [Bacillus subtilis]	70	51	1353
36	2	959	1594	gi|500755	methyl purine glycosylase [Mus musculus]	70	47	636
38	8	4901	5860	gi|1408507	pyrimidine nucleoside transport protein [Bacillus subtilis]	70	44	960
44	8	5312	5989	gi|1006620	hypothetical protein [Synechocystis sp.]	70	49	678
46	10	8950	10020	gi|1403126	czcD gene product [Alcaligenes eutrophus]	70	45	1071
52	2	2727	1900	gi|1486247	unknown [Bacillus subtilis]	70	53	828
52	6	4048	4656	gi|244501	esterase II-carboxylesterase (EC 3.1.1.1) [Pseudomonas fluorescens. eptide. 218 aa]	70	50	609
56	8	8460	9962	gi|1339951	small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	70	51	1503
62	1	48	290	gi|142702	A competence protein 2 [Bacillus subtilis]	70	47	243
64	1	1080	541	gi|1204377	molybdopterin biosynthesis protein [Haemophilus influenzae]	70	47	540
70	5	5139	3595	gi|1204834	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Haemophilus influenzae]	70	47	1545
91	4	7793	5466	gi|886471	methionine synthase [Catharanthus roseus]	70	56	2328
96	5	8754	7255	pir|B39096|B390	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis	70	54	1500
110	2	767	1100	gi|145294	adenine phosphoribosyl-transferase [Escherichia coli]	70	51	334
116	6	7026	7976	gi|143607	sporulation protein [Bacillus subtilis]	70	50	951
121	8	6401	6988	gi|1107528	ttg start [Campylobacter coli]	70	45	588
131	8	6842	7936	gi|1150454	prolidase PepQ [Lactobacillus dalbrueckii]	70	48	1095

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
135	1	2	1489	gi|311309	putative membrane-bound protein with four times repetition of ro-Ser-Ala at the N-terminus; function unknown [Alcaligenes utrophus]	70	49	1488
138	3	418	714	gi|904181	hypothetical protein [Bacillus subtilis]	70	46	297
164	8	9344	9874	gi|49315	ORF1 gene product [Bacillus subtilis]	70	47	531
164	16	15626	16618	gi|1205212	hypothetical protein (GB:D10483_18) [Haemophilus influenzae]	70	50,	993
205	2	2735	1803	gi|1215695	peptide transport system protein SapF homolog; SapF homolog [Mycoplasma pneumoniae]	70	47	933
209	3	910	1386	gi|1204665	hypothetical protein (GB:X73124_26) [Haemophilus influenzae]	70	48	477
246	3	340	756	gi|215098	excisionase [Bacteriophage 154a]	70	46	417
263	7	7876	6749	gi|142540	aspartokinase II [Bacillus sp.]	70	51	1128
268	3	3212	4117	gi|1340128	ORF1 [Staphylococcus aureus]	70	50	906
302	6	3201	3827	gi|147782	ruvA protein (gtg start) [Escherichia coli]	70	46	627
302	10	5879	7051	pir|C38530|C385	queuine tRNA-ribosyltransferase (EC 2.4.2.29) - Escherichia coli	70	55	1173
313	1	2520	1414	gi|1205934	aminopeptidase a/i [Haemophilus influenzae]	70	46	1107
355	2	379	669	gi|1070013	protein-dependent [Bacillus subtilis]	70	48	291
403	1	1255	629	gi|733147	GumF [Xanthomonas campestris]	70	33	627
414	10	8770	9273	gi|1204752	high affinity ribose transport protein [Haemophilus influenzae]	70	52	504
449	1	2	1243	gi|619724	MgtE [Bacillus firmus]	70	44	1242
472	1	637	320	gi|727145	open reading frame; putative [Bacillus amyloliquefaciens] pir|B29091|B29091 hypothetical protein (bglA region) - Bacillus myloliquefaciens (fragment)	70	41	318
480	2	727	1608	gi|142560	ATP synthase gamma subunit [Bacillus megaterium]	70	44	882
524	1	2	307	gi|602292	RCH2 protein [Brassica napus]	70	45	306
525	1	823	413	gi|143372	phosphoribosyl glycinamide formyltransferase (PUR-N) [Bacillus subtilis]	70	52	411
565	4	3625	2552	gi|881434	ORFP [Bacillus subtilis]	70	51	1074
607	4	829	1284	gi|1511524	hypothetical protein (SP:P17002) [Methanococcus jannaschii]	70	50	456
633	1	1383	703	gi|431231	uracil permease [Bacillus caldolyticus]	70	53	681
646	3	1683	1309	gi|467340	unknown [Bacillus subtilis]	70	49	375
663	1	830	417	gi|1303873	YjjZ [Bacillus subtilis]	70	40	414

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
681	1	1488	781	gi|1001678	hypothetical protein (Synechocystis sp.)	70	53	708
708	1	2	448	sp|P33940|YOJH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	70	51	447
725	1	51	722	gi|1001644	hypothetical protein (Synechocystis sp.)	70	48	672
776	1	1371	787	gi|145165	putative (Escherichia coli)	70	47	585
A34	1	250	783	gi|552971	NADH dehydrogenase (ndhF) (Vicia faba)	70	47	534
865	2	1585	1379	gi|1204636	ATP-dependent helicase (Haemophilus influenzae)	70	45	207
894	1	535	269	gi|467364	DNA binding protein (probable) (Bacillus subtilis)	70	41	267
919	1	3	317	gi|1314847	CinA (Bacillus subtilis)	70	40	315
944	1	3	572	gi|709991	hypothetical protein (Bacillus subtilis)	70	44	570
988	2	772	605	gi|12441	ORF 3; putative (Bacillus subtilis)	70	50	168
1055	1	3	335	gi|529755	spec (Streptococcus pyogenes)	70	37	333
1093	1	2	904	gi|853754	ABC transporter (Bacillus subtilis)	70	49	903
1109	1	2	310	gi|1001827	hypothetical protein (Synechocystis sp.)	70	42	309
1220	1	468	235	pir|S23416|S234	epiB protein - Staphylococcus epidermidis	70	40	234
1279	1	73	348	gi|153015	FemA protein (Staphylococcus aureus)	70	47	276
1336	1	195	542	sp|P31776|PBPA_	PENICILLIN-BINDING PROTEIN 1A (PBP-1A) (PENICILLIN-BINDING PROTEIN A).	70	50	348
1537	2	232	402	gi|1146181	putative (Bacillus subtilis)	70	50	171
1574	1	451	272	gi|219630	endothelin-A receptor (Homo sapiens)	70	47	180
1640	1	690	346	gi|1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative (Bacillus subtilis)	70	46	345
2504	1	2	286	gi|495179	transmembrane protein (Lactococcus lactis)	70	51	285
3061	1	564	301	gi|508175	EIIC domain of PTS-dependent Gat transport and phosphorylation Escherichia coli]	70	44	264
3128	1	2	199	gi|1340096	unknown (Mycobacterium tuberculosis)	70	51	198
3218	1	3	488	gi|515938	glutamate synthase (ferredoxin) [Synechocystis sp.] pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - synechocystis sp.	70	50	486
3323	1	794	399	gi|1154891	ATP binding protein (Phormidium laminosum)	70	52	396
3679	1	599	399	gi|529385	chromosome condensation protein (Caenorhabditis elegans)	70	30	201

TABLE 2

S. aureus : Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3841	1	706	198	gi|1208965	hypothetical 23.3 kd protein [Escherichia coli]	70	47	309
3929	1	3	401	gi|149435	putative [Lactococcus lactis]	70	69	399
4044	1	595	374	gi|602031	similar to trimethylamine DH (Mycoplasma capricolum) pir|S49950|S49950 probable trimethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	70	40	222
4129	1	558	280	gi|339951	small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	70	49	279
4422	1	576	289	gi|296464	ATPase [Lactococcus lactis]	70	57	288
4647	1	361	200	gi|166412	NADH-glutamate synthase [Medicago sativa]	70	59	162
16	8	7571	9031	gi|1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	69	44	1461
16	9	9080	10033	gi|1353197	chloredoxin reductase [Eubacterium acidaminophilum]	69	54	954
30	1	1452	727	gi|1204910	hypothetical protein (GB:U14003_102) [Haemophilus influenzae]	69	52	726
38	4	1023	1298	gi|407773	devA gene product [Anabaena sp.]	69	41	276
44	9	5987	6595	gi|1205920	molybdate uptake system hydrophilic membrane-bound protein [Haemophilus influenzae]	69	45	609
62	15	9104	9475	gi|385178	unknown [Bacillus subtilis]	69	44	372
66	4	2402	2803	gi|1303893	YqhL [Bacillus subtilis]	69	51	402
67	15	14124	13627	gi|149647	ORF2 [Listeria monocytogenes]	69	37	498
67	17	14053	14382	gi|305002	ORF_f356 [Escherichia coli]	69	49	330
67	19	15130	15807	gi|1109684	ProV [Bacillus subtilis]	69	45	678
78	3	1447	2124	gi|1256633	putative [Bacillus subtilis]	69	53	678
78	4	4513	3725	gi|1303958	YqjG [Bacillus subtilis]	69	32	789
85	4	4521	4213	pir|E29326|E293	hypothetical protein (pur operon) - Bacillus subtilis	69	32	309
86	6	3253	2654	gi|973332	OrfC [Bacillus subtilis]	69	50	600
95	1	96	710	gi|786464	(A11 antigen, sperm tail membrane antigen=putative sucrose-specific phosphotransferase enzyme II homolog (mice, testis, Peptide Partial, 72 aa)	69	43	615
100	7	6023	7426	gi|1205355	Na+/H antiporter [Haemophilus influenzae]	69	39	1404
102	2	2678	1650	gi|561690	sialoglycoprotease [Pasteurella haemolytica]	69	47	1029
103	8	12241	8537	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	69	54	3705
103	11	14987	12552	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	69	51	2436

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
112	11	8708	10168	gi|154411	hexosephosphate transport protein (Salmonella typhimurium) pir|D41853|D41853 hexose phosphate transport system protein uhpT - almonella typhimurium	69	51	1461
112	16	16644	17414	gi|1204435	(pyruvate formate-lyase activating enzyme [Haemophilus influenzae]	69	50	771
113	2	33	953	gi|290509	o307 (Escherichia coli)	69	43	921
114	2	1537	1058	pir|A42771|A427	reticulocyte-binding protein 1 - Plasmodium vivax	69	39'	480
121	6	4309	5310	gi|154633	NrdF [Bacillus subtilis]	69	53	1002
125	2	267	854	gi|13931	tpa-7d gene product [Bacillus subtilis]	69	43	588
149	27	10666	10400	pir|S28089|S280	hypothetical protein A - yeast (Zygosaccharomyces bisporus) plasmid pSB1	69	39	267
161	1	1598	813	gi|1205538	hypothetical protein (GB:U14003_302) [Haemophilus influenzae]	69	47	786
165	4	2222	4633	gi|40054	phenylalanyl-tRNA synthetase beta subunit (AA 1-804) [Bacillus btilis]	69	52	2412
169	3	1210	1761	gi|296031	elongation factor Ts (Spirulina platensis)	69	45	552
175	12	8686	8339	gi|732682	FimE protein [Escherichia coli]	69	69	348
190	2	484	1671	sp|P17731|HIS8_	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-PHOSPHATE TRANSAMINASE).	69	48	1188
206	1	5551	2777	gi|41750	(hadR protein (AA 1-1033) [Escherichia coli]	69	49	2775
206	4	6038	5796	gi|1256135	YbhF [Bacillus subtilis]	69	46	243
249	1	636	319	gi|1405456	YncP [Bacillus subtilis]	69	80	318
302	8	4820	5776	gi|1001768	hypothetical protein [Synechocystis sp.]	69	44	957
324	2	7384	3893	gi|1256798	pyruvate carboxylase [Rhizobium etli]	69	53	3492
351	3	2098	1808	gi|1491664	T04H1.4 [Caenorhabditis elegans]	69	30	291
369	3	2075	2305	gi|336458	ORF [Balaenoptera acutorostrata]	69	61	231
392	3	1999	2424	gi|556015	ORFl [Bacillus subtilis]	69	45	426
410	1	87	779	gi|155611	phosphoglyceromutase [Zymomonas mobilis]	69	58	693
421	1	2085	1129	gi|1276985	arginase [Bacillus caldovelox]	69	54	957
444	8	6713	7741	gi|1221782	purine synthesis repressor [Haemophilus influenzae]	69	40	1029
453	1	828	415	gi|1122758	unknown [Bacillus subtilis]	69	57	414
469	2	3286	2246	gi|1458228	mutY homolog [Homo sapiens]	69	44	1041

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
509	3	1730	1171	gi|49224	URF 4 [Synechococcus sp.]	69	39	360
520	5	3023	2823	gi|726427	similar to D. melanogaster HST101-2 protein (PIR:S34154) Caenorhabditis elegans	69	39	201
511	1	26	760	gi|509672	repressor protein (Bacteriophage Tuc2009]	69	33	735
589	1	107	253	gi|169101	17.9 kDa heat shock protein (hsp17.9) [Pinus sativum]	69	52	147
594	2	597	1391	gi|142783	DNA photolyase [Bacillus firmus]	69	48	795
604	4	2475	2114	gi|413930	ipa-6d gene product [Bacillus subtilis]	69	45	163
607	1	2	313	gi|1236103	W08D2.3 [Caenorhabditis elegans]	69	47	312
607	2	590	312	gi|536715	ORF YBR275c [Saccharomyces cerevisiae]	69	39	279
734	1	864	433	gi|467327	unknown [Bacillus subtilis]	69	44	432
759	1	3	338	gi|1009367	Respiratory nitrate reductase [Bacillus subtilis]	69	50	336
761	2	392	586	gi|3508	Leucyl-tRNA synthetase (cytoplasmic) [Saccharomyces cerevisiae] |370340 ORF YPL160w [Saccharomyces cerevisiae]	69	46	195
802	1	72	1013	gi|143044	ferrochelatase [Bacillus subtilis]	69	55	942
816	1	2573	1368	gi|1510268	restriction modification system s subunit [Methanococcus jannaschii]	69	45	1206
838	2	133	387	gi|1255371	coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase [Caenorhabditis elegans]	69	46	255
851	2	745	1005	gi|3888998	secA gene product [Antithamnion sp.]	69	39	261
867	1	535	269	gi|1070014	protein-dependent [Bacillus subtilis]	69	47	267
995	1	954	478	gi|205569	transcription elongation factor [Haemophilus influenzae]	69	53	477
999	1	1009	506	gi|899254	predicted trithorax protein [Drosophila virilis]	69	21	504
1127	1	1315	659	gi|1205434	H. influenzae predicted coding region HI1191 [Haemophilus influenzae]	69	56	657
1118	1	248	460	gi|1510646	M. jannaschii predicted coding region MJ0568 [Methanococcus jannaschii]	69	48	213
2928	1	3	401	gi|290503	glutamate permease [Escherichia coli]	69	41	399
3090	1	444	223	gi|1204987	DNA polymerase III, alpha chain [Haemophilus influenzae]	69	36	222
3817	1	2	400	gi|1483199	peptide-synthetase [Amycolatopsis mediterranei]	69	45	399
3833	1	667	335	gi|1524193	unknown [Mycobacterium tuberculosis]	69	46	333

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4079	1	747	400	gi|546918	orfy 3' of comK [Bacillus subtilis, E26, Peptide Partial, 140 aa] pir|S43612|S43612 hypothetical protein Y - Bacillus subtilis sp|P40398|YHXD_BACSU HYPOTHETICAL PROTEIN IN COMK 3'REGION (ORFY) FRAGMENT).	69	64	348
4115	2	215	400	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	69	59	186
4139	1	1	333	gi|1208451	hypothetical protein [Synechocystis sp.]	69	36	333
4258	1	457	230	gi|496158	restriction-modification enzyme subunit M1 [Mycoplasma pulmonis] pir|S49395|S49395 HsdM1 protein - Mycoplasma pulmonis (SGC3)	69	43	228
4317	1	90	374	gi|413967	ipa-43d gene product [Bacillus subtilis]	69	44	285
4465	1	1	293	gi|396296	similar to phosphotransferase system enzyme II [Escherichia coli] sp|P26672|PTWC_ECOLI PTS SYSTEM, FRUCTOSE-LIKE-2 IIC COMPONENT PHOSPHOTRANSFERASE ENZYME II, C COMPONENT).	69	49	291
3	1	2102	1193	gi|1109685	ProW [Bacillus subtilis]	68	46	1110
15	4	2592	2074	gi|807973	unknown [Saccharomyces cerevisiae]	68	45	519
31	8	6328	8772	gi|290642	ATPase [Enterococcus hirae]	68	48	2445
40	2	1115	750	gi|606342	ORF_o622; reading frame open far upstream of start; possible rameshift, linking to previous ORF [Escherichia coli]	68	55	366
46	9	6886	8415	gi|155276	aldehyde dehydrogenase [Vibrio cholerae]	68	44	1530
48	3	3643	3404	gi|285608	241k polyprotein [Apple stem grooving virus]	68	47	240
48	4	3536	4132	gi|1045937	M. genitalium predicted coding region MG246 [Mycoplasma genitalium]	68	39	597
53	10	11671	10685	gi|1303952	YqjA [Bacillus subtilis]	68	46	987
70	9	7346	8155	gi|147198	phnE protein [Escherichia coli]	68	40	810
89	4	1899	2966	gi|145173	35 kDa protein [Escherichia coli]	68	43	1068
108	1	2187	1150	gi|38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus] 1r|A29277|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus	68	57	1038
112	5	2666	3622	gi|153724	MalC [Streptococcus pneumoniae]	68	55	957
115	7	7865	8638	gi|143608	sporulation protein [Bacillus subtilis]	68	48	774
118	3	2484	3698	gi|1303805	YqeR [Bacillus subtilis]	68	46	1215
120	2	1424	1594	sp|P38018|CYSJ_	SULFITE REDUCTASE (NADPH) FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2) (SIR-FP)	68	45	171
129	1	1	1011	gi|396307	argininosuccinate lyase [Escherichia coli]	68	50	1011

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Entry ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
32	3	1867	2739	gi|1.6267	ORF2 (Bacillus megaterium)	68	48	873
14	2	848	1012	gi|147545	DNA recombinase (Escherichia coli)	68	50	165
41	2	372	614	gi|872116	sti (stress inducible protein) (Glycine max)	68	36	243
49	7	2454	2260	gi|145774	hsp70 protein (dnaK gene) (Escherichia coli)	68	48	195
55	2	1776	1534	gi|216583	ORF1 (Escherichia coli)	68	36	243
58	3	1826	3289	sp|P33940|YOJH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	68	51	1464
169	6	2749	3318	gi|1401402	unknown [Mycobacterium tuberculosis]	68	46	570
175	10	2158	7365	gi|1072395	phaA gene product [Rhizobium meliloti]	68	51	1794
188	7	4184	5434	gi|1173843	3-ketoacyl-ACP synthase II [Vibrio harveyi]	68	48	1251
189	3	907	1665	gi|467383	DNA binding protein (probable) [Bacillus subtilis]	68	55	759
206	5	7683	6709	gi|1256138	YbbI [Bacillus subtilis]	68	48	975
206	8	10425	12176	gi|452687	pyruvate decarboxylase [Saccharomyces cerevisiae]	68	48	1752
212	8	3421	3648	gi|1369941	c1 gene product [Bacteriophage B1]	68	39	228
214	8	5457	6482	gi|1420467	ORF YOR196c [Saccharomyces cerevisiae]	68	45	1026
237	4	2507	3088	gi|149381	HisH [Lactococcus lactis]	68	46	582
243	5	5540	4542	gi|1235684	mevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae]	68	47	999
262	1	3	164	gi|150974	4-oxalocrotonate tautomerase [Pseudomonas putida]	68	42	162
262	2	1984	1118	gi|1147744	PSR [Enterococcus hirae]	68	49	867
276	6	3702	3139	sp|P30750|ABC_E	ATP-BINDING PROTEIN ABC (FRAGMENT).	68	50	564
306	6	6345	5725	gi|1256617	adenine phosphoribosyltransferase [Bacillus subtilis]	68	53	621
333	3	4599	3850	gi|467473	unknown [Bacillus subtilis]	68	45	750
365	6	5017	4838	gi|1130643	T22B3.3 [Caenorhabditis elegans]	68	45	180
376	2	549	1646	gi|1277026	DAPA aminotransferase [Bacillus subtilis]	68	51	1098
405	1	1741	872	gi|1303917	YqiB [Bacillus subtilis]	68	47	870
406	2	853	539	gi|1511513	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	68	44	315
426	6	3558	3391	gi|624632	GltL [Escherichia coli]	68	48	168
438	1	108	329	gi|146923	nitrogenase reductase [Escherichia coli]	68	43	222

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
443	1	476	240	gi|535810	hippuricase [Campylobacter jejuni]	68	42	237
443	2	518	1015	gi|1204742	H. influenzae predicted coding region HI0491 [Haemophilus influenzae]	68	48	498
443	5	4447	3779	gi|409660	deoxyribose-phosphate aldolase [Bacillus subtilis] pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	68	55	669
476	2	240	1184	gi|571345	unknown, similar to E.coli cardiolipin synthase [Bacillus subtilis] sp|P45860|YWIE_BACSU HYPOTHETICAL 58.2 PROTEIN IN NARI-ACDA NTERGENIC REGION.	68	45	945
486	2	1876	1046	gi|147328	transport protein [Escherichia coli]	68	41	831
517	3	1764	2084	gi|523809	orf2 [Bacteriophage A2]	68	64	321
572	1	2	571	sp|P39237|YO5L_	HYPOTHETICAL 6.8 KD PROTEIN IN NRDC-TK INTERGENIC REGION.	68	47	570
646	1	914	459	gi|413982	ipa-56r gene product [Bacillus subtilis]	68	52	456
659	3	1668	1901	gi|1407541	C33D9.8 [Caenorhabditis elegans]	68	36	234
864	5	1510	1716	gi|145774	hsp70 protein (dnaK gene) [Escherichia coli]	68	48	207
920	1	860	432	gi|1510416	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	68	54	429
952	1	1096	611	gi|623456	reductase [Leishmania major]	68	46	486
970	1	91	402	gi|1354775	pfoS/R [Treponema pallidum]	68	46	312
1028	1	1064	534	gi|410117	diaminopimelate decarboxylase [Bacillus subtilis]	68	47	531
1029	1	428	216	gi|1135714	Plasmodium falciparum mRNA for asparagine-rich antigen (clone 17C1) [Plasmodium falciparum]	68	31	211
1058	1	692	348	gi|81649	epic gene product [Staphylococcus epidermidis]	68	46	345
1096	2	665	465	gi|143434	Rho Factor [Bacillus subtilis]	68	43	201
1308	1	2	694	gi|69939	group B oligopeptidase.PepB [Streptococcus agalactiae]	68	50	693
1679	1	2	238	gi|17205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	68	53	237
2039	1	3	383	gi|153898	transport protein [Salmonella typhimurium]	68	51	381
2077	1	3	326	pir|C33496|C334	hisC homolog - Bacillus subtilis	68	47	324
2112	1	613	374	gi|64884	lamin LII [Xenopus laevis]	68	50	240
2273	1	793	398	gi|581648	eplB gene product [Staphylococcus epidermidis]	68	45	396
2948	1	2	385	gi|216869	branched-chain amino acid transport carrier [Pseudomonas aeruginosa] pir|A38534|A38534 branched-chain amino acid transport protein braZ Pseudomonas aeruginosa	68	41	384

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
2955	1	768	400	gi|704179	hypothetical protein (Bacillus subtilis)	68	49	369
2981	1	572	288	gi|508979	GTP-binding protein (Bacillus subtilis)	68	48	285
3014	1	584	294	gi|1524394	ORF-2 upstream of gbsAB operon (Bacillus subtilis)	68	45	291
3042	1	336	169	gi|1204696	[fructose-permease IIBC component (Haemophilus influenzae)	68	53	168
3108	1	103	258	gi|217855	heat-shock protein (Arabidopsis thaliana)	68	48	156
3639	1	919	461	gi|1510490	nitrate transport permease protein (Methanococcus jannaschii)	68	47	459
3657	1	1	330	gi|155269	PTS enzyme-II fructose (Xanthomonas campestris)	68	48	330
3823	1	780	391	gi|603768	HutI protein, imidazolone-5-propionate hydrolase (Bacillus subtilis) gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis	68	54	390
3982	1	2	277	gi|149435	putative (Lactococcus lactis)	68	47	276
4051	1	1	342	gi|450688	hsdM gene of Ecoprrl gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	68	48	342
4085	1	12	209	gi|1353678	heavy-metal transporting P-type ATPase (Proteus mirabilis)	68	47	198
4143	1	47	187	gi|603769	HutU protein, urocanase (Bacillus subtilis)	68	55	141
4146	1	2	352	gi|450688	hsdM gene of Ecoprrl gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	68	51	351
4172	1	2	382	gi|1041097	Pyruvate Kinase (Bacillus psychrophilus)	68	48	381
4182	1	498	250	gi|411968	ipa-44d gene product (Bacillus subtilis)	68	50	249
4362	2	148	318	gi|450688	hsdM gene of Ecoprrl gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	68	44	171
5	11	9493	8300	gi|103727	putative (Bacillus subtilis)	67	46	1194
31	11	10318	9833	gi|216746	D-lactate dehydrogenase (Lactobacillus plantarum)	67	41	486
32	1	1560	3155	gi|1098557	renal sodium/dicarboxylate cotransporter (Homo sapiens)	67	46	1596
32	5	4945	4145	gi|1510720	prephenate dehydratase (Methanococcus jannaschii)	67	51	801
36	5	5350	4268	gi|146216	45% identity with the product of the ORF6 gene from the Erwinia herbicola carotenoid biosynthesis cluster; putative (Bacillus subtilis)	67	58	1083
44	7	4492	5304	gi|1006621	hypothetical protein (Synechocystis sp.)	67	43	813

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
56	7	3943	8481	gi|304131	glutamate synthase large subunit precursor [Azospirillum brasilense] pir|B46602|B46602 glutamate synthase (NADPH) (EC 1.4.1.13) alpha hain - Azospirillum brasilense	67	52	4539
56	12	13923	14678	gi|1000453	TreR [Bacillus subtilis]	67	48	756
62	8	5092	4757	gi|1113949	orf3 [Bacillus, C-125, alkali-sensitive mutant 18224, Peptide Mutant, 112 aa]	67	45	336
62	10	7570	6338	gi|054655	Na/H antiporter system [Bacillus alcalophilus]	67	49	1233
99	3	2119	3321	gi|1204349	hypothetical protein (GB:GB:D90212_3) [Haemophilus influenzae]	67	50	1203
102	9	5695	7176	gi|149432	putative [Lactococcus lactis]	67	51	1482
103	13	14549	14049	gi|1408497	LP9D gene product [Bacillus subtilis]	67	48	501
109	15	14821	13982	gi|413976	ipa-52r gene product [Bacillus subtilis]	67	49	840
109	17	14811	15194	gi|413983	ipa-59d gene product [Bacillus subtilis]	67	29	384
121	4	1713	2153	gi|1262335	YmaA [Bacillus subtilis]	67	54	441
122	1	1	1149	gi|143047	ORFB [Bacillus subtilis]	67	35	1149
124	5	4060	3518	gi|556885	Unknown [Bacillus subtilis]	67	47	543
131	2	4584	3589	gi|1046081	hypothetical protein (GB:D26185_10) [Mycoplasma genitalium]	67	30	996
140	3	2899	2297	gi|146549	kdnC [Escherichia coli]	67	45	603
142	4	5409	4198	gi|1212775	GTP cyclohydrolase II [Bacillus amyloliquefaciens]	67	55	1212
147	5	2913	2374	gi|1303709	YrkJ [Bacillus subtilis]	67	44	540
152	8	6341	6673	gi|1377841	unknown [Bacillus subtilis]	67	48	333
161	4	2720	1763	gi|496319	Sphx [Synechococcus sp.]	67	47	1044
163	6	1989	3428	gi|599681	2-oxoglutarate/malate translocator [Spinacia oleracea]	67	47	1440
193	3	1351	1626	gi|1511101	shikimate 5-dehydrogenase [Methanococcus jannaschii]	67	53	276
200	2	917	2179	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	67	48	1263
206	10	12445	12801	sp|P37347|YECD_	HYPOTHETICAL 21.8 KD PROTEIN IN ASPS 5'REGION.	67	47	357
206	11	13047	14432	gi|732813	branched-chain amino acid carrier [Lactobacillus delbrueckii]	67	46	1386
208	2	1321	809	gi|1033037	100 kDa heat shock protein (Hsp100) [Leishmania major]	67	36	513
238	3	1039	2052	gi|809542	CbrB protein [Erwinia chrysanthemi]	67	42	1014

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
246	2	176	367	gi|215098	excisionase [Bacteriophage 154x]	67	37	192
276	2	2260	1412	gi|303560	ORF271 [Escherichia coli]	67	50	849
297	6	2223	3056	gi|142784	CtaA protein [Bacillus firmus]	67	46	834
307	7	5220	4186	gi|1070013	protein-dependent [Bacillus subtilis]	67	43	1035
316	1	36	1028	gi|1161061	dioxygenase [Methylobacterium extorquens]	67	52	993
324	3	5650	5030	gi|169784	putative cell division protein ftsW [Enterococcus hirae]	67	49	621
336	1	524	264	gi|173122	urea amidolyase [Saccharomyces cerevisiae]	67	45	261
360	1	108	1194	gi|P3005J|SYH_S	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).	67	47	1287
364	3	4890	3592	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	67	46	1299
365	3	2940	2113	gi|1296823	orf2 gene product [Lactobacillus helveticus]	67	47	828
367	2	325	918	gi|1039479	ORFU [Lactococcus lactis]	67	47	594
395	3	666	1271	gi|1204516	hypothetical protein (GB:U00014_4) [Haemophilus influenzae]	67	55	606
415	1	1800	901	gi|382579	CG Site No. 29739 [Escherichia coli]	67	46	900
419	1	1799	903	gi|520752	putative [Bacillus subtilis]	67	48	897
474	1	2	796	gi|AA6906	argininosuccinate synthetase [Streptomyces clavuligerus] pir|S57659|S57659 argininosuccinate synthase (EC 6.3.4.5) - streptomyces clavuligerus	67	49	794
485	2	1921	2226	gi|143434	Rho Factor [Bacillus subtilis]	67	43	306
556	1	1728	865	gi|1303853	YqgF [Bacillus subtilis]	67	47	864
700	1	433	218	gi|1204628	hypothetical protein (SP:P21498) [Haemophilus influenzae]	67	47	216
806	2	249	647	gi|677947	AppC [Bacillus subtilis]	67	51	399
828	2	340	900	gi|777761	llrA [Synechococcus sp.]	67	37	561
833	1	1407	916	gi|142996	regulatory protein [Bacillus subtilis]	67	41	492
856	1	1555	779	gi|780224	2K970.2 [Caenorhabditis elegans]	67	38	777
888	1	1614	850	gi|437315	TTG start codon [Bacillus licheniformis]	67	40	765
1034	1	1190	597	gi|1205113	hypothetical protein (GB:L19201_15) [Haemophilus influenzae]	67	45	594
1062	1	636	319	gi|1303850	YqgC [Bacillus subtilis]	67	41	318
1067	1	918	460	pir|A32950|A329	probable reductase protein - Leishmania major	67	54	459

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1358	1	3	293	gi|1001369	hypothetical protein (Synechocystis sp.)	67	44	291
2181	2	3	302	gi|1510416	hypothetical protein (SP:P31466) (Methanococcus jannaschii)	67	48	300
3000	1	1	507	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus yogenes)	67	56	507
3066	1	464	234	gi|308861	GTG start codon (Lactococcus lactis)	67	46	231
3087	1	454	251	gi|1205366	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	67	47	204
3101	1	2	256	gi|1531541	uroporphyrinogen III methyltransferase (Zea mays)	67	55	255
3598	1	728	193	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevaloni1) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	67	56	336
3765	2	584	166	gi|557489	menD (Bacillus subtilis)	67	45	219
3788	1	658	398	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	67	45	261
3883	1	2	265	gi|704397	cystathionine beta-lyase (Arabidopsis thaliana)	67	46	264
3926	1	2	340	gi|1483199	peptide-synthetase (Amycolatopsis mediterranei)	67	44	339
4417	1	82	396	gi|1205337	ribonucleotide transport ATP-binding protein (Haemophilus influenzae)	67	46	315
2	3	3075	3989	gi|535348	CodV (Bacillus subtilis)	66	42	915
15	6	2273	2542	gi|46491	SmtB (Synechococcus PCC7942)	66	37	270
11	9	8059	7826	gi|292046	mucin (Homo sapiens)	66	44	234
31	10	9034	9258	gi|1204545	mercury scavenger protein (Haemophilus influenzae)	66	48	225
32	6	6347	5253	gi|998342	inducible nitric oxide synthase (Gallus gallus)	66	47	1095
44	13	8856	10124	gi|1510751	molybdenum cofactor biosynthesis moeA protein (Methanococcus jannaschii)	65	46	1269
48	2	1276	2868	gi|150209	ORF 1 (Mycoplasma mycoides)	66	40	1593
58	8	7178	8428	gi|665999	hypothetical protein (Bacillus subtilis)	66	47	1251
62	7	5143	4370	gi|1072398	phaD gene product (Rhizobium meliloti)	66	40	774
70	14	11693	10998	gi|809660	deoxyribose-phosphate aldolase (Bacillus subtilis) pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acilius subtilis	66	55	696
76	1	1	1105	gi|142440	ATP-dependent nuclease (Bacillus subtilis)	66	42	1305
91	6	9236	8205	gi|704397	cystathionine beta-lyase (Arabidopsis thaliana)	66	43	1032
102	5	3810	3265	gi|1204323	hypothetical protein (SP:P31805) (Haemophilus influenzae)	66	41	546

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	Match gene name	% sim	% ident	Length (nt)
101	4	3418	2712	gi|971344	nitrate reductase gamma subunit [Bacillus subtilis] sp|P42177|NARI_BACSU NITRATE REDUCTASE GAMMA CHAIN (EC 1.7.99.4). g:|I009369 Respiratory nitrate reductase [Bacillus subtilis] (SUB -160)	66	48	687
109	6	4243	4674	gi|170886	glucosamine-6-phosphate deaminase [Candida albicans] pir|A46652|A46652 glucosamine-6-phosphate isomerase (EC 5.3.1.10) - east (Candida albicans)	66	45	432
112	17	17491	17712	gi|1323179	ORF YGR111w [Saccharomyces cerevisiae]	66	33	222
116	2	4667	2637	gi|1491813	gamma-glutamyltranspeptidase [Bacillus subtilis]	66	43	2031
150	5	3189	2989	gi|1146224	putative [Bacillus subtilis]	66	30	201
172	5	3264	3662	gi|755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	66	41	399
174	5	4592	3723	gi|1146261	pantothenate synthetase [Bacillus subtilis]	66	49	870
175	4	3209	2880	gi|642655	unknown [Rhizobium meliloti]	66	29	330
175	11	8743	7994	gi|854655	Na/H antiporter system [Bacillus alcalophilus]	66	43	750
190	5	7079	5727	gi|451072	di-tripeptide transporter [Lactococcus lactis]	66	40	1353
195	15	13919	13713	gi|1322411	unknown [Mycobacterium tuberculosis]	66	42	207
217	3	2822	2595	gi|1143582	alternative stop codon [Rattus norvegicus]	66	36	228
233	9	7133	6135	gi|1458327	F08F3.4 gene product [Caenorhabditis elegans]	66	47	999
238	1	41	1041	gi|A09541	ChrA protein [Erwinia chrysanthemi]	66	42	999
241	1	2102	1053	gi|153067	peptidoglycan hydrolase [Staphylococcus aureus]	66	51	1050
261	1	1178	648	gi|1510859	M. jannaschii predicted coding region MJ0790 [Methanococcus jannaschii]	66	40	531
263	3	3731	2973	gi|1205865	tetrahydrodipicolinate N-succinyltransferase [Haemophilus influenzae]	66	47	759
272	8	6548	5484	gi|882101	high affinity nickel transporter [Alcaligenes eutrophus] sp|P23516|HOXN_ALCEU HIGH-AFFINITY NICKEL TRANSPORT PROTEIN.	66	44	1065
276	3	2805	2104	gi|1200965	hypothetical 23.3 kd protein [Escherichia coli]	66	47	702
278	2	2830	1784	gi|1488662	phosphatase-associated protein [Bacillus subtilis]	66	48	1047
278	3	3830	2952	gi|303560	ORF271 [Escherichia coli]	66	45	879
279	2	3894	2218	gi|1185289	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1- carboxylate synthase [Bacillus subtilis]	66	48	1677
288	4	2535	2275	gi|1256625	putative [Bacillus subtilis]	66	42	261
292	2	1133	942	gi|1511604	M. jannaschii predicted coding region MJ1651 [Methanococcus jannaschii]	66	30	192

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
294	1	1116	559	gi|216314	esterase [Bacillus stearothermophilus]	66	45	558
297	4	2913	1978	gi|994794	cytochrome a assembly facto (Bacillus subtilis) sp|P24009|COXX_BACSU PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR.	66	45	936
316	4	2053	2682	gi|1107839	alginate lyase [Pseudomonas aeruginosa]	66	40	630
338	4	2460	2302	gi|520750	biotin synthetase [Bacillus sphaericus]	66	59	159
339	1	1214	735	gi|467468	7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase [Bacillus ubtilis]	66	52	480
363	1	3	863	gi|581649	epiC gene product (Staphylococcus epidermidis]	66	47	861
366	2	232	483	gi|1103505	unknown [Schizosaccharomyces pombe]	66	53	252
367	4	2468	1845	sp|P20692|TYRA_	PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).	66	50	624
372	3	2150	1599	gi|467416	unknown [Bacillus subtilis]	65	38	552
378	1	212	1009	gi|147309	purine nucleoside phosphorylase [Escherichia coli]	66	50	798
401	1	1	462	gi|388263	p-aminobenzoic acid synthase (Streptomyces griseus) pir|JNO531|JNO531 p-aminobenzoic acid synthase - Streptomyces riseus	66	46	462
404	7	4826	5254	gi|606744	cytidine deaminase [Bacillus subtilis]	66	51	429
411	2	1738	1103	gi|1160081	unknown [Mycobacterium tuberculosis]	66	44	636
420	1	2	541	gi|1046024	Na+ ATPase subunit J [Mycoplasma genitalium]	66	49	540
431	1	1	858	gi|1500008	M. jannaschii predicted coding region KJ1154 [Methanococcus jannaschii]	64	60	858
443	7	5679	5299	gi|852076	MrgA [Bacillus subtilis]	66	46	381
444	3	3405	2413	gi|153047	lysostaphin (ttg start codon) (Staphylococcus simulans) pir|A25881|A25881 lysostaphin precursor - Staphylococcus simulans sp|P10547|LSTP_STASI LYSOSTAPHIN PRECURSOR (EC 3.5.1.-).	66	51	993
561	1	956	480	gi|1204905	DNA-3-methyladenine glycosidase I [Haemophilus influenzae]	66	45	477
562	3	1066	1383	gi|1046082	M. genitalium predicted coding region MG372 [Mycoplasma genitalium]	66	52	318
576	1	11	724	gi|305014	ORF_o234 (Escherichia coli)	66	43	714
577	3	1190	903	gi|1001353	hypothetical protein (Synechocystis sp.)	66	52	288
584	1	2	331	sp|P24204|YEBA_	HYPOTHETICAL 46.7 KD PROTEIN IN MSBB-RUVB INTERGENIC REGION (ORFU).	66	48	330
592	1	1410	706	gi|928839	ORF266: putative (Lactococcus lactis phage BK5-T)	66	51	705
601	1	1433	720	gi|1488695	novel antigen; orf-2 (Staphylococcus aureus)	66	55	714

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
619	3	468	845	gi|746573	similar to M. musculus transport system membrane protein, Nramp PIR:A40739) and S. cerevisiae SMF1 protein (PIR:A45154) Caenorhabditis elegans)	66	45	378
706	2	561	355	gi|804808	unknown protein (Rattus norvegicus)	66	46	207
734	2	673	512	gi|1519085	phosphatidylcholine binding immunoglobulin heavy chain IgH variable region (Mus musculus)	66	60	162
740	1	3	317	gi|1209272	argininosuccinate-lyase (Campylobacter jejuni)	66	47	315
764	1	310	747	gi|435296	alkaline phosphatase like protein (Lactococcus lactis) pir[S39339|S39339 alkaline phosphatase-like protein - Lactococcus actis	66	42	438
852	1	338	171	gi|536955	CG site No. 361 (Escherichia coli)	66	43	168
886	1	3	158	gi|289272	ferrichrome-binding protein (Bacillus subtilis)	66	44	156
889	1	462	232	gi|833061	HCMVUL77 (AA 1-642) (Human cytomegalovirus)	66	66	231
893	1	2	247	gi|149008	putative (Helicobacter pylori)	66	45	246
900	1	1425	733	gi|580842	F3 (Bacillus subtilis)	66	51	693
906	2	2300	1473	gi|790945	aryl-alcohol dehydrogenase (Bacillus subtilis)	66	53	828
947	1	79	549	gi|410117	diaminopimelate decarboxylase (Bacillus subtilis)	66	47	471
950	1	1100	552	gi|48713	orf145 (Staphylococcus aureus)	66	35	549
955	2	89	475	gi|1204390	uridine kinase (uridine monophosphokinase) (Haemophilus influenzae)	66	50	387
981	2	1308	997	gi|457146	rhoptry protein (Plasmodium yoelii)	66	18	311
986	1	25	315	gi|305002	ORF_f356 (Escherichia coli)	66	31	291
1057	1	3	203	gi|1303853	YqgF (Bacillus subtilis)	66	40	201
1087	1	1	294	gi|575913	unknown (Saccharomyces cerevisiae)	66	53	294
1105	1	1	231	gi|1045799	methylgalactoside permease ATP-binding protein (Mycoplasma genitalium)	66	46	231
1128	1	2	574	gi|1001493	hypothetical protein (Synechocystis sp.)	66	46	573
1150	1	498	250	gi|1499034	M. jannaschii predicted coding region MJ0255 (Methanococcus jannaschii)	66	40	249
1180	2	707	453	gi|215908	DNA polymerase (g43) (Bacteriophage T4)	66	46	255
1208	1	1123	587	gi|1256653	DNA-binding protein (Bacillus subtilis)	66	58	537
1342	1	1	402	gi|1208474	hypothetical protein (Synechocystis sp.)	66	53	402
1761	2	589	398	gi|215811	tail fiber protein (Bacteriophage T3)	66	50	192

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1983	1	499	251	gi|1045935	DNA helicase II [Mycoplasma genitalium]	66	40	249
2103	2	176	400	gi|929798	precursor for the major merozoite surface antigens [Plasmodium falciparum]	66	46	225
2341	1	373	188	gi|1256621	exodeoxyribonuclease [Bacillus subtilis]	66	38	186
2458	1	325	164	gi|1019410	unknown [Schizosaccharomyces pombe]	66	47	162
2505	1	468	235	gi|1510394	putative transcriptional regulator [Methanococcus jannaschii]	66	39	234
2525	1	558	280	gi|1000695	cytotoxin L [Clostridium sordellii]	66	44	279
2935	1	3	275	gi|765073	autolysin [Staphylococcus aureus]	66	47	273
3005	1	114	305	gi|1205784	heterocyst maturation protein [Haemophilus influenzae]	66	46	192
3048	1	80	277	gi|1303813	YqeW [Bacillus subtilis]	66	42	198
3071	1	1	189	gi|1070014	protein-dependent [Bacillus subtilis]	66	41	189
3081	1	404	225	gi|984212	unknown [Schizosaccharomyces pombe]	66	44	180
3090	2	580	386	gi|1204987	DNA polymerase III, alpha chain [Haemophilus influenzae]	66	48	195
3318	1	1	387	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	66	49	387
3739	1	798	400	gi|1109684	ProV [Bacillus subtilis]	66	47	399
3796	1	402	202	gi|853760	acyl-CoA dehydrogenase [Bacillus subtilis]	66	60	201
3924	1	197	347	gi|563952	gluconate permease [Bacillus licheniformis]	66	46	249
4240	1	3	350	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.88) Pseudomonas sp.	66	51	348
4604	1	7	234	pir|A26713|BHHC	hemocyanin subunit II - Atlantic horseshoe crab	66	46	228
4	9	8845	9750	gi|145646	cynR [Escherichia coli]	65	35	906
6	5	2708	3565	gi|887824	ORF_o110 [Escherichia coli]	65	47	858
13	1	1993	998	gi|143402	recombination protein (ttg start codon) [Bacillus subtilis] gi|1303923 RecN [Bacillus subtilis]	65	44	996
15	7	2493	3524	gi|1403126	czcD gene product [Alcaligenes eutrophus]	65	38	1032
18	3	1908	1372	gi|349187	acyltransferase [Saccharomyces cerevisiae]	65	50	537
21	3	1467	2492	gi|149518	phosphoribosyl anthranilate transferase [Lactococcus lactis] pir|S35126|S35126 anthranilate phosphoribosyltransferase (EC 4.2.18) - Lactococcus lactis subsp. lactis	65	52	1026
25	4	3374	4312	gi|1502420	malonyl-CoA:Acyl carrier protein transacylase [Bacillus subtilis]	65	44	939

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
27	2	390	626	gi|1212729	YqhJ (Bacillus subtilis)	65	45	237
11	12	11040	10187	gi|509245	D-hydroxyisocaproate dehydrogenase (Lactobacillus delbrueckii)	65	41	654
38	24	19172	19528	gi|547:	M-protein (Flaveria cronquistii)	65	41	357
44	2	790	1746	gi|405882	yelx (Escherichia coli)	65	46	957
44	12	9356	8832	gi|1205905	molybdenum cofactor biosynthesis protein (Haemophilus influenzae)	65	50	525
45	8	6615	7588	gi|493074	ApbA protein (Salmonella typhimurium)	65	46	954
51	2	580	1503	gi|580897	OppB gene product (Bacillus subtilis)	65	45	924
52	1	225	953	gi|1205518	NAD(P)H-flavin oxidoreductase (Haemophilus influenzae)	65	41	729
55	4	1339	1058	pir|A44459|A444	troponin T beta TnT-5 - rabbit	65	42	282
67	9	7421	8272	gi|143607	sporulation protein (Bacillus subtilis)	65	42	852
73	5	4446	5375	gi|1204896	lysophospholipase L2 (Haemophilus influenzae)	65	37	930
74	1	954	478	gi|1204844	H. influenzae predicted coding region HI0594 (Haemophilus influenzae)	65	50	477
77	1	2	757	gi|1046082	M. genitalium predicted coding region MG372 (Mycoplasma genitalium)	65	46	756
77	2	795	1433	gi|1222116	permease (Haemophilus influenzae)	65	37	639
81	3	4728	3454	gi|1001708	hypothetical protein (Synechocystis sp.)	65	49	1275
91	7	8548	8357	gi|1399263	cystathionine beta-lyase (Emericella nidulans)	65	40	192
98	3	1608	1988	gi|467423	unknown (Bacillus subtilis)	65	38	381
96	4	2250	2987	gi|467424	unknown (Bacillus subtilis)	65	45	738
102	3	2598	2119	gi|1511532	N-terminal acetyltransferase complex, subunit ARD1 (Methanococcus jannaschii)	65	39	480
102	4	3647	2862	gi|1204637	H. influenzae predicted coding region HI0388 (Haemophilus influenzae)	65	32	786
103	9	10851	9841	gi|142695	S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium	65	47	1011
103	10	10439	10119	gi|710021	nitrite reductase (nirD) (Bacillus subtilis)	65	51	321
106	2	262	1140	gi|39881	ORF 311 (AA 1-311) (Bacillus subtilis)	65	44	879
109	5	3909	4268	gi|1204399	glucosamine-6-phosphate deaminase protein (Haemophilus influenzae)	65	44	360
109	10	7165	8595	gi|536955	CG Site No. 361 (Escherichia coli)	65	41	1431

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
110	4	3688	3915	gi|407881	stringent response-like protein [Streptococcus equisimilis] pir|S39975|S39975 stringent response-like protein - Streptococcus quisimilis	65	45	228
110	5	3882	4295	gi|407880	ORF1 [Streptococcus equisimilis]	65	50	414
110	6	4231	4380	gi|1139574	Orf2 [Streptomyces griseus]	65	56	150
112	10	9218	8640	gi|1204571	H. influenzae predicted coding region HI0318 [Haemophilus influenzae]	65	52	579
112	12	12049	11288	gi|710496	transcriptional activator protein [Bacillus brevis]	65	32	762
125	12	2	202	gi|1151158	repeat organellar protein [Plasmodium chabaudi]	65	39	201
126	11	3	422	gi|37589	precursor [Homo sapiens]	65	46	420
127	11	10733	12658	gi|1064809	homologous to sp:MTRA_ECOLI [Bacillus subtilis]	65	41	1926
143	8	7543	7004	gi|216513	mutator mutT (AT-GC transversion) [Escherichia coli]	65	56	540
145	5	3587	3838	gi|1209768	D02_orf569 [Mycoplasma pneumoniae]	65	27	252
150	4	3482	2841	gi|1146225	putative [Bacillus subtilis]	65	37	642
166	1	3858	1948	gi|148304	Beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir|A42296|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790)	65	50	1911
188	6	3195	4178	gi|151963	ORF3; putative [Rhodobacter capsulatus]	65	46	984
189	7	4982	4785	gi|158812	ORF IV (AA 1-489) [Figwort mosaic virus]	65	40	198
195	6	7908	5272	gi|145220	alanyl-tRNA synthetase [Escherichia coli]	65	44	2637
195	7	10599	8104	gi|82711	exonuclease V alpha-subunit [Escherichia coli]	65	38	2496
206	16	16896	18191	gi|468115	ornithine acetyltransferase [Bacillus subtilis]	65	53	1296
217	4	3844	3215	gi|1205974	5'guanylate kinase [Haemophilus influenzae]	65	41	630
220	4	5265	3751	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13484|TAGF_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPIIA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E)	65	40	1515
236	5	2327	3709	gi|1146200	DNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis]	65	46	1383
237	3	1902	2513	gi|149379	HisBd [Lactococcus lactis]	65	46	612
241	4	4968	4195	gi|1205308	ribonuclease HII (EC 3.1.26.4) (RNASE HII) [Haemophilus influenzae]	65	50	774
252	1	1278	940	gi|1204989	hypothetical protein (GB:U00022_9) [Haemophilus influenzae]	65	40	339
261	5	4780	3794	gi|145927	fecD [Escherichia coli]	65	43	987

TABLE 2

S aureus : Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
274	1	3	278	gi|496558	orfX [Bacillus subtilis]	65	42	276
301	2	982	815	gi|67418	unknown [Bacillus subtilis]	65	45	168
307	4	3586	2864	gi|1070014	protein-dependent [Bacillus subtilis]	65	40	723
335	2	2286	1399	gi|46913	N-acetylglucosamine transport protein (Escherichia coli) pir|B29895|WQEC2N phosphotransferase system enzyme II (EC .7.1.69), N-acetylglucosamine-specific - Escherichia coli sp|P09323|PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC OMPONENT (EIIA	65	50	888
338	5	4120	3170	gi|1277029	biotin synthase [Bacillus subtilis]	65	49	951
343	3	1490	2800	gi|143264	membrane-associated protein [Bacillus subtilis]	65	48	1311
344	4	2763	2531	gi|1050540	tRNA-glutamine synthetase [Lupinus luteus]	65	34	233
358	3	3421	3621	gi|146220	NAD+ dependent glycerol-3-phosphate dehydrogenase [Bacillus subtilis]	65	47	201
364	1	238	699	gi|140128	ORF1 [Staphylococcus aureus]	65	51	462
379	1	1	576	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTIESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	65	40	576
329	3	3666	4346	gi|143268	dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) [Bacillus ubtilis]	65	50	681
428	1	187	483	gi|420465	ORF YOR195w [Saccharomyces cerevisiae]	65	45	297
438	2	272	838	gi|143498	dcgS protein [Bacillus subtilis]	65	38	567
444	11	9280	10215	gi|1204756	ribokinase [Haemophilus influenzae]	65	47	936
449	2	1241	1531	gi|599848	Na/H antiporter homolog [Lactococcus lactis]	65	41	291
478	2	1452	865	gi|1045942	glycyl-tRNA synthetase [Mycoplasma genitalium]	65	39	588
479	1	1032	517	gi|498192	putative [Pseudomonas aeruginosa]	65	40	516
480	6	4312	5637	gi|415662	UDP-N-acetylglucosamine 1-carboxyvinyl transferase [Acinetobacter alcoaceticus]	65	48	1326
484	1	2	430	gi|146551	transmembrane protein (kdpD) [Escherichia coli]	65	44	429
499	1	54	932	gi|601456	reductase [Leishmania major]	65	53	879
505	1	914	459	gi|518853	OafA [Salmonella typhimurium]	65	39	456
571	2	1509	883	gi|49399	open reading frame upstream glnE [Escherichia coli] ir|S37754|S37754 hypothetical protein XE (glnE 5' region) - cherichia coli	65	44	627
611	2	506	270	gi|10961	RAP-2 [Plasmodium falciparum]	65	40	237

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
705	1	564	283	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	65	52	282
712	1	1	177	gi|289272	[ferrichrome-binding protein [Bacillus subtilis]	65	37	177
712	2	196	354	gi|289272	[ferrichrome-binding protein [Bacillus subtilis]	65	37	159
743	1	2	631	gi|310631	ATP binding protein [Streptococcus gordonii]	65	45	610
749	2	393	779	gi|167376	single strand DNA binding protein [Bacillus subtilis]	65	29'	387
762	1	1698	850	gi|160399	multidrug resistance protein [Plasmodium falciparum]	65	48	849
788	1	85	315	gi|1129096	unknown protein [Bacillus sp.]	65	35	231
850	1	1	408	gi|1006604	hypothetical protein [Synechocystis sp.]	65	37	408
908	1	1	444	gi|1199546	[2362 [Saccharomyces cerevisiae]	65	46	444
925	1	1	174	gi|1256653	DNA-binding protein [Bacillus subtilis]	65	54	174
1031	1	26	232	gi|238657	AppC=cytochrome d oxidase, subunit I homolog [Escherichia coli, K12, eptide, 514 aa]	65	47	207
1037	1	414	262	gi|1491813	gamma-glutamyltranspeptidase [Bacillus subtilis]	65	46	153
1053	1	1	175	gi|642655	[unknown [Rhizobium meliloti]	65	33	174
1149	1	1399	752	gi|1162980	ribulose-5-phosphate 3-epimerase [Spinacia oleracea]	65	48	648
1214	1	881	495	gi|1205959	lactam utilization protein [Haemophilus influenzae]	65	45	387
1276	1	476	276	pir|[535493|S354]	site-specific DNA-methyltransferase StsI (EC 2.1.1.-) - Streptococcus sanguis	65	35	201
1276	2	900	577	gi|473794	'ORF' [Escherichia coli]	65	34	324
2057	1	272	138	gi|633699	TrsH [Yersinia enterocolitica]	65	21	135
2521	1	336	169	gi|1045789	hypothetical protein [GB:U14003_76] [Mycoplasma genitalium]	65	41	168
2974	1	590	297	gi|152052	enantiomerase-selective amidase [Rhodococcus sp.]	65	45	294
3031	1	306	154	pir|[JQ1024|JQ10]	hypothetical 30K protein [DmNP140 5' region] - fruit fly (Drosophila melanogaster)	65	35	153
3069	1	3	278	gi|144906	product homologous to E.coli thioredoxin reductase: J.Biol.Chem. 1988) 263:9015-9019, and to F52a protein of alkyl hydroperoxide eductase from S.typhimurium: J.Biol.Chem. (1990) 265:10535-10540. pen reading frame A [Clostridium pasteurianum]	65	46	276
3146	1	282	142	gi|49315	ORF1 gene product [Bacillus subtilis]	65	47	141
3170	1	679	341	gi|1507711	indolepyruvate decarboxylase [Erwinia herbicola]	65	44	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
046	1	1	301	gi|450688	hsdM gene of Ecoprrl gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	65	42	301
782	1	2	328	gi|166412	NADH-glutamate synthase [Medicago sativa]	65	42	327
990	1	374	189	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	65	53	186
1032	1	613	308	gi|1123127	ORF YGR087c [Saccharomyces cerevisiae]	65	50	306
1278	2	726	364	gi|1197667	vitellogenin [Anolis pulchellus]	65	42	363
19	4	4259	5518	gi|145727	deaD [Escherichia coli]	64	45	1260
19	6	7639	6926	gi|1016232	ycf27 gene product [Cyanophora paradoxa]	64	36	714
20	8	7053	6454	gi|765073	autolysin [Staphylococcus aureus]	64	47	600
31	13	12706	11537	gi|414009	ipa-85d gene product [Bacillus subtilis]	64	45	1170
33	4	2388	4364	gi|1204696	fructose-permease IIBC component [Haemophilus influenzae]	64	47	1977
36	3	1871	3013	gi|290503	glutamate permease [Escherichia coli]	64	40	1143
37	6	4065	4409	gi|39815	orf 2 gene product [Bacillus subtilis]	64	46	345
45	9	7852	8760	gi|1220585	nucleotide sugar epimerase [Vibrio cholerae 0139]	64	53	909
51	3	1540	1899	gi|1303961	YqjJ [Bacillus subtilis]	64	50	360
56	6	4793	3855	gi|457514	gltC [Bacillus subtilis]	64	45	919
56	24	30002	30247	gi|470031	similar to zinc fingers [Caenorhabditis elegans]	64	42	246
62	4	2759	2421	gi|642655	unknown [Rhizobium meliloti]	64	28	339
85	6	7178	6027	gi|457702	5-aminoimidazole ribonucleotide-carboxilase [Pichia methanolica] pir|S39112|S39112 phosphoribosylaminoimidazole carboxylase (EC .1.1.21) - yeast [Pichia methanolica]	64	46	1152
96	9	9251	10030	gi|1511513	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	64	42	780
100	1	1	600	gi|765073	autolysin [Staphylococcus aureus]	64	44	600
106	5	3868	4854	gi|466778	lysine specific permease [Escherichia coli]	64	46	987
123	2	838	554	gi|467484	unknown [Bacillus subtilis]	64	47	285
127	8	7514	7810	gi|10061	serotype-specific antigen [African horse sickness virus] pir|S27891|S27891 capsid protein VP2 - African horse sickness virus	64	28	297
131	7	7134	6721	gi|1511160	M. jannaschii predicted coding region MJ1163 [Methanococcus jannaschii]	64	46	414

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
142	5	5455	4817	gi|1173517	riboflavin synthase alpha subunit (Actinobacillus pleuropneumoniae)	64	44	639
143	1	709	356	pir|A32950|A329	probable reductase protein - Leishmania major	64	52	354
149	10	3555	3295	gi|398151	major surface antigen MSG2 (Pneumocystis carinii)	64	44	261
154	4	3134	2307	gi|984587	DinP (Escherichia coli)	64	50	828
161	5	3855	4880	gi|903304	ORF72 (Bacillus subtilis)	64	37	1026
165	1	33	791	gi|467483	unknown (Bacillus subtilis)	64	38	759
175	6	6355	4844	gi|1072398	phaD gene product (Rhizobium meliloti)	64	42	1512
188	3	2042	2500	gi|1001961	MHC class II analog (Staphylococcus aureus)	64	45	459
195	14	13667	13446	gi|396380	No definition line found (Escherichia coli)	64	47	222
206	15	16429	16938	gi|304134	argC (Bacillus stearothermophilus)	64	49	510
215	1	560	282	gi|142359	ORF 6 (Azotobacter vinelandii)	64	39	279
243	7	7818	6928	gi|414014	ipa-90d gene product (Bacillus subtilis)	64	49	891
258	2	1330	845	gi|664754	P17 (Listeria monocytogenes)	64	38	486
259	1	462	232	gi|1499663	M. jannaschii predicted coding region MJ0837 (Methanococcus jannaschii)	64	52	231
263	6	6565	5567	gi|142828	aspartate semialdehyde dehydrogenase [Bacillus subtilis] sp|Q04797|DHAS_BACSU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC .2.1.11) (ASA DEHYDROGENASE).	64	48	999
271	1	3	1163	gi|467091	hflX; B2235_C2_202 (Mycobacterium leprae)	64	44	1161
280	1	173	1450	gi|1303839	YqfR (Bacillus subtilis)	64	43	1278
293	1	2532	1267	gi|147345	primosomal protein n' (Escherichia coli)	64	45	1266
295	2	742	1488	gi|459266	Potential membrane spanning protein (Staphylococcus hominis) pir|S42932|S42932 potential membrane spanning protein - taphylococcus hominis	64	39	747
301	5	1625	1446	gi|580035	lysine decarboxylase (Bacillus subtilis)	64	35	180
315	4	5064	3949	gi|143396	quinol oxidase (Bacillus subtilis)	64	45	1116
321	1	1264	635	gi|710496	transcriptional activator protein (Bacillus brevis)	64	41	630
333	5	4520	4239	gi|1314295	ORF2; putative 19 kDa protein (Listeria monocytogenes)	64	43	282
342	1	1	549	gi|142940	ftsA (Bacillus subtilis)	64	38	549
353	3	2878	2324	gi|537049	ORF_0470 (Escherichia coli)	64	44	555

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
379	2	827	3658	pir|S25295|A328	oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Bacillus subtilis	64	47	2832
404	6	4429	4839	pir|A36933|A369	diacylglycerol kinase homolog - Streptococcus mutans	64	35	411
407	1	2020	1133	gi|969026	orfx (Bacillus subtilis)	64	41	888
425	1	1109	591	gi|1146177	phosphotransferase system glucose-specific enzyme II (Bacillus subtilis)	64	44	519
443	6	4082	4798	gi|147309	purine nucleoside phosphorylase (Escherichia coli)	64	51	717
450	2	1035	1604	gi|606176	ORF_o162 (Escherichia coli)	64	38	570
470	5	1680	6107	gi|1369948	host interacting protein (Bacteriophage B1)	64	45	4428
486	4	1911	1471	gi|1205582	spermidine/putrescine transport system permease protein (Haemophilus influenzae)	64	35	441
497	1	2217	1159	sp|P36929|FMU_E	FMU PROTEIN.	64	38	1059
501	1	3	410	gi|142450	ahrC protein (Bacillus subtilis)	64	38	408
514	1	3	290	gi|1204496	H. influenzae predicted coding region HI0238 (Haemophilus influenzae)	64	34	288
551	4	3162	3323	gi|1204511	bacterioferritin comigratory protein (Haemophilus influenzae)	64	41	162
603	4	759	956	gi|755823	NADH dehydrogenase F (Streptogyna americana)	64	35	198
651	2	940	746	gi|211234	dicarboxylic amino acids Dip5p permease (Saccharomyces cerevisiae)	64	41	195
660	1	3601	2257	sp|P46133|YUAH_	HYPOTHETICAL PROTEIN IN OGT 5'REGION (FRAGMENT).	64	39	1345
695	1	11	502	gi|1001383	hypothetical protein (Synechocystis sp.)	64	41	492
702	1	3	752	gi|142865	DNA primase (Bacillus subtilis)	64	46	750
826	1	1	339	gi|971336	arginyl tRNA synthetase (Bacillus subtilis)	64	50	339
838	1	1831	917	gi|1354775	pfoS/R (Treponema pallidum)	64	41	915
864	3	675	944	gi|39833	cyclomaltodextrin glucanotransferase (Bacillus stearothermophilus) i|39835 cyclomaltodextrin glucanotransferase (Bacillus earothermophilus)	64	47	270
AA7	1	3	677	gi|153002	enterotoxin type E precursor (Staphylococcus aureus) pir|A28179|A28179 enterotoxin E precursor - Staphylococcus aureus sp|P12293|ETXE_STAAU ENTEROTOXIN TYPE E PRECURSOR (SEE).	64	46	675
92H	2	1172	963	gi|311976	[fibrinogen-binding protein (Staphylococcus aureus) pir|S34270|S34270 fibrinogen-binding protein - Staphylococcus ureus	64	41	210
1049	2	800	606	gi|1049115	Rap60 (Bacillus subtilis)	64	42	195
1067	2	999	748	gi|1151072	HhdA precursor [Haemophilus ducreyi]	64	50	252

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1120	1	50	202	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	64	30	153
1125	1	751	377	gi|581648	epiB gene product [Staphylococcus epidermidis]	64	44	375
1688	1	402	214	pir|A01365|TVMS	transforming protein K-ras - mouse	64	47	189
2472	1	2	358	gi|487282	Na+ -ATPase subunit J [Enterococcus hirae]	64	36	357
2989	1	520	356	gi|304134	argC [Bacillus stearothermophilus]	64	50	165
3013	1	630	352	gi|551699	cytochrome oxidase subunit I [Bacillus firmus]	64	51	279
3034	1	546	274	gi|1204349	hypothetical protein (GB:GB:D90212_3) [Haemophilus influenzae]	64	50	273
3197	1	613	308	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	64	46	306
3303	1	90	362	gi|1107839	alginate lyase [Pseudomonas aeruginosa]	64	43	273
3852	2	82	288	gi|216746	D-lactate dehydrogenase [Lactobacillus plantarum]	64	42	207
1868	1	1	312	gi|149435	putative [Lactococcus lactis]	64	48	312
3918	1	660	331	gi|5532	acetyl-CoA acyltransferase [Yarrowia lipolytica]	64	46	330
4000	1	112	378	gi|994688	unknown [Saccharomyces cerevisiae]	64	44	267
4009	1	81	368	gi|39372	grsB gene product [Bacillus brevis]	64	41	288
4166	1	2	349	gi|149435	putative [Lactococcus lactis]	64	46	348
4366	1	2	307	gi|216257	ORF2 [Bacillus megaterium]	64	44	306
4457	1	2	400	gi|1197667	vitellogenin [Anolis pulchellus]	64	43	399
11	3	1539	2438	gi|438228	ORF C [Staphylococcus aureus]	63	32	900
24	7	5611	5423	gi|369943	al gene product [Bacteriophage B1]	63	34	189
29	1	1	390	gi|467441	expressed at the end of exponential growyh under condtions in which he enzymes of the TCA cycle are repressed [Bacillus subtilis] gi|467441 expressed at the end of exponential growyh under ondtions in which the enzymes of the TCA cycle are repressed Bacil	63	43	390
31	6	6329	5712	gi|496943	ORF [Saccharomyces cerevisiae]	63	47	618
44	123	14669	15019	pir|A04446|QQEC	hypothetical protein F-92 - Escherichia coli	63	36	351
48	6	4403	6250	gi|43498	pyruvate synthase [Halobacterium halobium]	63	42	1848
50	5	3869	4738	gi|413967	ipa-43d gene product [Bacillus subtilis]	63	43	870
53	6	6764	5742	gi|474176	regulator protein [Staphylococcus xylosus]	63	49	1023

TABLE 2

Turbus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	# nim	% ident	length (nt)
56	14	15880	17607	gi|467409	DNA polymerase III subunit (Bacillus subtilis)	63	44	1728
57	11	7945	7376	gi|137016	ORF_o158 (Escherichia coli)	63	39	570
62	3	2479	2114	gi|42656	unknown (Rhizobium meliloti)	63	41	366
70	8	6562	7353	gi|1199821	PhoC (Rhizobium meliloti)	63	46	792
75	2	223	927	gi|49376	HisG (Lactococcus lactis)	63	45	705
78	5	4912	4403	gi|413950	ipa-26d gene product (Bacillus subtilis)	63	42	510
91	5	9076	7220	gi|466997	metH2; B2126_C1_157 (Mycobacterium leprae)	63	41	1857
91	8	10566	9448	gi|1204344	cystathionine gamma-synthase (Haemophilus influenzae)	63	45	1119
120	1	21	1508	gi|882657	sulfite reductase (NADPH) flavoprotein beta subunit (Escherichia oli)	63	46	1488
120	4	2722	4125	gi|665994	hypothetical protein (Bacillus subtilis)	63	34	1404
127	7	6064	7566	gi|40162	murE gene product (Bacillus subtilis)	63	44	1503
149	6	2321	2106	gi|148503	dnaK (Erysipelothrix rhusiopathiae)	63	40	216
149	26	10445	10170	gi|4870	ORF 2, has similarity to DNA polymerase (Saccharomyces kluyveri) r|S15961|S15961 hypothetical protein 2 - yeast (Saccharomyces yveri) plasmid pSKL	63	42	276
164	2	507	1298	gi|145476	CDP-diglyceride synthetase (Escherichia coli)	63	44	792
166	6	9907	8164	gi|151932	fructose enzyme II (Rhodobacter capsulatus)	63	41	1746
169	4	1704	1886	gi|152886	elongation factor Ts (tsf) (Spiroplasma citri)	63	48	183
188	5	3145	2951	gi|1334547	GTY COI 114 grp IB protein (Podospora anserina)	63	42	195
195	13	11767	12804	gi|606100	ORF_o335 (Escherichia coli)	63	40	1038
201	2	607	2283	gi|433534	arginyl-tRNA synthetase (Corynebacterium glutamicum) pir|A49936|A49936 arginine--tRNA ligase (EC 6.1.19) - orynebacterium glutamicum	63	46	1677
206	14	15891	16489	gi|580828	N-acetyl-glutamate-gamma-semialdehyde dehydrogenase (Bacillus subtilis)	63	49	597
220	5	7763	5766	gi|216334	secA protein (Bacillus subtilis)	63	42	2004
221	1	74	907	gi|677945	AppA (Bacillus subtilis)	63	42	834
227	3	944	1708	gi|1510558	cobyric acid synthase (Methanococcus jannaschii)	63	46	765
261	2	804	1070	gi|486511	ORF YKR054c (Saccharomyces cerevisiae)	63	45	267
269	2	1606	1960	gi|148221	DNA-dependent ATPase, DNA helicase (Escherichia coli) pir|JS0117|BVECRQ recQ protein - Escherichia coli	63	42	1647

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
278	8	7417	6176	gi|699273	cystathionine gamma-synthase (Mycobacterium leprae) sp|P46807|METB_MYCLE CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) O-SUCCINYLHOMOSERINE (THIOL)-LYASE).	63	41	1242
287	2	738	1733	gi|405133	putative [Bacillus subtilis]	63	38	996
295	1	2	748	gi|1239983	hypothetical protein [Bacillus subtilis]	63	41	747
128	3	2148	3134	gi|45302	carrier protein (AA 1 - 417) (Pseudomonas aeruginosa) ir|S11497|S11497 branched-chain amino acid transport protein braB - Pseudomonas aeruginosa	63	36	987
362	2	1626	1216	sp|P35136|SERA_	[D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).	63	38	411
404	1	326	1051	gi|1303816	YqeZ [Bacillus subtilis]	63	35	726
405	3	2101	1715	gi|1303914	YqhY [Bacillus subtilis]	63	42	387
406	1	451	227	gi|142152	sulfate permease (gtg start codon) [Synechococcus PCC6301] pir|A30301|GRYCS7 sulfate transport protein - Synechococcus sp. PCC 7942)	63	43	225
415	2	1048	2718	gi|1205402	transport ATP-binding protein [Haemophilus influenzae]	63	41	1671
426	4	3575	2679	gi|393268	29-kiloDalton protein (Streptococcus pneumoniae) sp|P42362|P29K_STRPN 29 KD MEMBRANE PROTEIN IN PSAA 5'REGION ORF1).	63	39	897
505	3	1347	2195	gi|1418999	orf4 [Lactobacillus sake]	63	40	849
507	1	2	574	gi|546917	comK [Bacillus subtilis, E26, Peptide, 192 aa]	63	35	573
562	2	146	1084	gi|43985	nifS-like gene [Lactobacillus delbrueckii]	63	45	939
675	1	427	215	gi|1510994	serine aminotransferase [Methanococcus jannaschii]	63	29	213
686	1	3	230	gi|517356	nitrate reductase (NADH) [Lotus japonicus]	63	52	228
701	1	3	392	gi|881940	NorQ protein [Paracoccus denitrificans]	63	41	390
720	1	2	400	gi|47168	open reading frame [Streptomyces lividans]	63	35	399
779	1	571	287	gi|1261932	unknown [Mycobacterium tuberculosis]	63	41	285
907	1	22	321	gi|149445	ORF1 [Lactococcus lactis]	63	27	300
972	1	794	399	gi|1511235	M. jannaschii predicted coding region MJ1232 [Methanococcus jannaschii]	63	27	396
1085	1	1154	618	gi|1204277	hypothetical protein (GB:U00019_14) [Haemophilus influenzae]	63	38	537
1094	1	3	542	gi|790943	urea amidolyase [Bacillus subtilis]	63	39	540
1108	1	3	482	pir|S49892|S498	regulation protein - Bacillus subtilis	63	44	480
1113	1	1231	617	gi|493017	endocarditis specific antigen [Enterococcus faecalis]	63	45	615

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1100	1	1	695	sp|P33940|YOJH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	63	46	693
1325	1	1	204	gi|928989	p100 protein [Borrelia burgdorferi]	63	30	204
1814	1	3	245	gi|1303914	YqhY [Bacillus subtilis]	63	34	243
2021	1	498	250	pir|C33496|C334	hisC homolog - Bacillus subtilis	63	46	249
2325	1	2	193	gi|436132	product is similar to TnpA of transposon Tn554 from Staphylococcus ureus [Clostridium butyricum]	63	40	192
2335	1	1	195	gi|1184298	flagellar MS-ring protein [Borrelia burgdorferi]	63	47	195
2406	1	451	227	gi|1041785	rhoptry protein [Plasmodium yoelii]	63	33	225
2961	2	136	360	gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolyticus]	63	52	225
2965	1	1	402	gi|1407784	orf-1; novel antigen [Staphylococcus aureus]	63	50	402
2987	1	583	293	gi|1224069	amidase [Moraxella catarrhalis]	63	35	291
2994	1	266	135	gi|836646	phosphoribosylformimino-praic ketoisomerase [Rhodobacter phaeroides]	63	51	132
1043	1	440	252	gi|1480237	phenylacetaldehyde dehydrogenase [Escherichia coli]	63	40	189
3078	1	609	400	gi|1487982	intrinsic membrane protein [Mycoplasma hominis]	63	36	210
3139	1	2	217	gi|439126	glutamate synthase (NADPH) [Azospirillum brasilense] pir|A49916|A49916 glutamate synthase (NADPH) (EC 1.4.1.13) - zospirillum brasilense	63	47	216
1625	1	791	198	gi|623071	ORF160; putative [bacteriophage (L..)]	63	48	494
3658	1	1	399	gi|1303697	YrkA [Bacillus subtilis]	63	37	399
3659	1	3	395	gi|1256135	YbbF [Bacillus subtilis]	63	48	393
3783	1	720	361	gi|1256902	Pyruvate decarboxylase isozyme 2 (Swiss Prot. accession number P16467) [Saccharomyces cerevisiae]	63	36	160
3900	1	338	171	sp|P10537|AMYB_	BETA-AMYLASE (EC 3.2.1.2) (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE).	63	54	168
4309	1	3	176	pir|A37967|A379	neural cell adhesion molecule Ng-CAM precursor - chicken	63	57	174
4367	1	1	195	gi|1121932	Per6p gene product [Pichia pastoris]	63	30	195
4432	1	1	312	gi|45259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	63	51	312
4468	1	6	308	gi|296464	ATPase [Lactococcus lactis]	63	36	303
33	3	1411	2400	gi|153675	tagatose 6-P kinase [Streptococcus mutans]	62	44	990
36	9	5985	6218	gi|1490521	HHSH3 [Homo sapiens]	62	51	234

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
37	1	2	721	gi|1107531	ceuE gene product [Campylobacter coli]	62	33	720
38	15	10912	11589	gi|1222058	H. influenzae predicted coding region HIN1279 [Haemophilus influenzae]	62	38	678
38	25	19526	20329	gi|695280	ORF2 [Alcaligenes eutrophus]	62	41	804
57	2	2523	1780	gi|171234	orf1 [Haemophilus influenzae]	62	55	744
57	9	6646	6350	gi|508174	EIIB domain of PTS-dependent Gat transport and phosphorylation Escherichia coli]	62	35	297
58	1	2	559	gi|755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	62	34	558
67	10	8250	9014	gi|470683	Shows similarity with ATP-binding proteins from other ABC-transport perons. Swiss Prot Accession Numbers P24137, P08007, P04285, P24136 Escherichia coli]	62	31	765
69	8	8315	7494	gi|46816	actVA 4 gene product [Streptomyces coelicolor]	62	44	822
80	3	1793	1320	gi|39993	UDP-N-acetylmuramoylalanine-D-glutamate ligase [Bacillus subtilis]	62	43	474
87	7	7034	9205	gi|217191	5'-nucleotidase precursor [Vibrio parahaemolyticus]	62	38	2172
100	3	4051	3089	gi|1511047	phosphoglycerate dehydrogenase [Methanococcus jannaschii]	62	42	963
102	1	2	520	gi|153655	mismatch repair protein [Streptococcus pneumoniae] pir|C28667|C28667 DNA mismatch repair protein hexA - Streptococcus neumoniae	62	34	519
112	2	466	1068	gi|153741	ATP-binding protein [Streptococcus mutans]	62	37	603
114	7	6855	7562	gi|1204866	L-fucose operon activator [Haemophilus influenzae]	62	38	708
116	4	6823	5613	gi|677947	AppC [Bacillus subtilis]	62	37	1191
124	8	6855	6004	gi|853777	product similar to E.coli PRFA2 protein [Bacillus subtilis] pir|S55438|S55438 ywkE protein - Bacillus subtilis sp|P45873|HEMK_BACSU POSSIBLE PROTOPORPHYRINOGEN OXIDASE (EC .3.3.-).	62	44	852
148	1	24	554	gi|467456	unknown [Bacillus subtilis]	62	30	531
149	20	7591	6725	gi|1205807	replicative DNA helicase [Haemophilus influenzae]	62	41	867
163	3	1503	1153	gi|40067	X gene product [Bacillus sphaericus]	62	42	351
164	15	14673	15632	gi|42219	P35 gene product (AA 1 - 314) [Escherichia coli]	62	38	960
165	2	1166	1447	gi|1403936	phenylalanyl-tRNA synthetase alpha subunit (Gly294 variant) unidentified cloning vector]	62	38	282
166	2	2084	5089	gi|306861	GTG start codon [Lactococcus lactis]	62	43	1006
171	1	1225	614	gi|1046053	hypothetical protein (SP:P32049) [Mycoplasma genitalium]	62	41	612

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
183	1	2521	1310	gi|143045	hemY [Bacillus subtilis]	62	45	1212
200	1	3	956	gi|142419	ATP-dependent nuclease [Bacillus subtilis]	62	32	954
237	2	935	1966	gi|41695	hisC protein [Escherichia coli]	62	44	1032
261	3	4008	2605	gi|143121	ORF A: putative [Bacillus firmus]	62	42	1404
299	8	4477	4719	gi|467441	expressed at the end of exponential growh under conditions in which he enzymes of the TCA cycle are repressed [Bacillus subtilis] gi|467461 expressed at the end of exponential growth under ondtions in which the enzyms of the TCA cycle are repressed Bact]	62	47	243
304	6	5018	3819	gi|153015	FemA protein [Staphylococcus aureus]	62	43	1200
324	1	2	262	gi|142717	cytochrome aa3 controlling protein [Bacillus subtilis] pir|A33960|A33960 cta protein - Bacillus subtilis sp|P12946|CTA_BACSU CYTOCHROME AA3 CONTROLLING PROTEIN.	62	30	261
325	2	269	1207	gi|581088	methionyl-tRNA formyltransferase [Escherichia coli]	62	39	939
332	6	4894	4631	gi|1499960	uridine 5'-monophosphate synthase [Methanococcus jannaschii]	62	36	264
355	1	2	370	gi|143925	fecB [Escherichia coli]	62	32	369
365	8	6628	6804	gi|413943	ipa-19d gene product [Bacillus subtilis]	62	54	177
369	2	2744	1626	pir|A41577|A41S	regulatory protein pfoR - Clostridium perfringens	62	42	1119
370	1	34	264	gi|40665	beta-glucosidase [Clostridium thermocellum]	62	37	231
415	3	2109	3176	gi|1205401	transport ATP-binding protein [Haemophilus influenzae]	62	35	468
429	1	1578	790	gi|1046024	Na+ ATPase subunit J [Mycoplasma genitalium]	62	40	789
444	2	704	1369	gi|581510	nodulation gene; integral membrane protein; homology to Rhizobium equinosarum nodI [Rhizobium loti]	62	37	666
477	2	751	1869	pir|A48440|A484	ring-infected erythrocyte surface antigen 2, RESA-2 - Plasmodium falciparum	62	44	1119
485	1	241	1707	gi|17934	betaine aldehyd dehydrogenase [Beta vulgaris]	62	43	1467
487	3	1141	1311	gi|149445	ORF1 [Lactococcus lactis]	62	31	171
494	2	1134	1313	gi|166835	ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis haliana]	62	37	180
518	1	193	882	gi|153491	O-methyltransferase [Streptomyces glaucescens]	62	39	690
534	2	369	2522	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	62	35	2154
551	6	4371	4820	gi|511113	ferric uptake regulation protein [Campylobacter jejuni]	62	37	450
574	1	1	570	gi|153000	enterotoxin B [Staphylococcus aureus]	62	43	570

TABLE 2

S. aureus : putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
590	2	344	1171	gi|40367	ORFC [Clostridium acetobutylicum]	62	37	828
655	1	396	830	gi|147195	phnB protein [Escherichia coli]	62	44	435
656	1	2	478	gi|1205451	cell division inhibitor [Haemophilus influenzae]	62	36	477
676	1	692	348	gi|1511613	methyl coenzyme M reductase system, component A2 [Methanococcus jannaschii]	62	36	345
687	1	493	248	gi|49272	Asparaginase [Bacillus licheniformis]	62	46	246
700	2	267	944	gi|1205822	hypothetical protein (GB:X75627_4) [Haemophilus influenzae]	62	40	678
840	2	1715	1041	gi|1045865	M. genitalium predicted coding region MG181 [Mycoplasma genitalium]	62	36	675
864	4	898	1491	gi|1144332	deoxyuridine nucleotidohydrolase [Homo sapiens]	62	38	594
916	1	35	400	gi|413931	ipa-7d gene product [Bacillus subtilis]	62	45	366
1071	1	1	771	gi|1510649	aspartokinase I [Methanococcus jannaschii]	62	40	771
1084	1	19	609	gi|688011	AgX-1 antigen (human, infertile patient, testis. Peptide, 505 aa]	62	39	591
1103	1	1	201	gi|581261	ORF homologous to E.coli metB [Herpetosiphon aurantiacus] pir|S14030|S14030 hypothetical protein - Herpetosiphon aurantiacus (fragment)	62	51	201
1217	1	463	233	gi|460025	ORF2, putative [Streptococcus pneumoniae]	62	41	231
1533	1	644	414	gi|413968	ipa-44d gene product [Bacillus subtilis]	62	48	231
1537	1	3	257	gi|1510641	alanyl-tRNA synthetase [Methanococcus jannaschii]	62	23	255
2347	1	3	161	gi|485956	mpiC gene product [Proteus mirabilis]	62	45	159
2386	1	3	245	gi|285708	nontoxic component [Clostridium botulinum]	62	31	243
2484	1	331	167	gi|142092	DNA-repair protein (recA) [Anabaena variabilis]	62	35	165
2490	1	798	400	gi|581648	epiB gene product [Staphylococcus epidermidis]	62	42	399
3016	1	596	300	gi|710022	uroporphyrinogen III [Bacillus subtilis]	62	51	297
3116	1	1	213	gi|466883	nifS: B1496_C2_191 [Mycobacterium leprae]	62	44	213
3297	1	823	413	gi|475715	acetyl coenzyme A acetyltransferase (thiolase) [Clostridium cetobutylicum]	62	42	411
3609	1	31	276	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	62	48	246
3665	2	584	402	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	62	40	183
3731	1	3	374	gi|1353197	[thioredoxin reductase [Eubacterium acidaminophilum]	62	42	372

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	start (nt)	stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3R98	1	1	237	gi|1536675	tagatose 6-P kinase (Streptococcus mutans)	62	45	237
4027	1	283	143	gi|330705	homologue to gene 30 (aa 1-59); putative (Bovine herpesvirus 4)	62	43	141
4109	1	727	365	gi|41748	hsdM protein (AA 1-520) (Escherichia coli)	62	45	363
4303	1	1	303	gi|1303813	YqeW (Bacillus subtilis)	62	43	303
4380	1	530	267	gi|1235684	mevalonate pyrophosphate decarboxylase (Saccharomyces cerevisiae)	62	55	264
4494	1	2	256	gi|510692	enterotoxin H (Staphylococcus aureus)	62	34	255
4598	1	411	221	gi|763513	ORF4: putative (Streptomyces violaceoruber)	62	45	189
4624	1	1	222	gi|41748	hsdM protein (AA 1-520) (Escherichia coli)	62	45	222
5	5	4288	3932	gi|92883	(ORF95; putative (Lactococcus lactis phage BK5-T)	61	36	357
11	1	320	162	pir|C33356|C33	prothymosin alpha homolog (clone 12) - human (fragment)	61	33	159
16	11	10291	11238	gi|1205391	hypothetical protein (SP:P33995) (Haemophilus influenzae)	61	44	948
22	1	283	801	gi|1066504	exo-beta 1,3 glucanase (Cochliobolus carbonum)	61	50	519
38	3	616	1107	gi|1510864	glutamine transport ATP-binding protein Q (Methanococcus jannaschii)	61	41	492
45	4	3082	4038	gi|1109686	ProX (Bacillus subtilis)	61	45	957
48	8	7118	7504	gi|498839	ORF2 (Clostridium perfringens)	61	33	387
51	9	4605	5570	gi|38269	traC (Plasmid pAD1)	61	42	966
60	6	1689	2243	gi|1205893	hypothetical protein (GB:U00011.3) (Haemophilus influenzae)	61	32	555
62	9	5559	5122	gi|854656	Na/H antiporter system ORF2 (Bacillus alcalophilus)	61	38	438
67	5	4330	5646	gi|466612	nikA (Escherichia coli)	61	36	1317
74	2	2400	1504	gi|1204846	carbamate kinase (Haemophilus influenzae)	61	40	897
85	1	2198	1101	gi|1498756	amidophosphoribosyltransferase PurF (Rhizobium etli)	61	41	1098
86	4	1995	1582	gi|1499931	M. jannaschii predicted coding region MJ1083 (Methanococcus jannaschii)	61	44	414
97	1	74	649	gi|1518679	orf (Bacillus subtilis)	61	44	576
99	2	2454	1990	gi|413958	ipa-34d gene product (Bacillus subtilis)	61	18	465
124	7	6223	5123	gi|556881	Similar to Saccharomyces cerevisiae SUA5 protein (Bacillus subtilis) pir|S49358|S49358 ipc-29d protein - Bacillus subtilis sp|P39153|YWLC_BACSU HYPOTHETICAL 37.0 KD PROTEIN IN SPOIIR-GLYC INTERGENIC REGION.	61	46	1101
125	4	1668	2531	gi|1491643	ORFA gene product (Chloroflexus aurantiacus)	61	43	864

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
132	1	1250	627	pir|PQ0259|PQ02	hypothetical protein 1 - Enterococcus (faecalis plasmid pAM-beta-1 (fragment)	61	43	624
149	9	3617	3075	gi|1144332	deoxyuridine nucleotidohydrolase (Homo sapiens)	61	40	543
149	22	8690	7869	gi|160047	pIO1/acidic basic repeat antigen (Plasmodium falciparum) pir|A29232|A29232 101K malaria antigen precursor - Plasmodium alciparum (strain Camp)	61	35	822
16A	3	1915	2361	gi|1499694	HIT protein, member of the HIT-family (Methanococcus jannaschii)	61	41	447
171	9	9675	7948	gi|467416	similar to SpoVB (Bacillus subtilis)	61	38	1728
174	3	1042	2340	gi|216374	glutaryl 7-ACA acylase precursor (Bacillus laterosporus)	61	49	1299
190	4	5034	4111	gi|409286	bmrU (Bacillus subtilis)	61	37	924
216	1	2	190	gi|415861	eukaryotic initiation factor 2 beta (eIF-2 beta) (Oryctolagus uniculus)	61	29	189
227	7	4161	5048	gi|216341	ORF for methionine amino peptidase (Bacillus subtilis)	61	41	888
238	4	1959	3047	gi|809543	CbrC protein (Erwinia chrysanthemi)	61	38	1089
247	1	2	694	gi|537231	ORF_f579 (Escherichia coli)	61	38	693
247	2	678	1034	gi|142226	chvD protein (Agrobacterium tumefaciens)	61	40	357
257	2	1523	2627	gi|699379	glvr-1 protein (Mycobacterium leprae)	61	40	897
268	2	3419	3051	gi|40364	ORFA1 (Clostridium acetobutylicum)	61	41	369
275	4	4621	4827	gi|1204848	hypothetical protein (GP:M87049_57) (Haemophilus influenzae)	61	36	207
277	1	1	1445	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - streptococcus pneumoniae	61	45	1445
27A	9	8003	7032	gi|467462	cysteine synthetase A (Bacillus subtilis)	61	43	972
278	10	9878	8535	gi|1205919	Na+ and Cl- dependent gamma-aminobutyric acid transporter (Haemophilus influenzae)	61	38	1344
283	1	1	366	gi|755607	polyA polymerase (Bacillus subtilis)	61	36	366
288	2	1918	1496	gi|388108	cell wall enzyme ..nterococcus faecalis)	61	43	423
291	1	86	334	gi|454265	FBP3 (Petunia hybrida)	61	38	249
318	1	1104	694	gi|290531	similar to beta-glucoside transport protein (Escherichia coli) sp|P14251|PTIB_ECOLI PTS SYSTEM, ARBUTIN-LIKE IIB COMPONENT PHOSPHOTRANSFERASE ENZYME II, B COMPONENT) (EC 2.7.1.69)	61	47	411
330	2	1912	1190	gi|1001805	hypothetical protein (Synechocystis sp.)	61	41	723

TABLE 2

S. aureus : Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
385	2	1513	1025	gi|533098	DnaD protein (Bacillus subtilis)	61	42	489
426	1	794	399	gi|1103853	YqgF (Bacillus subtilis)	61	44	396
438	3	810	1421	gi|1293660	AbsA2 (Streptomyces coelicolor)	61	36	612
454	1	1580	792	gi|733522	phosphatidylinositol-4,5-diphosphate 3-kinase (Dictyostelium [scoideum]	61	30	789
464	2	784	560	gi|1123120	C51B7.5 gene product (Caenorhabditis elegans)	61	38'	225
470	8	6077	7357	gi|623073	ORF360: putative (Bacteriophage LL-H)	61	47	1281
509	1	554	279	gi|467484	unknown (Bacillus subtilis)	61	45	276
555	3	1916	1296	gi|141800	anthranilate synthase glutamine amidotransferase (Acinetobacter alcoaceticus]	61	42	621
569	1	1711	857	gi|467090	B2235_C2_195 (Mycobacterium leprae)	61	47	855
585	2	961	803	sp|P16686|SURE_	SURVIVAL PROTEIN SURE HOMOLOG (FRAGMENT)	61	33	159
592	3	1694	1422	gi|1221602	immunity repressor protein (Haemophilus influenzae)	61	32	273
601	1	43	357	gi|507738	Hmp (Vibrio parahaemolyticus)	61	33	315
669	1	2467	1235	gi|1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative (Bacillus subtilis)	61	37	1233
675	3	805	1101	gi|403373	glycerophosphoryl diester phosphodiesterase (Bacillus subtilis) pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	61	36	297
703	1	1656	829	gi|537181	ORF_f470 (Escherichia coli)	61	32	828
728	1	1628	815	gi|806281	DNA polymerase I (Bacillus stearothermophilus)	61	39	813
821	1	61	318	gi|709992	hypothetical protein (Bacillus subtilis)	61	38	258
856	2	2313	1567	gi|609310	portal protein gp3 (Bacteriophage HK97)	61	40	747
923	1	1081	542	gi|143213	putative (Bacillus subtilis)	61	38	540
1124	1	59	370	gi|1107541	C33D9.8 (Caenorhabditis elegans)	61	26	312
1492	1	548	276	gi|406397	unknown (Mycoplasma genitalium)	61	32	273
1602	1	46	318	gi|733522	phosphatidylinositol-4,5-diphosphate 3-kinase (Dictyostelium [scoideum]	61	34	273
2500	1	577	290	gi|1045964	hypothetical protein (GB:U14003_297) (Mycoplasma genitalium)	61	31	288
2968	1	2	808	gi|397526	clumping factor (Staphylococcus aureus)	61	55	807
3076	1	3	248	gi|(9373	ORF 1 (Lactococcus lactis)	61	41	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3609	2	207	401	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	61	39	195
3662	1	1477	740	gi|1303813	YqeW [Bacillus subtilis]	61	42	738
3672	1	2	442	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	441
3724	1	2	220	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	61	41	219
3728	1	3	398	gi|677943	AppD [Bacillus subtilis]	61	46	396
3884	1	3	401	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	47	399
3971	1	3	383	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	45	381
4038	1	661	359	gi|1133997	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	61	24	303
4041	1	546	274	gi|1413953	ipa-29d gene product [Bacillus subtilis]	61	48	273
4047	1	1	402	gi|528991	unknown [Bacillus subtilis]	61	42	402
4102	1	1	345	gi|976025	HrsA [Escherichia coli]	61	46	345
4155	1	1	336	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	336
4268	1	463	233	gi|450688	hsdM gene of EcoprrI gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	61	38	231
4374	1	542	273	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	270
4189	1	2	172	gi|147516	ribokinase [Escherichia coli]	61	35	171
4621	1	2	268	gi|784897	beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	47	267
4663	1	27	227	gi|976025	HrsA [Escherichia coli]	61	50	201
4	6	6661	5536	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	60	43	1128

TABLE 2

S aureus Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
11	6	3426	3725	gi|410748	ring-infested erythrocyte surface antigen (Plasmodium falciparum) pir|A25526|A25526 ring-infected erythrocyte surface antigen recursor - Plasmodium falciparum (strain FC27/Papua New Guinea) sp|P13830|RESA_PLAFF RING-INFECTED ERYTHROCYTE SURFACE ANTIGEN RE	60	24	300
11	14	11035	10313	gi|1217651	carbonyl reductase (NADPH) [Rattus norvegicus]	60	28	723
16	12	11917	12930	gi|1001453	hypothetical protein [Synechocystis sp.]	60	37	1014
33	1	26	469	gi|388109	regulatory protein [Enterococcus faecalis]	60	41	444
37	13	10914	9834	gi|1336656	OrfI [Bacillus subtilis]	60	40	981
39	4	4364	4522	gi|4872	ORF 4 [Saccharomyces kluyveri]	60	47	159
41	1	2047	1025	gi|142822	D-alanine racemase cds [Bacillus subtilis]	60	39	1023
43	4	2474	3607	gi|468046	para-nitrobenzyl esterase [Bacillus subtilis]	60	40	1134
44	10	6756	7769	gi|414234	thiF [Escherichia coli]	60	52	1014
45	10	8874	9074	gi|343949	var1(40.0) [Saccharomyces cerevisiae]	60	44	201
56	18	27842	26410	gi|468764	mocR gene product [Rhizobium meliloti]	60	35	1413
60	2	173	388	gi|1303864	YqgQ [Bacillus subtilis]	60	33	216
63	2	357	1619	gi|467124	ureD: B229_C3_234 [Mycobacterium leprae]	60	43	1263
65	1	787	395	gi|1518853	OafA [Salmonella typhimurium]	60	36	393
MA	1	1	1188	gi|480029	putative transcriptional regulator [Bacillus stearothermophilus]	60	30	1188
92	1	4735	3881	gi|349227	transmembrane protein [Escherichia coli]	60	37	855
92	7	5996	4923	gi|466631	nikB [Escherichia coli]	60	38	1074
93	1	949	476	gi|1510925	coenzyme F420-reducing hydrogenase, beta subunit [Methanococcus jannaschii]	60	27	474
96	6	7366	7578	gi|472715	accessory protein [Carnobacterium piscicola]	60	30	213
98	6	3212	4069	gi|467425	unknown [Bacillus subtilis]	60	42	858
102	10	7158	7430	gi|143092	acetolactate synthase small subunit [Bacillus subtilis] sp|P37252|ILVN_BACSU ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC .1 3.18) (AHAS) (ACETOHYDROXY-ACID SYNTHASE SMALL SUBUNIT) (ALS1).	60	37	273
109	11	9127	10515	gi|1253259	o-succinylbenzoic acid (OSB) CoA ligase [Staphylococcus aureus]	60	28	1389
109	12	10499	11656	gi|141954	beta-ketothiolase [Alcaligenes eutrophus]	60	41	1158
119	2	4630	3134	gi|1524280	unknown [Mycobacterium tuberculosis]	60	45	1497

TABLE 2

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
121	9	6957	7646	gi|1107529	ceuC gene product (Campylobacter coli)	60	35	690
140	7	7704	6013	gi|146547	kdpA (Escherichia coli)	60	45	1692
145	1	2	703	gi|1460077	unknown (Mycobacterium tuberculosis)	60	23	702
150	3	2809	2216	gi|1146230	putative (Bacillus subtilis)	60	40	594
157	2	1389	961	gi|1303975	YqjX (Bacillus subtilis)	60	30'	429
158	5	5125	4769	gi|1449288	unknown (Mycobacterium tuberculosis)	60	36	357
159	1	511	257	gi|580932	murD gene product (Bacillus subtilis)	60	43	255
160	1	159	1187	gi|1204532	hypothetical protein (GB:L19201_29) (Haemophilus influenzae)	60	34	1029
161	14	8249	7866	gi|1496003	ORF3; PepY; putative oligoendopeptidase based on homology with Lactococcus lactis PepF (GenBank Accession Number Z32522) [Caldicellulosiruptor saccharolyticus]	60	34	384
172	3	1331	2110	gi|485280	28.2 kDa protein (Streptococcus pneumoniae)	60	33	780
173	2	4082	2460	gi|1524397	glycine betaine transporter OpuD (Bacillus subtilis)	60	41	1623
173	4	4963	4953	gi|1100737	NADP dependent leukotreine b4 12-hydroxydehydrogenase (Sus scrofa)	60	44	1011
198	1	3	995	gi|413943	ipa-19d gene product (Bacillus subtilis)	60	42	993
201	4	3641	4573	sp|P37028|YADT_	HYPOTHETICAL 29.4 KD PROTEIN IN HEML-PPS INTERGENIC REGION PRECURSOR.	60	37	933
201	7	3269	2415	gi|927798	D9719.34p; CAI: 0.14 [Saccharomyces cerevisiae]	60	43	855
206	9	12234	12515	sp|P37347|YECD_	HYPOTHETICAL 21.8 KD PROTEIN IN ASPS 5'REGION	60	47	282
212	4	1213	1410	gi|332711	hemagglutinin-neuraminidase fusion protein (Human parainfluenza irus 3)	60	34	198
214	1	65	1153	gi|1204366	hypothetical protein (GB:U14003_130) [Haemophilus influenzae]	60	36	1089
237	1	2	937	gi|149377	HisD (Lactococcus lactis)	60	40	936
241	6	5696	4998	gi|1046160	hypothetical protein (GB:U00021_5) (Mycoplasma genitalium)	60	37	699
260	6	5919	6485	gi|431950	similar to a B.subtilis gene (GB: BACHEMHY_5) (Clostridium asteurianum)	60	35	567
264	1	2432	1218	gi|397526	clumping factor (Staphylococcus aureus)	60	53	1215
267	1	3	1409	gi|148016	NaH-antiporter protein (Enterococcus hirae)	60	27	1407
275	3	3804	4595	pir;F36A89|F368	leuD 3'-region hypothetical protein - Lactococcus lactis subsp. lactis (strain IL1403)	60	35	792
291	3	860	1198	gi|1208889	coded for by C. elegans cDNA yk130e12.5; contains C2H2-type zinc fingers [Caenorhabditis elegans]	60	33	339

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
307	6	3421	3176	gi|1070014	protein-dependent (Bacillus subtilis)	60	36	246
316	8	4957	5823	gi|413952	ipa-28d gene product (Bacillus subtilis)	60	41	867
328	4	2995	3484	gi|1204484	membrane-associated component, branched amino acid transport system (Haemophilus influenzae)	60	39	489
312	5	4887	4363	gi|1205449	colicin V production protein (pur regulon) (Haemophilus influenzae)	60	37	525
357	1	1062	532	gi|AR7842	single-stranded DNA specific exonuclease (Escherichia coli)	60	41	531
375	2	96	362	gi|1057	adenylyl cyclase gene product (Saccharomyces kluyveri) r|JQ1145|OYBYK adenylate cyclase (EC 4.6.1.1) - yeast ccharomyces kluyveri)	60	47	267
397	1	66	416	gi|709999	Glucarate dehydratase (Bacillus subtilis)	60	37	351
409	1	2	163	gi|499700	glycogen phosphorylase (Saccharomyces cerevisiae)	60	35	162
453	4	914	1237	gi|1196899	unknown protein (Staphylococcus aureus)	60	36	324
453	7	3818	3620	sp|P12222|YCF1_	HYPOTHETICAL 226 KD PROTEIN (ORF 1901).	60	31	219
470	2	622	945	pir|S30782|S307	integrin homolog - yeast (Saccharomyces cerevisiae)	60	31	324
500	1	114	606	gi|467407	unknown (Bacillus subtilis)	60	36	489
503	3	752	982	gi|167835	myosin heavy chain (Dictyostelium discoideum)	60	34	231
505	4	2238	3563	gi|1510732	NADH oxidase (Methanococcus jannaschii)	60	26	1326
523	1	3	1043	gi|143311	alkaline phosphatase regulatory protein (Bacillus subtilis) pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3.-).	60	41	1041
543	1	1	465	gi|1511103	cobalt transport ATP-binding protein O (Methanococcus jannaschii)	60	40	465
545	1	1	726	gi|1498192	putative (Pseudomonas aeruginosa)	60	40	726
556	1	2	1054	gi|1477402	tex gene product (Bordetella pertussis)	60	42	1053
578	1	974	489	gi|1205129	H. Influenzae predicted coding region HI0882 (Haemophilus influenzae)	60	42	486
594	1	1	624	gi|1212755	adenylyl cyclase (Aeromonas hydrophila)	60	35	624
604	1	3	530	gi|145925	fecB (Escherichia coli)	60	42	528
620	1	926	465	gi|1205483	bicyclomycin resistance protein (Haemophilus influenzae)	60	33	462
630	2	871	1122	gi|1486242	unknown (Bacillus subtilis)	60	41	252
645	2	574	425	gi|1205136	serine hydroxymethyltransferase (serine methylase) (Haemophilus influenzae)	60	28	150

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
684	1	1082	843	gi|1205538	[hypothetical protein (GB:U14003_302) [Haemophilus influenzae]	60	39	240
786	1	967	485	gi|1402944	orfRM1 gene product [Bacillus subtilis]	60	46	483
844	1	588	346	gi|790943	urea amidolyase [Bacillus subtilis]	60	40	243
851	1	1	726	gi|159661	GMP reductase [Ascaris lumbricoides]	60	41	726
871	1	1746	874	gi|1001493	hypothetical protein [Synechocystis sp.]	60	39.	873
896	1	1558	839	gi|604926	NADH dehydrogenase, subunit 5 [Schizophyllum commune] sp|P50168|NU5M_SCHCO NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 6.5.3).	60	39	720
908	2	448	753	gi|662880	novel hemolytic factor [Bacillus cereus]	60	31	306
979	1	2	595	gi|1429255	putative; orf1 [Bacillus subtilis]	60	30	594
1078	1	669	502	gi|581055	inner membrane copper tolerance protein [Escherichia coli] gi|87029 disulphide isomerase like protein [Escherichia coli] pir|S47295|S47295 inner membrane copper tolerance protein - scherichia coli	60	40	168
1112	1	1150	620	gi|407885	ORF3 [Streptomyces griseus]	60	34	531
1135	1	484	275	gi|1171407	vpa8p [Saccharomyces cerevisiae]	60	36	210
1146	1	17	562	gi|1235981	hypothetical protein [Bacillus subtilis]	60	36	546
1291	1	716	360	pir|S57530|S575	carboxyl esterase - Acinetobacter calcoaceticus	60	30	357
1332	1	336	169	gi|1222056	aminotransferase [Haemophilus influenzae]	60	44	168
1429	1	3	146	gi|1205619	ferritin like protein [Haemophilus influenzae]	60	39	144
1722	1	570	286	gi|240052	dihydroflavonol-4-reductase, DFR [Hordeum vulgare=barley, cv. Gula, eptide, 354 aa]	60	36	285
2350	1	385	200	gi|497626	ORF 1 [Plasmid pAQ1]	60	20	186
2936	1	519	310	gi|508981	prephenate dehydratase [Bacillus subtilis]	60	48	210
3027	1	568	302	gi|1146199	putative [Bacillus subtilis]	60	37	267
3084	1	20	208	gi|1407784	orf-1; novel antigen [Staphylococcus aureus]	60	51	189
3155	1	2	226	gi|1046097	cytadherence-accessory protein [Mycoplasma genitalium]	60	34	225
3603	1	368	186	gi|510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA ehydrogenase alpha-subunit [Rattus norvegicus]	60	42	183
3665	1	486	244	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.88) Pseudomonas sp.	60	42	243
3747	1	3	146	gi|474192	iucC gene product [Escherichia coli]	60	36	144

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3912	1	3	335	gi|488695	novel antigen: orf-2 [Staphylococcus aureus]	60	44	333
4072	1	3	272	gi|405839	yeiH [Escherichia coli]	60	33	270
4134	1	510	352	gi|780656	chemoreceptor protein [Rhizobium leguminosarum bv. viciae] gi|780656 chemoreceptor protein [Rhizobium leguminosarum bv. iciae]	60	28	159
4207	2	677	402	gi|602001	similar to trimethylamine DH [Mycoplasma capricolum] pir|S49950|S49950 probable trimethylamine dehydrogenase (EC 1.5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	60	41	276
4243	1	127	324	gi|899317	peptide synthetase module [Microcystis aeruginosa] pir|S49111|S49111 probable amino acid activating domain - Icrocystis aeruginosa (fragment) (SUB 144-528)	60	42	198
4110	1	624	313	gi|508980	phcB [Bacillus subtilis]	60	28	312
4345	1	343	173	gi|510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxycyl-CoA ehydrogenase alpha-subunit [Rattus norvegicus]	60	42	171
43R2	1	498	280	gi|47382	acyl-CoA-dehydrogenase [Streptomyces purpurascens]	60	48	219
4474	1	53	223	gi|510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxycyl-CoA ehydrogenase alpha-subunit [Rattus norvegicus]	60	42	171
23	4	4518	3523	gi|426446	VipB protein [Salmonella typhi]	59	39	996
33	2	707	1483	pir|S48604|S486	hypothetical protein - Mycoplasma capricolum (SGC3) (fragment)	59	33	777
33	5	4651	5853	gi|6721	F55B2.3 [Caenorhabditis elegans]	59	33	1203
17	2	1228	2292	gi|142833	ORF2 [Bacillus subtilis]	59	37	910
38	21	16784	16593	gi|912576	BiP [Phaeodactylum tricornutum]	59	40	192
52	3	2848	2349	gi|536972	ORF_o90a [Escherichia coli]	59	44	300
54	12	14181	13402	gi|483940	transcription regulator [Bacillus subtilis]	59	37	780
57	3	4397	3339	gi|508176	Gat-1-P-DH, NAD dependent [Escherichia coli]	59	40	1059
66	1	986	495	gi|1303901	YqhT [Bacillus subtilis]	59	34	492
67	7	6552	7460	gi|912461	nikC [Escherichia coli]	59	37	909
70	7	5383	6365	gi|1399822	PhoD precursor [Rhizobium meliloti]	59	46	984
78	1	1	1449	gi|971345	unknown, similar to E.coli cardiolipin synthase [Bacillus subtilis] sp|P45860|YWIE_BACSU HYPOTHETICAL 58.2 PROTEIN IN NARI-ACDA NTERGENIC REGION.	59	39	1449
82	10	14329	15534	gi|490328	LORF F (unidentified)	59	44	1206

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
89	2	1602	958	gi|642801	unknown [Saccharomyces cerevisiae]	59	32	645
96	4	4940	5473	gi|1333802	protein of unknown function (Rhodobacter capsulatus)	59	33	534
98	1	2	820	gi|467421	similar to B. subtilis DnaH [Bacillus subtilis]	59	34	819
119	1	166	1557	gi|143122	ORF B; putative [Bacillus firmus]	59	36	1392
120	10	6214	6756	gi|15354	ORF 55.9 [Bacteriophage T4]	59	39'	543
120	16	12476	13510	gi|1086575	BatA [Rhizobium meliloti]	59	44	1035
123	1	386	195	gi|984737	catalase [Campylobacter jejuni]	59	38	192
130	1	370	645	gi|1256634	25.8% identity over 120 aa with the Synecococcus sp. MpeV protein; putative [Bacillus subtilis]	59	31	276
131	4	5278	5712	gi|1510655	hypothetical protein (SP:P42297) [Methanococcus jannaschii]	59	39	435
164	1	3	509	gi|1001342	hypothetical protein [Synechocystis sp.]	59	41	507
164	4	1529	2821	gi|1205165	hypothetical protein (SP:P37764) [Haemophilus influenzae]	59	35	1293
164	19	19643	21376	gi|1001381	hypothetical protein [Synechocystis sp.]	59	34	1734
173	3	4727	3717	gi|1184121	auxin-induced protein [Vigna radiata]	59	50	1011
179	2	2218	1688	gi|143036	unidentified gene product [Bacillus subtilis]	59	33	531
195	12	12659	11503	gi|762778	NifS gene product [Anabaena azollae]	59	41	1167
201	5	4702	5670	gi|1510240	hemin permease [Methanococcus jannaschii]	59	32	969
201	7	5719	6315	gi|1511456	M. jannaschii predicted coding region MJ1437 [Methanococcus jannaschii]	59	34	597
209	1	102	461	gi|1204666	hypothetical protein (GB:X73124_53) [Haemophilus influenzae]	59	42	360
214	3	1050	2234	gi|551531	2-nitropropane dioxygenase [Williopsis saturnus]	59	36	1185
214	5	3293	4135	gi|1303709	YrkJ [Bacillus subtilis]	59	32	843
217	2	3381	2167	gi|290489	dfp (CG Site NO. 18430) [Escherichia coli]	59	44	1215
237	5	3078	3785	gi|149382	HisA [Lactococcus lactis]	59	38	708
251	2	376	960	gi|1303791	YqoJ [Bacillus subtilis]	59	34	585
286	1	1621	812	gi|146551	transmembrane protein (kdpD) [Escherichia coli]	59	31	810
316	5	4978	3860	gi|405879	yeiH [Escherichia coli]	59	32	1119
370	3	600	761	gi|1303794	YqeM [Bacillus subtilis]	59	35	162

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3R2	1	1009	506	gi|147513	orf3 [Haemophilus influenzae]	59	34	504
391	1	1620	1273	gi|152901	ORF 3 [Spirochaeta aurantia]	59	37	348
406	3	2805	1705	gi|709992	hypothetical protein [Bacillus subtilis]	59	34	1101
426	5	3802	3245	gi|1204610	iron(III) dicitrate transport ATP-binding protein FECE [Haemophilus influenzae]	59	36	558
429	2	1513	1148	gi|1064809	homologous to sp:NTRA_ECOLI [Bacillus subtilis]	59	42	366
460	2	708	1301	gi|466882	ppsi: B1496_C2_189 [Mycobacterium leprae]	59	37	594
461	4	2212	3135	gi|1498295	homoserine kinase homolog [Streptococcus pneumoniae]	59	37	924
473	1	2929	1607	gi|147989	trigger factor [Escherichia coli]	59	40	1323
480	8	5862	6110	gi|1205311	(3R)-hydroxymyristol acyl carrier protein dehydrase [Haemophilus influenzae]	59	40	249
521	1	14	1354	pir|A25620|A256	staphylocoagulase - Staphylococcus aureus ((fragment)	59	32	1341
534	4	2994	4073	gi|153746	mannitol-phosphate dehydrogenase [Streptococcus mutans] pir|C44798|C44798 mannitol-phosphate dehydrogenase Mt1D - streptococcus mutans	59	36	1080
535	1	1	954	gi|1469939	group B oligopeptidase PepB [Streptococcus agalactiae]	59	33	954
551	3	2836	3186	gi|1204511	bacterioferritin comigratory protein [Haemophilus influenzae]	59	45	351
573	2	449	940	gi|386681	ORF YALO22 [Saccharomyces cerevisiae]	59	36	492
650	1	5	748	gi|396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp|P12703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549).	59	30	744
664	1	566	285	gi|1262748	LukF-PV like component [Staphylococcus aureus]	59	33	282
670	1	3	455	gi|1122758	unknown [Bacillus subtilis]	59	42	453
674	3	543	929	gi|293033	integrase [Bacteriophage phi-LC3]	59	46	387
758	1	349	176	gi|1500472	M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]	59	37	174
771	2	2270	1461	gi|522150	bromoperoxidase BPO-A1 [Streptomyces aureofaciens] sp|P33912|BPA1_STRAU NON-HAEM BROMOPEROXIDASE BPO-A1 (EC 1.11.1.-) BROMIDE PEROXIDASE) (BPO1). (SUB 2-275)	59	44	810
825	1	2191	1097	gi|397526	clumping factor [Staphylococcus aureus]	59	47	1095
1052	2	1094	723	gi|289262	comE ORF3 [Bacillus subtilis]	59	36	372
1152	1	373	188	gi|1276668	ORF238 gene product [Porphyra purpurea]	59	37	186

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1198	1	492	247	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	59	26	246
1441	1	468	235	gi|1045942	glycyl-tRNA synthetase [Mycoplasma genitalium]	59	37	234
2103	1	1	186	gi|459250	triacylglycerol lipase [Galactomyces geotrichum]	59	33	186
2205	1	793	398	gi|1301794	YqeM [Bacillus subtilis]	59	38	396
2578	1	484	284	gi|258003	insulin-like growth factor binding protein complex acid-labile subunit [rats, liver, Peptide, 603 aa]	59	48	201
2967	2	145	348	gi|1212730	YqhK [Bacillus subtilis]	59	44	204
3012	1	3	248	gi|1773571	neurofilament protein NF70 [Helix aspersa]	59	31	246
3544	1	3	401	gi|1055218	crotonase [Clostridium acetobutylicum]	59	42	399
3548	1	3	401	gi|1055218	crotonase [Clostridium acetobutylicum]	59	42	399
3580	1	698	351	gi|1055218	crotonase [Clostridium acetobutylicum]	59	42	348
3720	1	722	363	gi|1408494	homologous to penicillin acylase [Bacillus subtilis]	59	36	360
4171	1	3	296	gi|1055218	crotonase [Clostridium acetobutylicum]	59	42	294
4305	1	618	310	gi|1524193	unknown [Mycobacterium tuberculosis]	59	39	309
18	1	1242	622	gi|146913	N-acetylglucosamine transport protein (Escherichia coli) pir|B29895|WQEC2N phosphotransferase system enzyme II (EC 7.1.69), N-acetylglucosamine-specific - Escherichia coli sp|P09323|PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC OMPONENT (EIIA	58	43	621
20	7	7020	5845	gi|50502	collagen alpha chain precursor (AA -27 to 1127) [Mus musculus]	58	50	1176
21	5	3224	3626	gi|1054860	phosphoribosyl anthranilate isomerase [Thermotoga maritima]	58	32	393
23	2	2841	1669	gi|1276880	EpsG [Streptococcus thermophilus]	58	29	1173
23	10	9301	8090	pir|A31133|A311	diaminopimelate decarboxylase (EC 4.1.1.20) - Pseudomonas aeruginosa	58	37	1212
38	29	22555	22884	gi|973249	vestitone reductase [Medicago sativa]	58	37	330
44	1	2	406	gi|289272	ferrichrome-binding protein [Bacillus subtilis]	58	33	405
45	1	1	552	gi|29464	embryonic myosin heavy chain (1085 AA) [Homo sapiens] lr|S12460|S12460 myosin beta heavy chain - human	58	33	552
55	2	759	538	gi|158852	glucose regulated protein [Echinococcus multilocularis]	58	32	222
62	13	8493	8068	gi|975353	kinase-associated protein B [Bacillus subtilis]	58	35	426
63	3	1553	1717	gi|166926	[Arabidopsis thaliana unidentified mRNA sequence, complete cds.], ene product (Arabidopsis thaliana)	58	35	165

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
67	13	12017	11229	gi|1228083	NADH dehydrogenase subunit 2 (Chorthippus parallelus)	58	41	789
96	8	8208	9167	gi|709992	hypothetical protein (Bacillus subtilis)	58	42	960
107	2	2065	1364	gi|806327	Escherichia coli hrpA gene for A protein similar to yeast PRP16 and RP22 (Escherichia coli)	58	37	702
112	7	4519	5613	gi|155588	glucose-fructose oxidoreductase (Zymomonas mobilis) pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) precursor - Zymomonas mobilis	58	38,	1095
114	6	7118	6503	gi|1377843	unknown (Bacillus subtilis)	58	38	816
143	2	2261	1395	pir|A45605|A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	58	31	867
161	2	717	950	gi|1370261	unknown (Mycobacterium tuberculosis)	58	31	234
154	6	6015	4627	gi|1209227	pCTHoo1 gene product (Chlamydia trachomatis)	58	41	1389
154	16	14281	13541	gi|146613	DNA ligase (EC 6.5.1.2) (Escherichia coli)	58	39	741
155	3	2269	1892	gi|1303917	YqiB (Bacillus subtilis)	58	34	378
174	1	1056	529	ni|904198	hypothetical protein (Bacillus subtilis)	58	26	528
189	4	1533	1769	gi|467383	DNA binding protein (probable) (Bacillus subtilis)	58	25	237
201	3	2669	3307	gi|1511451	endonuclease III (Methanococcus jannaschii)	58	34	639
208	1	2	238	gi|1276729	phycobilisome linker polypeptide (Porphyra purpurea)	58	29	237
220	11	14575	13058	gi|397526	clumping factor (Staphylococcus aureus)	58	51	1518
231	3	1629	1474	gi|1002520	HutS (Bacillus subtilis)	58	45	156
233	6	4201	3497	gi|1463023	No definition line found (Caenorhabditis elegans)	58	39	705
243	10	9303	10082	gi|537207	ORF_[277 (Escherichia coli)	58	32	780
257	1	331	1143	gi|1340128	ORF1 (Staphylococcus aureus)	58	44	813
302	2	460	801	gi|40174	ORF x (Bacillus subtilis)	58	30	342
307	11	6984	6127	gi|1303842	YqfU (Bacillus subtilis)	58	34	858
321	3	1914	2747	gi|1239996	hypothetical protein (Bacillus subtilis)	58	41	834
342	4	2724	3497	gi|454838	ORF 6: putative (Pseudomonas aeruginosa)	58	41	774
348	1	1	663	gi|467478	unknown (Bacillus subtilis)	58	36	663
401	2	384	605	gi|143407	para-aminobenzoic acid synthase, component I (pab) (Bacillus subtilis)	58	53	222

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
437	1	125	1554	gi|1303866	Yqgs [Bacillus subtilis]	58	35	1230
445	1	105	1442	gi|581583	protein A [Staphylococcus aureus]	58	32	1338
453	3	789	965	gi|1009455	unknown [Schizosaccharomyces pombe]	58	34	177
451	5	2748	2047	gi|537214	yjjG gene product [Escherichia coli]	58	40	702
479	2	731	1444	gi|1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative [Bacillus subtilis]	58	36´	714
490	1	909	547	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13484|TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS ROTEIN E).	58	36	363
517	1	1	1164	sp|P47264|YO18_	HYPOTHETICAL HELICASE MG018.	58	30	1164
517	6	4182	4544	gi|453422	orf268 gene product [Mycoplasma hominis]	58	29	363
546	3	2802	4019	gi|886052	restriction modification system S subunit [Spiroplasma citri] gi|886052 restriction modification system S subunit [Spiroplasma itri]	58	37	1218
562	1	3	179	gi|43031	nifS protein (AA 1-400) [Klebsiella pneumoniae]	58	34	177
600	2	1347	1156	gi|1183839	unknown [Pseudomonas aeruginosa]	58	48	192
604	2	1231	1001	gi|1001353	hypothetical protein [Synechocystis sp.]	58	41	231
619	1	1	504	gi|903748	integral membrane protein [Homo sapiens]	58	43	504
625	1	2	364	gi|1208474	hypothetical protein [Synechocystis sp.]	58	43	363
635	1	1492	755	ni|1510995	transaldolase [Methanococcus jannaschii]	58	41	738
645	1	1	846	gi|677882	ileal sodium-dependent bile acid transporter [Rattus norvegicus] gi|677882 ileal sodium-dependent bile acid transporter [Rattus orvegicus]	58	33	846
645	3	906	1556	gi|1239999	hypothetical protein [Bacillus subtilis]	58	41	651
665	1	771	532	gi|1204262	hypothetical protein (GB:L10228_61) [Haemophilus influenzae]	58	39	240
674	1	635	327	gi|498817	ORF8; homologous to small subunit of phage terminases [Bacillus ubtilis]	58	39	309
675	2	1312	806	gi|42181	osmC gene product [Escherichia coli]	58	28	507
745	1	618	310	gi|1205432	coenzyme PQQ synthesis protein III (pqqIII) [Haemophilus influenzae]	58	32	309
799	2	242	1174	gi|1204669	collagenase [Haemophilus influenzae]	58	36	933
800	2	1096	614	gi|171963	tRNA isopentenyl transferase [Saccharomyces cerevisiae] sp|P07884|MOD5_YEAST TRNA ISOPENTENYLTRANSFERASE (EC 2.5.1.8) ISOPENTENYL-DIPHOSPHATE: TRNA ISOPENTENYLTRANSFERASE) (IPP RANSFERASE) (IPPT).	58	37	483

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

ontig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
854	1	1108	605	gi|466778	lysine specific permease (Escherichia coli)	58	44	504
885	1	481	242	gi|861199	protoporphyrin IX Mg-chelatase subunit precursor (Hordeum vulgare)	58	33	240
891	1	3	527	gi|1293660	AbsA2 (Streptomyces coelicolor)	58	31	525
942	1	931	467	gi|405567	traH (Plasmid pSK41)	58	30	465
1002	1	952	521	gi|577669	preLUKM (Staphylococcus aureus)	58	34	432
1438	1	1	261	gi|581558	isoleucyl tRNA synthetase (Staphylococcus aureus) sp|P41368|SYIP_STAU ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS) (MUPIROCIN RESISTANCE ROTEIN).	58	30	261
1442	1	2	463	gi|971394	similar to Acc.No. D26185 (Escherichia coli)	58	34	462
1473	1	480	241	gi|1339951	small subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	58	38	240
1876	1	3	158	gi|529216	No definition line found (Caenorhabditis elegans) sp|P46503|YLX7_CAEEL HYPOTHETICAL 7.3 KD PROTEIN F23F12.7 IN HROMOSOME III	58	33	156
1989	1	108	401	gi|1405458	YneR (Bacillus subtilis)	58	29	294
2109	1	3	401	gi|1001801	hypothetical protein (Synechocystis sp.)	58	31	399
2473	1	288	145	gi|510140	oligoendopeptidase F (Lactococcus lactis)	58	38	144
2523	1	452	228	gi|644873	catabolic dehydroquinate dehydratase (Acinetobacter calcoaceticus)	58	37	225
3041	1	2	211	gi|1205367	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	58	39	210
3094	1	3	263	gi|1185288	isochorismate synthase (Bacillus subtilis)	58	38	261
3706	1	3	383	gi|416614	mevalonate kinase (Arabidopsis thaliana)	58	48	381
3454	1	1	402	gi|808869	human gcp372 (Homo sapiens)	58	32	402
4042	1	51	224	gi|508551	ribulose-1,5 bisphosphate carboxylase large subunit -methyltransferase (Pisum sativum)	58	37	174
4278	1	3	206	gi|180189	cerebellar-degeneration-related antigen (CDR34) (Homo sapiens) gi|182737 cerebellar degeneration-associated protein (Homo sapiens) cerebellar degeneration-related protein - human pir|A29770|A29770 cerebellar degeneration-related protein [Synechocystis sp.]	58	37	204
19	7	7818	7363	gi|1001516	hypothetical protein (Synechocystis sp.)	57	31	456
23	11	9663	8872	gi|1605066	ORF_f256 (Escherichia coli)	57	29	792
31	1	4801	2402	gi|153146	ORF3 (Streptomyces coelicolor)	57	32	2400
38	14	11611	10796	gi|144859	ORF B (Clostridium perfringens)	57	31	816
46	14	12063	13046	gi|1001319	hypothetical protein (Synechocystis sp.)	57	25	984

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
51	3	1411	1187	pir|B33856|B338	hypothetical 80K protein - Bacillus sphaericus	57	38	225
54	1	1	453	gi|684950	staphylococcal accessory regulator A [Staphylococcus aureus]	57	31	453
75	1	3	239	gi|1000470	C27B7.7 [Caenorhabditis elegans]	57	42	237
92	5	3855	3061	gi|143607	sporulation protein [Bacillus subtilis]	57	35	795
96	3	4006	4773	gi|144297	acetyl esterase (XynC) [Caldocellum saccharolyticum] pir|B37202|B37202 acetylesterase (EC 3.1.1.6) (XynC) - Caldocellum saccharolyticum	57	34'	768
107	3	1480	2076	gi|460955	TagE [Vibrio cholerae]	57	42	597
109	8	5340	5933	gi|1438846	Unknown [Bacillus subtilis]	57	41	594
112	9	6679	7701	gi|1486250	unknown [Bacillus subtilis]	57	33	1023
114	4	6384	4108	gi|871456	putative alpha subunit of formate dehydrogenease [Methanobacterium thermoautotrophicum]	57	37	2277
126	2	430	1053	gi|288301	ORF2 gene product [Bacillus megaterium]	57	37	624
131	5	6537	6277	gi|1511160	M. jannaschii predicted coding region MJ1163 [Methanococcus jannaschii]	57	38	261
133	3	2668	2201	gi|1303912	YqhW [Bacillus subtilis]	57	40	468
133	4	3383	2784	gi|1221884	(urea?) amidolyase [Haemophilus influenzae]	57	37	600
147	4	2164	1694	gi|467469	unknown [Bacillus subtilis]	57	33	471
160	2	1293	1060	gi|558604	chitin synthase 2 [Neurospora crassa]	57	28	234
163	8	5687	4764	gi|145580	rarD gene product [Escherichia coli]	57	38	924
168	6	4336	5325	gi|39782	33kDa lipoprotein [Bacillus subtilis]	57	32	990
170	5	3297	3455	gi|603404	Yer164p [Saccharomyces cerevisiae]	57	37	159
221	6	8026	6809	gi|1136221	carboxypeptidase [Sulfolobus solfataricus]	57	32	1218
228	3	1348	1791	gi|288969	fibronectin binding protein [Streptococcus dysgalactiae] pir|S33850|S33850 fibronectin-binding protein - Streptococcus ysgalactiae	57	32	444
263	4	4411	3686	gi|1185002	dihydrodipicolinate reductase [Pseudomonas syringae pv. tabaci]	57	42	726
276	1	494	255	gi|396380	No definition line found [Escherichia coli]	57	40	240
283	2	335	1324	gi|773349	BirA protein [Bacillus subtilis]	57	32	990
297	1	469	236	gi|1334820	reading frame V [Cauliflower mosaic virus]	57	46	234
342	3	1993	2805	gi|1204431	hypothetical protein (SP:P33644) [Haemophilus influenzae]	57	35	813

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
375	6	3340	3741	gi|385177	cell division protein (Bacillus subtilis)	57	26	402
433	6	3286	4011	gi|1524117	alpha-acetolactate decarboxylase (Lactococcus lactis)	57	40	726
470	3	903	1145	gi|R04819	protein serine/threonine kinase (Toxoplasma gondii)	57	30	243
487	5	1391	1723	gi|507323	ORF1 (Bacillus stearothermophilus)	57	28	333
498	1	274	852	gi|1334549	NADH-ubiquinone oxidoreductase subunit 4L (Podospora anserina)	57	34'	579
503	1	343	173	gi|1502283	organic cation transporter OCT2 (Rattus norvegicus)	57	30	171
505	2	1619	1284	gi|466884	B1436_C2_194 (Mycobacterium leprae)	57	40	336
519	2	1182	2549	gi|1303707	YrkH (Bacillus subtilis)	57	34	1368
522	2	3234	1945	gi|1064809	homologous to sp:HTRA_ECOLI (Bacillus subtilis)	57	36	1290
538	2	909	1415	gi|153179	phosphorinothyrcin n-acetyltransferase (streptomyces coelicolor) pir|JH02446|JH02446 phosphinothricin N-acetyltransferase (EC 2.3.1.-) Streptomyces coelicolor	57	40	507
547	1	968	486	gi|467340	unknown (Bacillus subtilis)	57	50	483
599	1	1062	532	sp|P20692|TYRA_	PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).	57	41	531
620	2	757	572	gi|1107894	unknown (Schizosaccharomyces pombe)	57	38	186
622	2	1600	1130	gi|173028	thioredoxin II (Saccharomyces cerevisiae)	57	39	471
625	2	362	1114	gi|1262366	hypothetical protein (Mycobacterium leprae)	57	34	753
680	1	1	204	gi|143544	RNA polymerase sigma-30 factor (Bacillus subtilis) pir|A28625|A28625 transcription initiation factor sigma H - acillus subtilis	57	30	204
690	1	3	629	gi|466520	pocR (Salmonella typhimurium)	57	29	627
696	1	2	433	gi|413972	ipa-48r gene product (Bacillus subtilis)	57	33	432
704	1	36	638	gi|1499931	M. jannaschii predicted coding region MJ1083 (Methanococcus jannaschii)	57	36	603
732	1	2316	1621	gi|1418999	orf4 (Lactobacillus sake)	57	37	696
746	1	451	227	gi|392973	Rab3 (Aplysia californica)	57	42	225
757	1	20	466	gi|143579	L curvatus small cryptic plasmid gene for rep protein (Lactobacillus rvatus)	57	45	447
862	1	2	295	gi|1303827	YqfI (Bacillus subtilis)	57	21	294
1049	1	907	455	gi|1510108	ORF-1 (Agrobacterium tumefaciens)	57	35	453
1117	1	1187	695	gi|896286	NH2 terminus uncertain (Leishmania tarentolae)	57	28	693

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1136	1	2	322	gi|1303653	YqgF [Bacillus subtilis]	57	38	321
1144	2	1033	611	gi|310083	voltage-activated calcium channel alpha-1 subunit [Rattus orvegicus]	57	40	421
1172	1	1472	738	gi|1511146	M. jannaschii predicted coding region MJ1143 [Methanococcus jannaschii]	57	28	735
1500	2	746	558	gi|142780	putative membrane protein; putative [Bacillus subtilis]	57	35	189
1676	1	659	399	gi|313777	uracil permease [Escherichia coli]	57	31*	261
2481	1	2	400	gi|1237015	ORF4 [Bacillus subtilis]	57	23	399
3099	1	3	230	gi|1204540	isochorismate synthase [Haemophilus influenzae]	57	29	228
3122	1	360	181	gi|882472	ORF_0464 [Escherichia coli]	57	40	180
3560	1	2	361	gi|153490	tetracenomycin C resistance and export protein [Streptomyces lauceacens]	57	37	360
3850	1	856	434	gi|155588	glucose-fructose oxidoreductase [Zymomonas mobilis] pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis	57	40	423
3931	1	704	354	gi|1413953	ipa-29d gene product [Bacillus subtilis]	57	36	351
3993	1	1	384	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.88) Pseudomonas sp.	57	39	384
4065	1	793	398	pir|JV0017|RDEC	nitrate reductase (EC 1.7.99.4) alpha chain - Escherichia coli	57	31	396
4100	1	596	300	gi|1086633	T06C10.5 gene product [Caenorhabditis elegans]	57	47	297
4163	1	571	287	gi|21512	patatin [Solanum tuborosum]	57	50	285
4267	2	631	335	gi|1000365	SpoIIAG [Bacillus subtilis]	57	38	297
4358	1	3	302	gi|298032	EF [Streptococcus suis]	57	32	300
4389	2	108	290	gi|405894	1-phosphofructokinase [Escherichia coli]	57	37	183
4399	1	2	232	gi|1483603	Pristinamycin I synthase I [Streptomyces pristinaespiralis]	57	35	231
4481	1	572	288	gi|405879	yeiH [Escherichia coli]	57	44	285
4486	1	512	258	gi|515938	glutamate synthase (ferredoxin) [Synechocystis sp.] pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	57	42	255
4510	1	481	242	gi|1205301	leukotoxin secretion ATP-binding protein [Haemophilus influenzae]	57	38	240
4617	1	468	256	gi|1511222	restriction modification enzyme, subunit M1 [Methanococcus jannaschii]	57	35	213
4	11	12201	11524	gi|149204	histidine utilization repressor G (Klebsiella aerogenes) pir|AJ6730|AJ6730 hutG protein - Klebsiella pneumoniae (fragment) sp|P19452|HUTG_KLEAE FORMIMINOGLUTAMASE (EC 3.5.3.8) FORMIMINOGLUTAMATE HYDROLASE) (HISTIDINE UTILIZATION PROTEIN G) FRAGMENT).	56	31	678

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
22	8	4248	5177	gi|1322222	RACH1 [Homo sapiens]	56	33	930
38	28	21179	22264	gi|1480705	lipoate-protein ligase [Mycoplasma capricolum]	56	34	1086
44	3	1861	2421	gi|490320	Y gene product [unidentified]	56	31	561
44	15	10103	10606	gi|1205099	hypothetical protein (GB:L19201_1) [Haemophilus influenzae]	56	39	504
50	6	4820	5161	gi|209931	fiber protein [Human adenovirus type 5]	56	48'	342
51	4	2076	2972	gi|623476	transcriptional activator [Providencia stuartii] sp|P43463|AARP_PROST TRANSCRIPTIONAL ACTIVATOR AARP.	56	30	897
67	6	5656	6594	gi|466613	nikB [Escherichia coli]	56	32	939
89	3	2364	1810	gi|482922	protein with homology to pai repressor of B.subtilis [Lactobacillus albrueckii]	56	39	555
96	1	203	913	gi|145594	cAMP receptor protein (crp) [Escherichia coli]	56	35	711
109	21	18250	17846	gi|1204367	hypothetical protein (GB:U14003_270) [Haemophilus influenzae]	56	27	405
112	8	5611	6678	gi|155588	glucose-fructose oxidoreductase [Zymomonas mobilis] pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis	56	40	1068
131	3	6404	5100	gi|619724	MgtE [Bacillus firmus]	56	30	1305
134	2	65	232	gi|413948	ipa-24d gene product [Bacillus subtilis]	56	31	168
138	4	823	1521	gi|580868	ipa-22r gene product [Bacillus subtilis]	56	31	699
146	2	740	447	gi|1046009	M. genitalium predicted coding region MG309 [Mycoplasma genitalium]	56	37	294
149	2	1619	1067	gi|945380	terminase small subunit [Bacteriophage LL-H]	56	35	573
163	1	2	221	gi|143947	glutamine synthetase [Bacteroides fragilis]	56	30	222
166	5	6745	6449	gi|405792	ORF154 [Pseudomonas putida]	56	26	297
187	1	31	393	gi|311237	H(+)-transporting ATP synthase [Zea mays]	56	30	363
190	1	2	373	gi|1109686	Prox [Bacillus subtilis]	56	35	372
191	8	11538	9943	gi|581070	acyl coenzyme A synthetase [Escherichia coli]	56	35	1596
195	1	1293	647	gi|1510242	collagenase [Methanococcus jannaschii]	56	34	645
230	3	2323	2072	gi|40363	heat shock protein [Clostridium acetobutylicum]	56	39	252
238	5	3383	3775	gi|1477533	sarA [Staphylococcus aureus]	56	31	393
270	2	813	1712	gi|765073	autolysin [Staphylococcus aureus]	56	41	900

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
290	1	3221	1612	gi|547513	orf3 [Haemophilus influenzae]	56	34	1590
297	5	1140	1373	gi|1511556	M. jannaschii predicted coding region MJ1561 [Methanococcus jannaschii]	56	40	234
321	2	2947	1799	gi|1001801	hypothetical protein [Synechocystis sp.]	56	31	1149
359	2	1279	641	gi|46336	nolI gene product [Rhizobium meliloti]	56	26	639
371	2	360	1823	gi|145304	L-ribulokinase [Escherichia coli]	56	39*	1464
391	4	1762	2409	gi|1001634	hypothetical protein [Synechocystis sp.]	56	34	648
402	1	380	192	gi|1143904	5-HT4L receptor [Homo sapiens]	56	48	189
416	4	2480	2109	gi|1408486	HS74A gene product [Bacillus subtilis]	56	31	372
424	3	1756	2334	gi|142471	acetolactate decarboxylase [Bacillus subtilis]	56	32	579
457	1	1907	1017	gi|1205194	formamidopyrimidine-DNA glycosylase [Haemophilus influenzae]	56	36	891
458	2	2423	1812	gi|15466	terminase [Bacteriophage SPP1]	56	37	612
504	2	2152	1283	gi|1142681	Lpp38 [Pasteurella haemolytica]	56	38	870
511	1	1	1284	gi|217049	brnQ protein [Salmonella typhimurium]	56	37	1284
603	3	1099	1701	gi|467109	rim; 30S Ribosomal protein S18 alanine acetyltransferase; 229_Cl_170 [Mycobacterium leprae]	56	43	603
660	5	3547	3774	gi|1229106	ZK930.1 [Caenorhabditis elegans]	56	30	228
707	1	35	400	gi|153929	NADPH-sulfite reductase flavoprotein component [Salmonella typhimurium]	56	38	366
709	2	1385	1095	gi|1510801	hydrogenase accessory protein [Methanococcus jannaschii]	56	38	291
718	1	1	495	gi|413948	ipa-24d gene product [Bacillus subtilis]	56	35	495
744	1	87	677	gi|928836	repressor protein [Lactococcus lactis phage BK5-T]	56	35	591
790	1	776	399	gi|1511513	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	56	33	378
795	1	3	407	gi|1205382	cell division protein [Haemophilus influenzae]	56	34	405
813	1	19	930	gi|1222161	permease [Haemophilus influenzae]	56	28	912
855	1	3	515	gi|1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative [Bacillus subtilis]	56	33	513
968	1	2	466	gi|547513	orf3 [Haemophilus influenzae]	56	37	465
973	2	1049	732	gi|A86022	MexR [Pseudomonas aeruginosa]	56	21	318
1203	1	5	223	gi|184251	HMG-1 [Homo sapiens]	56	34	219

TABLE 2

S aureus   Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1976	1	452	237	gi|9806	lysine-rich aspartic acid-rich protein [Plasmodium chabaudi] r|S2218|S2218| lysine/aspartic acid-rich protein - Plasmodium baudi	56	33	216
2161	1	2	400	gi|1237015	ORF4 [Bacillus subtilis]	56	27	399
2958	1	362	183	gi|466685	No definition line found [Escherichia coli]	56	26	180
2979	1	421	212	gi|1204154	spore germination and vegetative growth protein [Haemophilus influenzae]	56	40	210
2994	2	526	326	gi|836646	phosphoribosylformimino-praic ketoisomerase [Rhodobacter phaeroides]	56	29	201
3026	1	177	328	gi|143306	penicillin v amidase [Bacillus sphaericus]	56	30	150
3149	1	289	146	gi|1166604	Similar to aldehyde dehydrogenase [Caenorhabditis elegans]	56	37	144
3770	1	63	401	gi|1129145	acetyl-CoA C-acyltransferase [Mangifera indica]	56	43	339
4054	2	720	361	gi|1205355	Na+/H+ antiporter [Haemophilus influenzae]	56	21	360
4145	1	1	324	gi|726095	long-chain acyl-CoA dehydrogenase [Mus musculus]	56	36	324
4200	1	505	254	gi|155588	glucose-fructose oxidoreductase [Zymomonas mobilis] pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis	56	40	252
4273	1	675	355	gi|308861	GTG start codon [Lactococcus lactis]	56	33	321
1	3	4095	3436	gi|5341	Putative orf YCLX8c, len:192 [Saccharomyces cerevisiae] r|S53591|S53591 hypothetical protein - yeast [Saccharomyces evisiae]	55	25	660
11	12	9377	8505	gi|216773	haloacetate dehalogenase H-1 [Moraxella sp.]	55	32	873
12	4	5133	4534	gi|467337	unknown [Bacillus subtilis]	55	26	600
19	5	5404	5844	gi|1001719	hypothetical protein [Synechocystis sp.]	55	25	441
23	13	14047	12339	gi|474190	lucA gene product [Escherichia coli]	55	30	1749
32	7	5364	6888	gi|1140096	unknown [Mycobacterium tuberculosis]	55	37	1521
34	3	2569	1808	gi|1303968	YqjQ [Bacillus subtilis]	55	39	762
34	5	3960	3412	gi|1303962	YqjK [Bacillus subtilis]	55	33	549
36	1	1291	647	gi|1606045	ORF_o118 [Escherichia coli]	55	27	645
36	6	6220	5243	gi|1001341	hypothetical protein [Synechocystis sp.]	55	31	978
47	3	3054	3821	gi|1001819	hypothetical protein [Synechocystis sp.]	55	21	768
49	1	2065	1127	gi|1403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	55	36	939

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match/gene name	% sim	% ident	length (nt)
67	11	8966	9565	gi|153053	norA1199 protein [Staphylococcus aureus]	55	23	600
75	3	881	1273	gi|21698	L-histidinol: NAD+ oxidoreductase (EC 1.1.1.23) (aa 1-434) scherichia coli]	55	33	393
82	9	15387	14194	gi|136221	carboxypeptidase [Sulfolobus solfataricus]	55	35	1194
87	4	3517	4917	gi|1064812	function unknown [Bacillus subtilis]	55	26	1401
88	2	1172	1636	gi|882463	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia oli]	55	35'	465
92.	1	127	516	gi|1377832	unknown [Bacillus subtilis]	55	36	390
100	2	836	2035	gi|1170274	zeaxanthin epoxidase [Nicotiana plumbaginifolia]	55	36	1200
100	5	5137	4658	gi|396660	unknown open reading frame [Buchnera aphidicola]	55	29	480
108	3	4266	2986	gi|1499A66	M. jannaschii predicted coding region MJ1024 [Methanococcus jannaschii]	55	31	1281
114	3	2616	1834	gi|1511367	formate dehydrogenase, alpha subunit [Methanococcus jannaschii]	55	29	783
144	3	1805	1476	gi|1100787	unkown [Saccharomyces cerevisiae]	55	35	330
165	5	6212	5508	gi|1045884	M. genitalium predicted coding region MG199 [Mycoplasma genitalium]	55	27	705
189	5	2205	2576	gi|142569	ATP synthase a subunit [Bacillus firmus]	55	35	372
191	6	9136	6857	gi|559411	B0272.3 [Caenorhabditis elegans]	55	39	2280
194	2	364	636	gi|1145768	K7 kinesin-like protein [Dictyostelium discoideum]	55	34	273
209	4	1335	1676	gi|473357	thi4 gene product [Schizosaccharomyces pombe]	55	35	342
211	2	1693	1145	gi|410130	ORFX6 [Bacillus subtilis]	55	37	549
213	2	644	1372	gi|633692	TrsA [Yersinia enterocolitica]	55	28	729
214	7	4144	5481	gi|1001793	hypothetical protein [Synechocystis sp.]	55	30	1338
221	7	11473	9197	gi|466520	pocR [Salmonella typhimurium]	55	32	2277
233	8	5908	4817	gi|1237063	unknown [Mycobacterium tuberculosis]	55	18	1092
236	4	1375	2340	gi|1146199	putative [Bacillus subtilis]	55	32	966
243	2	380	1885	gi|459907	mercuric reductase [Plasmid pI258]	55	29	1506
258	1	786	394	gi|455006	orf6 [Rhodococcus fascians]	55	36	393
281	1	126	938	gi|1408493	homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	55	35	813
316	3	1323	2102	gi|1486447	LuxA homologue [Rhizobium sp.]	55	30	780
326	5	2968	2744	gi|1296824	proline iminopeptidase [Lactobacillus helveticus]	55	36	225

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match/gene name	% sim	% ident	length (nt)
351	2	2322	1429	gi|1204820	hydrogen peroxide-inducible activator [Haemophilus influenzae]	55	28	894
353	4	2197	2412	gi|1272475	chitin synthase (Emericella nidulans)	55	50	216
380	1	14	379	gi|142554	ATP synthase 1 subunit (Bacillus megaterium)	55	37	366
383	1	462	232	gi|349272	[ferrichrome-binding protein [Bacillus subtilis]	55	36	231
386	1	3	938	gi|1510251	DNA helicase, putative [Methanococcus jannaschii]	55	30	936
410	2	1208	1891	gi|1205144	multidrug resistance protein [Haemophilus influenzae]	55	27	684
483	2	411	833	gi|413936	ipa-10r gene product [Bacillus subtilis]	55	26	423
529	3	1777	1433	gi|606150	ORF_f309 [Escherichia coli]	55	33	345
555	1	1088	585	gi|143407	para-aminobenzoic acid synthase, component I (pab) [Bacillus subtilis]	55	28	504
565	1	402	202	gi|1223961	CDP-tyvelose epimerase [Yersinia pseudotuberculosis]	55	41	201
582	1	751	452	gi|1256663	20.2% identity with NADH dehydrogenase of the Leishmania major mitochondrion; putative [Bacillus subtilis]	55	36	300
645	5	2260	2057	gi|410824	fusion protein F [Bovine respiratory syncytial virus] pir|JQ1481|VGNZBA [fusion glycoprotein precursor - bovine respiratory syncytial virus (strain A51908)]	55	25	204
672	2	957	2216	gi|1511333	M. jannaschii predicted coding region MJ1122 [Methanococcus jannaschii]	55	36	1260
730	1	955	479	gi|537007	ORF_f379 [Escherichia coli]	55	30	477
737	1	1859	945	gi|536963	CG site No. 1R166 [Escherichia coli]	55	10	915
742	1	228	572	gi|304160	product unknown [Bacillus subtilis]	55	38	345
817	2	1211	903	gi|1136289	histidine kinase A [Dictyostelium discoideum]	55	29	309
819	1	582	355	gi|558073	polymorphic antigen [Plasmodium falciparum]	55	22	228
832	2	1152	724	gi|40367	ORFC [Clostridium acetobutylicum]	55	32	429
840	1	769	386	gi|1205875	pseudouridylate synthase I [Haemophilus influenzae]	55	39	384
1021	1	21	529	gi|48563	beta-lactamase [Yersinia enterocolitica]	55	38	507
1026	1	60	335	gi|47804	Opp C (AA1-301) [Salmonella typhimurium]	55	26	276
1525	1	1	282	gi|1477533	sarA [Staphylococcus aureus]	55	29	282
1814	2	224	985	gi|1046078	M. genitalium predicted coding region MG369 [Mycoplasma genitalium]	55	38	762
3254	1	427	254	gi|413968	ipa-44d gene product [Bacillus subtilis]	55	30	174

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3695	1	686	345	gi|216773	haloacetate dehalogenase H-1 (Moraxella sp.)	55	32	342
3721	1	1	312	gi|42029	ORF1 gene product (Escherichia coli)	55	31	312
3799	1	3	272	gi|42029	ORF1 gene product (Escherichia coli)	55	38	270
3889	1	22	423	gi|1129145	acetyl-CoA C-acyltransferase (Mangifera indica)	55	45	402
3916	1	2	385	gi|529754	spoC (Streptococcus pyogenes)	55	38'	384
3945	1	4	198	gi|476252	phase 1 flagellin (Salmonella enterica)	55	36	195
4074	1	488	246	gi|42029	ORF1 gene product (Escherichia coli)	55	38	243
4184	1	2	343	gi|1524267	unknown (Mycobacterium tuberculosis)	55	28	342
4284	1	14	208	gi|1100774	ferredoxin-dependent glutamate synthase (Synechocystis sp.)	55	36	195
4457	2	644	378	gi|180189	cerebellar-degeneration-related antigen (CDR34) (Homo sapiens) gi|182737 cerebellar degeneration-associated protein (Homo sapiens) pir|A29770|A29770 cerebellar degeneration-related protein - human	55	38	267
4514	1	2	244	gi|216773	haloacetate dehalogenase H-1 (Moraxella sp.)	55	32	243
4599	1	432	217	gi|1129145	acetyl-CoA C-acyltransferase (Mangifera indica)	55	42	216
4606	1	416	210	gi|386120	myosin alpha heavy chain (S2 subfragment) (rabbits, masseter, eptide Partial, 234 aa)	55	27	207
5	A	5348	4932	gi|536069	ORF YBL047c (Saccharomyces cerevisiae)	54	27	417
12	7	7166	6165	gi|1205504	homoserine acetyltransferase (Haemophilus influenzae)	54	30	1002
23	16	17086	15326	gi|474192	iucC gene product (Escherichia coli)	54	31	1761
35	1	2	979	gi|48054	small subunit of soluble hydrogenase (AA 1-384) (Synechococcus sp.) lr|S06919|HQYCSS soluble hydrogenase (EC 1.12.-.-) small chain - nechococcus sp. (PCC 6716)	54	36	978
37	11	9437	8667	gi|337207	ORF_f277 (Escherichia coli)	54	38	771
37	12	8165	8332	gi|1160967	palmitoyl-protein thioesterase (Homo sapiens)	54	37	168
46	15	13025	13804	gi|438473	protein is hydrophobic, with homology to E. coli ProW; putative Bacillus subtilis]	54	28	780
56	2	203	736	gi|1256139	YbbJ (Bacillus subtilis)	54	34	534
57	13	11117	10179	gi|1151248	inosine-uridine preferring nucleoside hydrolase (Crithidia fasciculata)	54	32	939
66	2	515	1133	gi|1335781	Cap (Drosophila melanogaster)	54	29	618
70	10	8116	8646	gi|1399823	PhoE (Rhizobium meliloti)	54	31	531

TABLE 2

S. aureus   Putative coding regions of novel proteins similar to known proteins

ctig ID	ORF ID	Start (nt)	Stop (nt)	match acession	[match] gene name	% sim	% idenr	length (nt)
70	15	12556	11801	sp|P02981|TCR_S	TETRACYCLINE RESISTANCE PROTEIN.	54	29	756
87	5	4915	5706	gi|1064811	[function unknown (Bacillus subtilis)]	54	33	792
92	4	3005	2289	gi|1205366	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	54	33	717
103	2	2596	1556	gi|710495	protein kinase (Bacillus brevis)	54	33	1041
105	2	3585	2095	gi|143727	[putative (Bacillus subtilis)]	54	30'	1491
112	4	2317	2712	gi|153724	MalC (Streptococcus pneumoniae)	54	41	396
127	2	1720	2493	gi|144297	acetyl esterase (XynC) [Caldocellum saccharolyticum] pir|B37202|B37202 acetylesterase (EC 3.1.1.6) (XynC) - Caldocellum accharolyticum	54	34	774
138	5	1600	3306	gi|42473	pyruvate oxidase (Escherichia coli)	54	36	1707
152	2	525	1172	gi|1377834	unknown (Bacillus subtilis)	54	23	648
161	9	4831	5469	gi|901305	ORF73 (Bacillus subtilis)	54	28	639
161	13	6694	7251	gi|1511039	phosphate transport system regulatory protein (Methanococcus jannaschii)	54	32	558
164	6	3263	4543	gi|1204976	prolyl-tRNA synthetase (Haemophilus influenzae)	54	34	1281
164	20	21602	22243	gi|143582	spoIIIEA protein (Bacillus subtilis)	54	32	642
171	6	5683	4250	gi|1436965	[malA] gene products (Bacillus stearothermophilus) pir|S43914|S43914 hypothetical protein 1 - Bacillus tearothermophilus	54	37	1434
206	1R	19208	19720	gi|1240016	R09E10.3 (Caenorhabditis elegans)	54	38	513
218	2	1090	1905	gi|467378	unknown (Bacillus subtilis)	54	26	816
220	1	1322	663	gi|1353761	myosin II heavy chain (Naegleria fowleri)	54	22	660
220	13	12655	13059	pir-|S00485|S004	gene 11-1 protein precursor - Plasmodium falciparum (fragments)	54	35	405
221	3	2030	3709	gi|1303813	YqgW (Bacillus subtilis)	54	34	1680
272	7	5055	4219	gi|62964	arylamine N-acetyltransferase (AA 1-290) [Gallus gallus] sr|S06652|XYCHY3 arylamine N-acetyltransferase (EC 2.3.1.5) (clone NAT-3) - chicken	54	33	837
316	7	4141	4701	gi|6A2769	mccE gene product (Escherichia coli)	54	31	561
316	10	6994	8742	gi|413951	ipa-27d gene product (Bacillus subtilis)	54	28	1749
338	3	3377	2214	gi|490328	[ORF F (unidentified)]	54	28	1163
341	4	3201	3614	gi|171959	myosin-like protein (Saccharomyces cerevisiae)	54	25	414

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
346	1	1820	912	gi|396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp|P32703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549).	54	34	909
348	2	623	1351	gi|537109	ORF_f343a [Escherichia coli]	54	34	729
378	2	1007	1942	sp|P02983|TCR_S	TETRACYCLINE RESISTANCE PROTEIN.	54	3?	936
408	6	4351	5301	gi|474190	iucA gene product [Escherichia coli]	54	29*	951
444	9	7934	8854	gi|216267	ORF2 [Bacillus megaterium]	54	32	921
461	2	2717	2229	gi|104160	product unknown [Bacillus subtilis]	54	50	489
502	2	1696	1133	gi|1205015	hypothetical protein (SP:P10120) [Haemophilus influenzae]	54	38	564
505	6	6262	5357	gi|1500558	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase [Methanococcus jannaschii]	54	41	906
550	1	2736	1522	gi|40100	rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir|S06049|S06049 rodC protein - Bacillus subtilis p|P13485|TAGF_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F.	54	35	1215
551	5	3305	4279	gi|950197	unknown [Corynebacterium glutamicum]	54	34	975
558	2	1156	958	gi|485090	No definition line found [Caenorhabditis elegans]	54	32	399
580	1	91	936,	gi|331906	[fused envelope glycoprotein precursor [Friend spleen focus-forming irus]	54	45	846
603	3	554	757	gi|1323423	ORF YGR234w [Saccharomyces cerevisiae]	54	36	204
617	1	25	249	gi|219959	ornithine transcarbamylase [Homo sapiens]	54	40	225
622	3	1097	1480	gi|1303873	YqgZ [Bacillus subtilis]	54	25	384
623	1	3	404	gi|1063250	low homology to P20 protein of Bacillus lichiniformis and bleomycin acetyltransferase of Streptomyces verticilus [Bacillus subtilis]	54	45	402
689	1	1547	1011	gi|552446	NADH dehydrogenase subunit 4 [Apis mellifera ligustica] pir|S52968|S52968 NADH dehydrogenase chain 4 - honeybee itochondrion (SGC4)	54	30	537
725	2	686	1441	gi|987096	sensory protein kinase [Streptomyces hygroscopicus]	54	26	756
956	1	1	249	pir|S30782|S307	integrin homolog - yeast (Saccharomyces cerevisiae)	54	24	249
978	2	1137	859	gi|1301994	ORF YNL091w [Saccharomyces cerevisiae]	54	33	279
1314	1	3	281	gi|1001108	hypothetical protein [Synechocystis sp.]	54	33	279
2450	1	1	228	gi|1045057	ch-TOG [Homo sapiens]	54	32	228
2934	1	1	187	gi|580870	ipa-37d qoxA gene produc. [Bacillus subtilis]	54	36	387
2970	1	499	251	sp|P17J4P|YECE_	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	54	42	249

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

ontig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3002	1	1	309	gi|44027	Tma protein [Lactococcus lactis]	54	33	309
3561	1	9	464	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	54	35	456
3572	1	72	401	gi|450688	hsdM gene of Ecoprrl gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	54	36	330
3829	1	798	400	gi|1122245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	54	29	399
3909	1	1	273	gi|29865	CENP-E [Homo sapiens]	54	30	273
3921	1	1	209	pir|S24325|S243	glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Pseudomonas [fluorescens subsp. cellulosa]	54	34	207
4438	1	566	285	gi|1196657	unknown protein [Mycoplasma pneumoniae]	54	30	282
4459	1	3	272	gi|1046081	hypothetical protein (GB:D26185_10) [Mycoplasma genitalium]	54	38	270
4564	1	3	221	gi|216267	ORF2 [Bacillus megaterium]	54	38	219
23	12	12538	10685	gi|474192	iucC gene product [Escherichia coli]	53	35	1854
23	14	14841	13579	gi|42029	ORF1 gene product [Escherichia coli]	53	32	1263
24	3	4440	3940	gi|1369947	c2 gene product [Bacteriophage B1]	53	36	501
26	4	3818	4618	gi|1486247	unknown [Bacillus subtilis]	53	37	801
3H	6	2856	3998	gi|405880	yeiI [Escherichia coli]	53	40	1143
38	10	9380	7806	gi|1399954	thyroid sodium/iodide symporter NIS [Rattus norvegicus]	53	29	1575
56	10	12324	12100	pir|A54592|A545	110k actin filam. associated protein - chicken	53	32	225
57	6	5047	4583	pir|A00141|DEZP	alcohol dehydrogenase (EC 1.1.1.1) - fission yeast (Schizosaccharomyces pombe)	53	39	465
57	12	10515	8932	gi|480429	putative transcriptional regulator [Bacillus stearothermophilus]	53	30	1584
67	12	9496	10218	gi|1511555	quinolone resistance norA protein protein [Methanococcus jannaschii]	53	31	723
69	3	3125	2382	gi|1687017	arabinogalactan-protein, AGP [Nicotiana alata, cell-suspension culture filtrate. Peptide. 461 aa]	53	30	744
79	1	3	1011	gi|1523802	glucanase [Anabaena variabilis]	53	32	1029
80	1	673	338	gi|452428	ATPase 3 [Plasmodium falciparum]	53	36	336
88	4	1910	2524	gi|37014	ORF_o488 [Escherichia coli]	53	25	615
88	5	2467	3282	gi|537014	ORF_o488 [Escherichia coli]	53	29	816

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
92	8	5870	5505	gi|399598	amphotropic murine retrovirus receptor [Rattus norvegicus]	53	33	366
94	5	4417	3239	gi|173038	tropomyosin (TPM1) [Saccharomyces cerevisiae]	53	25	1179
99	5	4207	5433	sp|P28246|BCR_E	BICYCLOMYCIN RESISTANCE PROTEIN (SULFONAMIDE RESISTANCE PROTEIN).	53	30	1227
120	3	1639	2262	gi|576655	ORF1 [Vibrio anguillarum]	53	35	624
120	11	7257	8897	gi|1524397	glycine betaine transporter OpuD [Bacillus subtilis]	53	33'	1641
127	6	6893	5685	gi|1256630	putative [Bacillus subtilis]	53	32	1209
147	2	255	557	gi|581648	epiB gene product [Staphylococcus epidermidis]	53	34	303
158	4	4705	4256	gi|151004	mucoidy regulatory protein AlgR [Pseudomonas aeruginosa] pir|A32802|A32802 regulatory protein algR - Pseudomonas aeruginosa sp|P26275|ALGR_PSEAE POSITIVE ALGINATE BIOSYNTHESIS REGULATORY ROTEIN.	53	32	450
171	7	5717	5421	gi|1510669	hypothetical protein (GP:D64044_18) [Methanococcus jannaschii]	53	34	297
191	9	13087	11483	gi|298085	acetoacetate decarboxylase [Clostridium acetobutylicum] pir|B49346|B49346 butyrate-acetoacetate CoA-transferase (EC .8.3.9) small chain - Clostridium acetobutylicum sp|P31752|CTFA_CLOAB BUTYRATE-ACETOACETATE COA-TRANSFERASE SUBUNIT (EC 2.8.3.9) (COAT A)	53	31	1605
201	5	3763	4326	gi|143456	rpoE protein (ttg start codon) [Bacillus subtilis]	53	29	564
206	17	18204	18971	gi|304136	acetylglutamate kinase [Bacillus stearothermophilus] sp|O07905|ARGB_BACST ACETYLGLUTAMATE KINASE (EC 2.7.2.8) (NAG KINASE) (AGK) (N-ACETYL-L-GLUTAMATE 5-PHOSPHOTRANSFERASE).	53	36	768
212	10	4021	4221	gi|9878	protein kinase [Plasmodium falciparum]	53	28	201
231	2	1580	1350	gi|537506	paramyosin [Dirofilaria immitis]	53	34	231
272	6	2719	3249	pir|A33141|A331	hypothetical protein (gt(D 3' region) - Streptococcus mutans	53	34	531
308	3	927	2576	gi|606292	ORF_0696 [Escherichia coli]	53	33	1650
320	7	5645	5884	gi|160596	RNA polymerase III largest subunit [Plasmodium falciparum] sp|P27625|RPC1_PLAFA DNA-DIRECTED RNA POLYMERASE III LARGEST UBUNIT (EC 2.7.7.6).	53	33	240
327	1	218	901	gi|854601	unknown [Schizosaccharomyces pombe]	53	31	684
341	2	212	2500	gi|633732	ORF1 [Campylobacter jejuni]	53	31	2289
351	1	763	383	sp|P31675|VABM_	HYPOTHETICAL 42.7 KD PROTEIN IN TBPA-LEUD INTERGENIC REGION (ORF104).	53	32	381
433	7	5087	4731	gi|1001961	MHC class II analog [Staphylococcus aureus]	53	30	357
454	2	1240	980	pir|A60328|A603	40K cell wall protein precursor (sr 5' region) - Streptococcus mutans (strain OMZ175, serotype f)	53	27	261

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	Aafqh gene name	% sim	% ident	length (nt)
470	4	1123	1761	gi|516826	rat GCP360 [Rattus rattus]	53	30	639
483	1	432	217	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	53	(?)	216
544	1	516	1259	gi|46587	ORF 1 (AA 1 - 121) (1 is 2nd base in codon) [Staphylococcus aureus] tr|S15765|S15765 hypothetical protein 1 (hlb 5' region) - aphylococcus aureus (fragment)	53	38	744
55R	10	1957	3754	gi|15140	res gene [Bacteriophage P1]	53	32'	204
601	2	319	620	gi|507738	Hmp [Vibrio parahaemolyticus]	53	26	282
693	1	1669	941	gi|153123	toxic shock syndrome toxin-1 precursor [Staphylococcus aureus] pir|A24606|XCSAS1 toxic shock syndrome toxin-1 precursor - taphylococcus aureus	53	38	729
766	1	2	671	gi|687600	orfA2; orfA2 forms an operon with orfA1 [Listeria monocytogenes]	53	43	672
781	1	667	335	gi|1204551	pilin biogenesis protein [Haemophilus influenzae]	53	24	333
801	1	3	545	gi|279400	SapA protein [Escherichia coli]	53	25	543
803	1	2	910	gi|695278	lipase-like enzyme [Alcaligenes eutrophus]	53	30	909
872	1	1177	590	gi|298032	EF [Streptococcus suis]	53	30	588
910	1	2	184	gi|1044936	unknown [Schizosaccharomyces pombe]	53	29	183
943	1	794	399	gi|190508	similar to unidentified ORF near 47 minutes [Escherichia coli] sp|P31436|YICK_ECOLI HYPOTHETICAL 43.5 KD PROTEIN IN SELC-NLPA INTERGENIC REGION.	53	30	396
988	1	1004	504	gi|142441	ORF 3; putative [Bacillus subtilis]	53	28	501
1064	1	3	434	gi|305080	myosin heavy chain [Entamoeba histolytica]	53	26	432
1366	1	3	452	gi|308852	transmembrane protein [Lactococcus lactis]	53	33	450
1758	1	792	397	gi|1001774	hypothetical protein [Synechocystis sp.]	53	30	396
1897	1	1	447	gi|1303949	YqlX [Bacillus subtilis]	53	27	447
2381	1	798	400	gi|1146243	22.6% identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis]	53	37	399
3537	1	1	327	gi|450688	hsdM gene of Ecoprrl gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	53	35	327
3747	2	117	397	gi|1477486	transposase [Burkholderia cepacia]	53	53	261
11	5	3049	3441	gi|868224	No definition line found [Caenorhabditis elegans]	52	33	393

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
15	5	2205	2369	gi|215966	G41 protein (gtg start codon) [Bacteriophage T4]	52	34	165
19	3	2429	3808	gi|1205379	UDP-murnac-pentapeptide synthetase [Haemophilus influenzae]	52	31	1380
24	1	6920	3462	gi|579124	predicted 86.4kd protein; 52kd observed [Mycobacteriophage L5] pir|S30971|S30971 gene 26 protein - Mycobacterium phage L5 sp|Q05233|VG26_BPML5 MINOR TAIL PROTEIN GP26. (SUB 2-817)	52	32	3459
37	5	3015	3935	gi|1500543	P115 protein [Methanococcus jannaschii]	52	25	921
38	13	8795	9703	gi|46851	glucose kinase [Streptomyces coelicolor]	52	29	909
44	16	10617	11066	gi|42012	moaE gene product [Escherichia coli]	52	36	450
46	1	3	521	gi|1040957	NADH dehydrogenase subunit 6 [Anopheles trinkae]	52	25	519
51	10	5531	6280	gi|388269	traC [Plasmid pAD1]	52	32	750
56	5	3968	2826	gi|181949	endothelial differentiation protein (edg-1) [Homo sapiens] pir|A35300|A35300 G protein-coupled receptor edg-1 - human sp|P21453|EDG1_HUMAN PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.	52	23	1143
57	5	4850	4173	gi|304153	sorbitol dehydrogenase [Bacillus subtilis]	52	27	678
62	5	3364	2870	gi|1072399	phaE gene product [Rhizobium meliloti]	52	25	495
62	6	4445	3651	gi|46485	NADH dehydrogenase [Synechococcus PCC7942]	52	27	795
67	14	11355	12962	gi|1511365	glutamate synthase (NADPH), subunit alpha [Methanococcus jannaschii]	52	30	1608
67	21	16935	18158	gi|1204393	hypothetical protein (SP:P31122) [Haemophilus influenzae]	52	25	1224
70	4	2185	1997	gi|7227	cytoplasmic dynein heavy chain [Dictyostelium discoideum] r|A44357|A44357 dynein heavy chain, cytosolic - slime mold ctyosteluim discoideum]	52	36	189
96	10	10005	10664	gi|1408485	B65G gene product [Bacillus subtilis]	52	26	660
103	5	3986	3351	gi|1009368	Respiratory nitrate reductase [Bacillus subtilis]	52	42	636
109	3	4102	3350	gi|699274	lmbE gene product [Mycobacterium leprae]	52	39	753
109	19	15732	17300	gi|1526981	amino acid permease YaeF like protein [Salmonella typhimurium]	52	30	1569
121	3	1412	981	gi|732931	unknown [Saccharomyces cerevisiae]	52	32	432
125	3	865	1680	gi|1296975	puT gene product [Porphyromonas gingivalis]	52	38	816
130	2	659	1807	gi|1256634	25.8% identity over 120 aa with the Synenococcus sp. MpeV protein; putative MpeV protein; putative [Bacillus subtilis]	52	36	1149
149	1	1164	583	gi|1225943	PBSX terminase [Bacillus subtilis]	52	33	582
149	14	4687	4415	gi|1510368	M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii]	52	35	273

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

ntig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
167	1	216	1001	gi|146025	cell division protein (Escherichia coli)	52	43	786
188	1	120	1256	gi|147491S	orf 337; translated orf similarity to SW: BCR_ECOLI bicyclomycin resistance protein of Escherichia coli [Coxiella burnetii] pir|S44207|S44207 hypothetical protein 337 - Coxiella burnetii (SUB-338)	52	26	1137
195	9	9161	8760	gi|3028	mitochondrial outer membrane 72K protein [Neurospora crassa] r|A36682|A36682 72K mitochondrial outer membrane protein - rospora crassa	52	25	402
200	3	2065	2607	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	52	35	543
203	4	2776	3684	gi|1303698	BltD [Bacillus subtilis]	52	25	909
227	8	5250	5651	gi|305080	myosin heavy chain [Entamoeba histolytica]	52	24	402
242	1	21	1424	gi|1060877	EmrY [Escherichia coli]	52	32	1404
249	5	4526	4751	pir|C37222|C372	cytochrome P450 1A1, hepatic - dog (fragment)	52	23	228
255	1	2107	1055	gi|143290	penicillin-binding protein [Bacillus subtilis]	52	28	1053
276	7	3963	3664	gi|1001610	hypothetical protein [Synechocystis sp]	52	10	300
276	8	4456	4055	gi|416235	orf L3 [Mycoplasma capricolum]	52	26	402
289	2	1856	1449	gi|150900	GTP phosphohydrolase [Proteus vulgaris]	52	34	408
325	1	1	279	gi|1204874	polypeptide deformylase (formylmethionine deformylase) [Haemophilus influenzae]	52	33	279
340	1	2017	1010	gi|1215695	peptide transport system protein SapF homolog; SapF homolog [Mycoplasma pneumoniae]	52	31	100H
375	3	340	1878	gi|467446	similar to SpoVB [Bacillus subtilis]	52	28	1539
424	6	4104	3262	gi|1478239	unknown [Mycobacterium tuberculosis]	52	34	843
430	1	3	575	pir|A42606|A426	orfA 5' to orf405 - Saccharopolyspora erythraea (fragment)	52	28	573
444	4	4728	3712	gi|1408494	homologous to penicillin acylase [Bacillus subtilis]	52	31	1017
465	1	1802	903	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-)	52	36	900
469	5	4705	4169	gi|755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp|P42951|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	52	32	537
495	1	1262	633	gi|1204607	transcription activator [Haemophilus influenzae]	52	25	630
505	7	6004	5762	gi|142440	ATP-dependent nuclease [Bacillus subtilis]	52	28	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
517	2	1162	1614	gi|166162	Bacteriophage phi-11 int gene activator (Staphylococcus acteriophage phi 11)	52	35	453
543	2	444	1295	gi|1215693	putative orf; GT9_orf434 (Mycoplasma pneumoniae)	52	25	852
586	1	1	336	gi|581648	epiB gene product (Staphylococcus epidermidis)	52	36	336
773	1	848	426	gi|1279769	FdhC (Methanobacterium thermoformicicum)	52	30	423
1120	2	100	330	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	52	35	231
1614	1	691	347	gi|289262	comE ORF3 [Bacillus subtilis]	52	28	345
2495	1	1	324	gi|216151	DNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi|579197 SPO2 DNA polymerase (aa 1-648) [Bacteriophage SPO2] pir|A21498|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage PO2	52	34	324
2931	1	566	285	gi|1256136	YbbG [Bacillus subtilis]	52	30	282
2943	1	577	320	gi|41713	hisA ORF (AA 1-245) [Escherichia coli]	52	35	258
2993	1	588	295	gi|298032	EF [Streptococcus suis]	52	34	294
3667	1	612	307	gi|849025	hypothetical 64.7-kDa protein [Bacillus subtilis]	52	36	306
3944	1	478	260	gi|1218040	BAA [Bacillus licheniformis]	52	36	219
3954	2	613	347	gi|854064	U87 [Human herpesvirus 6]	52	50	267
3986	1	90	401	gi|1205919	Na+ and Cl- dependent gamma-aminobutyric acid transporter [Haemophilus influenzae]	52	33	312
4002	1	3	189	gi|40003	oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] p|P23129|ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE).	52	42	387
4020	1	1	249	gi|159388	ornithine decarboxylase [Leishmania donovani]	52	47	249
4098	1	438	220	gi|409795	No definition line found [Escherichia coli]	52	32	219
4248	1	3	212	gi|965077	Adr6p [Saccharomyces cerevisiae]	52	40	210
7	1	3	575	gi|895747	putative cel operon regulator [Bacillus subtilis]	51	28	573
21	4	2479	3276	gi|1510962	indole-3-glycerol phosphate synthase [Methanococcus jannaschii]	51	32	798
22	9	5301	5966	gi|1303933	YqiN [Bacillus subtilis]	51	25	666
43	3	1516	1283	gi|1519460	Srp1 [Schizosaccharomyces pombe]	51	31	234
44	17	11042	11305	gi|42011	moaD gene product [Escherichia coli]	51	35	264
51	11	6453	6731	gi|495471	vacuolating toxin [Helicobacter pylori]	51	37	279

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

ntig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
52	4	2537	2995	gi|1256652	25% identity to the E.coli regulatory protein MprA: putative [Bacillus subtilis]	51	32	459
57	10	7331	6843	gi|508173	EIIA domain of PTS-dependent Gat transport and phosphorylation Escherichia coli]	51	32	489
59	1	29	1111	gi|299163	alanine dehydrogenase [Bacillus subtilis]	51	33	1083
67	20	15791	16576	gi|1510977	M. jannaschii predicted coding region MJ0938 [Methanococcus jannaschii]	51	24	786
69	2	1559	1218	gi|467359	unknown [Bacillus subtilis]	51	34	342
71	1	3	1196	gi|298032	EF [Streptococcus suis]	51	32	1194
78	2	349	176	gi|1161242	proliferating cell nuclear antigen [Styela clava]	51	28	174
99	4	3357	4040	gi|642795	TFIID subunit TAFII55 [Homo sapiens]	51	25	684
109	1	2852	1428	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P11484|TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS ROTEIN E).	51	27	1425
109	9	6007	6693	gi|1204815	hypothetical protein (SP:P12662) [Haemophilus influenzae]	51	23	687
112	3	1066	2352	pir|S05330|S05	maltose-binding protein precursor - Enterobacter aerogenes	51	42	1287
112	13	14432	12855	gi|405857	yshU [Escherichia coli]	51	29	1578
114	9	9725	8967	gi|435098	orf1 [Mycoplasma capricolum]	51	30	759
115	1	1	912	gi|1431110	ORF YJL0R9w [Saccharomyces cerevisiae]	51	23	912
127	10	9647	10477	gi|1204314	H influenzae predicted coding region HI0056 [Haemophilus influenzae]	51	37	831
152	9	6814	7356	gi|431929	HunI regulatory protein [Mycoplasma sp.]	51	38	543
154	2	575	1153	gi|1237044	unknown [Mycobacterium tuberculosis]	51	36	579
154	7	6587	5634	gi|1409286	bmrU [Bacillus subtilis]	51	27	954
171	8	6943	6236	gi|1205484	hypothetical protein (SP:P33918) [Haemophilus influenzae]	51	32	708
184	1	1	291	gi|466886	B1496_C3_206 [Mycobacterium leprae]	51	33	291
212	5	1501	2139	pir|A45605|A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	51	23	639
228	2	707	1378	gi|8204	nuclear protein [Drosophila melanogaster]	51	27	672
216	8	8137	7481	gi|49272	Asparaginase [Bacillus licheniformis]	51	31	657
243	4	4637	3546	gi|1511102	mevalonate kinase [Methanococcus jannaschii]	51	29	1092

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
257	4	3540	3373	gi|204579	H. influenzae predicted coding region HI0326 [Haemophilus influenzae]	51	22	168
258	3	2397	1609	gi|160299	glutamic acid-rich protein [Plasmodium falciparum] pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum	51	34	789
265	5	2419	3591	gi|580841	F1 [Bacillus subtilis]	51	32	1171
298	2	518	748	gi|1336162	SCPB [Streptococcus agalactiae]	51	34	231
316	9	5817	7049	gi|313953	lpa-29d gene product [Bacillus subtilis]	51	39	1233
332	2	3775	2057	gi|209012	mutS [Thermus aquaticus thermophilus]	51	26	1719
364	4	3816	4991	gi|528991	[unknown [Bacillus subtilis]	51	32	1176
440	2	448	684	gi|2819	transferase (GAL10) (AA 1 - 687) [Kluyveromyces lactis] r|S01407|XUVKG UDPglucose 4-epimerase (EC 5.1.3.2) - yeast uyveromyces marxianus var. lactis]	51	32	237
495	2	1353	1177	gi|297861	protease G [Erwinia chrysanthemi]	51	41	177
495	3	2287	1718	gi|1511317	serine rich protein [Entamoeba histolytica]	51	25	570
506	1	840	421	gi|455320	cII protein [Bacteriophage P4]	51	33	420
600	1	1474	983	gi|587532	orf, len: 201, CAI: 0.16 [Saccharomyces cerevisiae] pir|S48818|S48818 hypothetical protein - yeast (Saccharomyces erevisiae]	51	30	492
607	3	479	934	gi|1511524	hypothetical protein (SP:P37002) [Methanococcus jannaschii]	51	40	456
6A6	2	127	600	gi|493017	endocarditis specific antigen [Enterococcus faecalis]	51	30	474
726	1	33	230	gi|1351851	[unknown [Prochlorococcus marinus]	51	45	198
861	1	176	652	gi|410145	dehydroquinate dehydratase [Bacillus subtilis]	51	34	477
A69	1	782	393	gi|40100	rodC (tagJ) polypeptide (AA 1-746) [Bacillus subtilis] ir|S06049|S06049 rodC protein - Bacillus subtilis p|P13485|TAGF_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F.	51	23	390
1003	1	642	322	gi|1279707	hypothetical phosphoglycerate mutase [Saccharomyces cerevisiae]	51	39	321
1046	2	866	624	gi|510257	glycosyltransferase [Escherichia coli]	51	29	243
1467	1	702	352	gi|1511175	M. jannaschii predicted coding region MJ1177 [Methanococcus jannaschii]	51	32	351
2558	1	457	230	sp|P10582|DPOM_	DNA POLYMERASE (EC 2.7.7.7) (S-1 DNA ORF 3).	51	26	228
3003	1	779	399	gi|809543	CbrC protein [Erwinia chrysanthemi]	51	27	381
3604	1	1	399	pir|JC4210|JC42	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - mouse	51	37	399
3732	1	2	316	gi|145906	acyl-CoA synthetase [Escherichia coli]	51	33	315

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3791	1	2	274	gi|1061351	semaphorin III family homolog (Homo sapiens)	51	37	273
3395	1	46	336	gi|-16346	surfactin synthetase [Bacillus subtilis]	51	38	291
4193	1	612	107	gi|42749	ribosomal protein L12 (AA 1-179) [Escherichia coli] ir|S04776|XXECPL peptide N-acetyltransferase rimL (EC 2.3.1.-) - cherichia coli	51	25	306
4539	1	367	185	gi|1408494	homologous to penicillin acylase [Bacillus subtilis]	51	60	183
4562	1	442	239	gi|1458280	coded for by C elegans cDNA cm01e7; Similar to hydroxymethylglutaryl-CoA synthase [Caenorhabditis elegans]	51	35	204
1	4	3576	4859	gi|559160	GRAIL score: null; cap site and late promoter motifs present patream; putative [Autographa californica nuclear polyhedrosis irus]	50	44	1284
11	7	4044	5165	gi|1146207	putative [Bacillus subtilis]	50	35	1122
11	11	10509	9496	gi|1208451	hypothetical protein [Synechocystis sp.]	50	39	1014
19	1	2034	1018	gi|413966	ipa-42d gene product [Bacillus subtilis]	50	29	1017
20	11	8586	8407	gi|1323159	ORF YGR103w [Saccharomyces cerevisiae]	50	28	180
24	5	5408	4824	gi|496280	structural protein [Bacteriophage Tuc2009]	50	29	585
34	4	1926	2759	gi|1303966	YqjO [Bacillus subtilis]	50	36	834
38	30	22865	23440	gi|1072179	Similar to dihydroflavonol 4-reductase (maize, petunia, tomato) [Caenorhabditis elegans]	50	32	576
47	2	1705	2976	gi|153015	FemA protein (Staphylococcus aureus)	50	29	1272
56	13	15290	15841	gi|606096	ORF_f167; end overlaps end of o100 by 14 bases; start overlaps f174, thor starts possible [Escherichia coli]	50	30	552
57	1	2135	1077	gi|640922	xylitol dehydrogenase [unidentified hemiascomycete]	50	29	1059
58	2	628	1761	gi|143725	putative [Bacillus subtilis]	50	29	1134
88	6	4393	3884	gi|1072179	Similar to dihydroflavonol 4-reductase (maize, petunia, tomato) [Caenorhabditis elegans]	50	32	510
89	5	3700	3356	gi|1276658	ORF174 gene product (Porphyra purpurea)	50	25	345
141	1	3	239	gi|1476024	carbamoyl phosphate synthetase II [Plasmodium falciparum]	50	33	237
151	1	186	626	gi|1401441	unknown [Mycobacterium tuberculosis]	50	35	441
166	7	11065	9623	gi|895747	putative cel operon regulator [Bacillus subtilis]	50	32	1443
201	6	5284	5096	gi|160229	circumsporozoite protein [Plasmodium reichenowi]	50	42	189
206	22	30784	29555	gi-11052754	LarP integral membrane protein [Lactococcus lactis]	50	24	1230

TABLE 2

s aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
211	4	1523	1927	gi|410131	ORFX7 [Bacillus subtilis]	50	29	405
214	4	2411	3295	sp|P37348|YECE_	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	50	37	885
228	7	5068	4406	gi|313580	envelope protein [Human immunodeficiency virus type 1] pir|S35835|S35835 envelope protein - human immunodeficiency virus ype 1 (fragment) (SUB 1-77)	50	35	661
272	2	3048	1723	gi|1408485	B65G gene product [Bacillus subtilis]	50	22	1326
273	2	1616	984	gi|JR41A6	[phosphoglycerate mutase [Saccharomyces cerevisiae]	50	28	611
328	2	2507	1605	gi|148896	lipoprotein [Haemophilus influenzae]	50	26	903
312	4	5469	3802	gi|1526547	DNA polymerase family X [Thermus aquaticus]	50	27	1668
342	5	3473	3931	gi|456562	G-box binding factor [Dictyostelium discoideum]	50	35	459
352	1	1478	741	gi|288301	ORF2 gene product [Bacillus megaterium]	50	29	738
408	7	5299	5523	gi|11665	ORF2136 [Marchantia polymorpha]	50	27	225
420	3	650	1825	gi|757842	UDP-sugar hydrolase [Escherichia coli]	50	30	1176
464	1	1	591	gi|487282	Na+-ATPase subunit J [Enterococcus hirae]	50	29	591
472	2	1418	864	gi|551875	BglR [Lactococcus lactis]	50	23	555
520	1	23	541	gi|567036	CapE [Staphylococcus aureus]	50	27	519
529	1	6	410	gi|1256652	25% identity to the E.coli regulatory protein MprA; putative [Bacillus subtilis]	50	34	405
534	5	7726	6059	gi|295671	selected as a weak suppressor of a mutant of the subunit AC40 of DNA ependant RNA polymerase I and III [Saccharomyces cerevisiae]	50	18	166H
647	1	2990	1497	gi|405568	TraI protein shares sequence similarity with a family of opoisomerases [Plasmid pSK41]	50	31	1494
664	3	1133	711	gi|410007	leukocidin F component [Staphylococcus aureus, MRSA No. 4, Peptide, 23 aa]	50	32	423
678	1	1	627	gi|298032	EF [Streptococcus suis]	50	29	627
755	3	947	1171	gi|150572	cytochrome c1 precursor (EC 1.10.2.2) [Paracoccus denitrificans] gi|45465 cytochrome c1 (AA 1-450) [Paracoccus denitrificans] pir|C29413|C29413 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) ytochrome c1 precursor - Paracoccus denitrificans sp|P13627|CY1	50	37	225
827	1	1363	683	gi|142020	heterocyst differentiation protein [Anabaena sp.]	50	21	681
892	1	3	752	gi|478485	B65G gene product [Bacillus subtilis]	50	27	750
910	2	438	887	gi|L04727	tyrosine-specific transport protein [Haemophilus influenzae]	50	25	450

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Coding ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
931	1	524	760	gi|1205451	cell division inhibitor [Haemophilus influenzae]	50	32	237
973	1	424	236	gi|486947	orf3 gene product [Saccharomyces cerevisiae]	50	40	189
1009	1	651	429	gi|153727	M protein [group G streptococcus]	50	28	225
1027	1	511	257	gi|143914	ipa-10r gene product [Bacillus subtilis]	50	25	255
1153	2	556	326	gi|773676	nccA [Alcaligenes xylosoxydans]	50	36	231
1272	1	798	400	gi|1408485	B65G gene product [Bacillus subtilis]	50	21	399
1350	1	692	399	gi|289272	[ferrichrome-binding protein [Bacillus subtilis]	50	32	294
2945	1	365	184	gi|171704	hexaprenyl pyrophosphate synthetase (COQ1) [Saccharomyces cerevisiae]	50	34	183
2968	2	1604	804	gi|197526	clumping factor [Staphylococcus aureus]	50	33	801
2998	2	657	394	gi|495696	F54E7.3 gene product [Caenorhabditis elegans]	50	40	264
3046	2	506	306	pir|S13A19|S138	acyl carrier protein - Anabaena variabilis (fragment)	50	32	201
3063	1	547	275	gi|474190	iucA gene product [Escherichia coli]	50	29	273
3174	1	3	146	gi|151900	alcohol dehydrogenase [Rhodobacter sphaeroides]	50	31	144
3792	1	625	314	gi|1001423	hypothetical protein [Synechocystis sp.]	50	35	312
3800	1	?	262	gi|114733	NAD-dependent beta-hydroxybutyryl coenzyme A dehydrogenase Clostridium acetobutylicum	50	24	261
3946	1	373	188	gi|576765	cytochrome b [Myrmecia pilosula]	50	38	146
3984	1	578	291	sp|P37348|YECE_	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	50	37	288
37	10	8250	7885	gi|1204367	hypothetical protein (GB:U14003_278) [Haemophilus influenzae]	49	30	166
46	16	13802	14848	ci|466860	acd; B1308_F1_34 [Mycobacterium leprae]	49	24	1047
59	5	2267	3601	gi|606304	ORF_o462 [Escherichia coli]	49	27	1335
112	18	17884	18615	gi|559502	ND4 protein (AA 1 - 409) [Caenorhabditis elegans]	49	25	732
138	9	6973	7902	gi|303953	esterase [Acinetobacter calcoaceticus]	49	29	930
217	6	4401	5138	gi|496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	49	31	738
220	12	11803	12657	gi|397526	clumping factor [Staphylococcus aureus]	49	31	855
228	4	842	2492	pir|S22692|S216	hypothetical protein 9 - Plasmodium falciparum	49	24	651
268	1	5016	2614	gi|143047	ORFB [Bacillus subtilis]	49	26	2403

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
271	2	1164	1373	gi|1001257	hypothetical protein [Synechocystis sp.]	49	38	210
300	3	4340	3180	gi|1510796	hypothetical protein (GP:X91006-2) [Methanococcus jannaschii]	49	26	1161
381	1	2281	1142	gi|396301	matches PS00041: Bacterial regulatory proteins, araC family ignature (Escherichia coli)	49	29	1140
466	1	3	947	gi|1303863	YqgP [Bacillus subtilis]	49	26	945
666	1	379	191	gi|633112	ORF1 [Streptococcus sobrinus]	49	29	189
670	2	403	1014	gi|1122758	unknown [Bacillus subtilis]	49	32	612
709	1	1433	795	gi|143830	xpaC [Bacillus subtilis]	49	29	639
831	1	943	473	gi|401786	phosphomannomutase [Mycoplasma pirum]	49	29	471
1052	1	422	213	gi|1303799	YqeN [Bacillus subtilis]	49	21	210
1800	1	342	172	gi|216300	peptidoglycan synthesis enzyme [Bacillus subtilis] sp|P37585|MURG_BACSU MURG PROTEIN UPD-N-ACETYLGLUCOSAMINE-N-ACETYLMURAMYL-PENTAPEPTIDE)PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE RANSFERASE).	49	28	171
2430	1	2	376	sp|P27434|YFGA_	HYPOTHETICAL 36.2 KD PROTEIN IN NDK-GCPE INTERGENIC REGION.	49	26	375
3096	1	542	273	gi|516360	surfactin synthetase [Bacillus subtilis]	49	25	270
32	4	3771	3100	gi|1217963	hepatocyte nuclear factor 4 gamma [HNF4(gamma] [Homo sapiens]	48	36	672
38	1	1	609	gi|1205790	H. influenzae predicted coding region HI1555 [Haemophilus influenzae]	48	28	609
45	6	5021	6427	gi|1524267	unknown [Mycobacterium tuberculosis]	48	20	1407
59	14	16346	31096	gi|1197336	Lmp1 protein [Mycoplasma hominis]	48	28	14751
61	1	3	608	gi|1511555	quinolone resistance norA protein protein [Methanococcus jannaschii]	48	30	606
61	3	3311	3646	gi|1303893	YqhL [Bacillus subtilis]	48	29	336
114	1	98	415	gi|671708	su(s) homolog: similar to Drosophila melanogaster suppressor of able (su(s)) protein. Swiss-Prot Accession Number P22293 Drosophila virilis]	48	25	318
121	1	1131	610	gi|1314584	unknown [Sphingomonas S88]	48	29	522
136	1	2014	1280	gi|1205968	H. influenzae predicted coding region HI1718 [Haemophilus influenzae]	48	23	735
171	10	8220	9557	gi|1208454	hypothetical protein [Synechocystis sp.]	48	34	1338
175	1	3625	1814	gi|396400	similar to eukaryotic Na+/H+ exchangers (Escherichia coli) sp|P12703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR--ACS NTERGENIC REGION (O549).	48	29	1812
194	1	2	385	gi|1510493	M. jannaschii predicted coding region MJ0419 [Methanococcus jannaschii]	48	25	384

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
197	1	901	452	gi|1045714	spermidine/putrescine transport ATP-binding protein [Mycoplasma genitalium]	48	25	450
203	1	1	396	gi|940288	protein localized in the nucleoli of pea nuclei. ORF; putative Pisum sativum	48	29	396
204	1	1363	698	gi|529202	No definition line found [Caenorhabditis elegans]	48	25	666
206	20	14815	27760	gi|511490	gramicidin S synthetase 2 [Bacillus brevis]	48	27	7056
212	1	2	166	gi|295899	nucleolin [Xenopus laevis]	48	34	165
220	10	12652	11426	gi|44073	SecY protein [Lactococcus lactis]	48	23	1227
243	6	6450	5491	gi|1184118	mevalonate kinase [Methanobacterium thermoautotrophicum]	48	30	960
264	4	5434	3308	gi|1015903	ORF YJR151c [Saccharomyces cerevisiae]	48	26	2127
441	1	1532	768	gi|142863	replication initiation protein [Bacillus subtilis] pir|B26580|B26580 replication initiation protein - Bacillus subtilis	48	23	765
444	5	3898	5298	gi|145836	putative [Escherichia coli]	48	24	1401
484	2	388	1110	gi|146551	[transmembrane protein (kdpD) [Escherichia coli]	48	18	723
542	3	1425	2000	pir|S28969|S289	N-carbamoylsarcosine amidohydrolase (EC 3.5.1.59) - Arthrobacter sp.	48	27	576
566	1	1	1019	gi|153490	tetracenomycin C resistance and export protein [Streptomyces laucescens]	48	24	1017
611	1	2	730	gi|1103507	unknown [Schizosaccharomyces pombe]	48	38	729
624	1	1255	665	gi|144859	ORF B [Clostridium perfringens]	48	26	591
846	1	1014	508	gi|537506	paramyosin [Dirofilaria immitis]	48	27	507
1020	1	66	950	gi|1499876	magnesium and cobalt transport protein [Methanococcus jannaschii]	48	10	885
1227	1	1	174	gi|493730	lipoxygenase [Pisum sativum]	48	35	174
1266	1	1	405	gi|882452	ORF_f211 alternate name yggA; orf5 of X14436 [Escherichia coli] gi|41425 ORF5 (AA 1-197) [Escherichia coli] (SUB 15-211)	48	24	405
2071	1	707	381	gi|1408486	HS74A gene product [Bacillus subtilis]	48	25	327
2198	1	463	233	gi|1500401	reverse gyrase [Methanococcus jannaschii]	48	40	231
2425	1	476	246	pir|H48563|H485	G1 protein - fowlpox virus (strain HP444) (fragment)	48	40	231
2432	1	446	225	gi|1353703	Trio [Homo sapiens]	48	31	222
2453	1	794	399	gi|142850	division initiation protein [Bacillus subtilis]	48	29	396
2998	1	469	236	gi|577569	PepV [Lactobacillus delbrueckii]	48	31	234

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3042	1	14	280	gi|945219	mucin [Homo sapiens]	48	35	267
1686	1	1	405	gi|145836	putative [Escherichia coli]	48	25	405
4027	2	492	301	pir SS1177|SS11	trans-activator protein - Equine infectious anemia virus	48	32	192
4	2	1641	2232	gi|1303989	YqkI [Bacillus subtilis]	47	24	1410
24	2	599	1084	gi|540083	PC4-1 gene product [Bradysia hygida]	47	28	486
36	10	7524	6925	gi|209223	esterase [Acinetobacter lwoffii]	47	26	600
43	2	196	1884	gi|403455	unknown [Mycobacterium tuberculosis]	47	27	1689
44	22	1611R	15108	gi|1511555	quinolone resistance norA protein protein [Methanococcus jannaschii]	47	31	1011
69	7	7141	6710	gi|438466	Possible operon with orfG. Hydrophilic, no homologue in the atabase; putative [Bacillus subtilis]	47	29	432
81	4	5022	4279	gi|466882	ppsl; B1496_C2_189 [Mycobacterium leprae]	47	24	744
120	12	9135	8863	gi|927340	D9509.27p; CAI: 0.12 [Saccharomyces cerevisiae]	47	38	273
142	1	2022	1174	gi|486143	ORF YKL094w [Saccharomyces cerevisiae]	47	32	849
168	1	2178	1093	gi|1177254	hypothetical EcsB protein [Bacillus subtilis]	47	29	1086
263	1	1884	943	gi|142822	D-alanine racemase cds [Bacillus subtilis]	47	34	942
279	1	1109	561	gi|516608	2 predicted membrane helices. homology with B. subtilis men Orf3 Rowland et. al. unpublished Accession number H74183), approximately 1 minutes on updated Rudd map; putative [Escherichia coli] sp|P37355|YFBB_ECOLI HYPOTHETICAL 26.7 KD PROTEIN IN MEND-MENB	47	31	549
145	2	2620	1676	gi|1204835	hippuricase [Haemophilus influenzae]	47	28	945
389	2	152	400	gi|456562	G-box binding factor [Dictyostelium discoideum]	47	32	249
391	1	1	831	gi|1420856	myo-inositol transporter [Schizosaccharomyces pombe]	47	19	831
404	3	2072	2773	gi|1255425	C33GB.2 gene product [Caenorhabditis elegans]	47	17	702
529	5	2145	3107	gi|1303973	YqjV [Bacillus subtilis]	47	29	963
565	2	2321	1257	gi|142824	processing protease [Bacillus subtilis]	47	28	1065
654	1	962	483	gi|243353	ORF 5' of ECRF3 [herpesvirus saimiri HVS. host-squirrel monkey. eptide. 407 aa]	47	23	480
692	1	115	633	gi|150756	40 kDa protein [Plasmid pJM1]	47	25	519
765	1	1634	819	gi|1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6. putative [Bacillus subtilis]	47	28	816

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
825	2	211	1023	gi|397526	clumping factor [Staphylococcus aureus]	47	32	813
914	1	1	615	gi|558073	polymorphic antigen [Plasmodium falciparum]	47	29	615
1076	1	1	753	gi|1147557	Aspartate aminotransferase [Bacillus circulans]	47	33	753
1351	1	793	398	gi|755153	ATP-binding protein [Bacillus subtilis]	47	20	396
4192	1	3	293	gi|145816	putative [Escherichia coli]	47	24*	291
5	6	4708	4161	gi|105080	myosin heavy chain [Entamoeba histolytica]	46	30	348
11	4	2777	3058	gi|603639	Yel040p [Saccharomyces cerevisiae]	46	28	282
46	11	10518	10300	gi|1246901	ATP-dependent DNA ligase [Candida albicans]	46	28	219
61	4	3941	7930	gi|298032	EF [Streptococcus suis]	46	35	3990
132	4	5028	4093	gi|1511057	hypothetical protein SP:P45869 [Methanococcus jannaschii]	46	25	936
170	4	4719	3652	pir|SS1910|SS19	1G4 protein - Saurole1shmania tarentolae	46	26	1068
191	7	9543	8284	gi|1041334	F54D5.7 [Caenorhabditis elegans]	46	25	1260
253	1	1	396	gi|1204449	dihydrolipoamide acetyltransferase [Haemophilus influenzae]	46	35	396
264	3	437	973	gi|180189	cerebellar-degeneration-related antigen (CDR34) [Homo sapiens] gi|182737 cerebellar degeneration-associated protein [Homo sapiens] pir|A29770|A29770 cerebellar degeneration-related protein - human	46	29	517
273	1	485	285	gi|607573	envelope glycoprotein C2V3 region [Human immunodeficiency virus type 1]	46	35	201
350	1	3	563	gi|537052	ORF_f286 [Escherichia coli]	46	35	561
343	1	.	862	gi|1221884	(urea?) amidolyase [Haemophilus influenzae]	46	31	861
410	4	1876	2490	gi|1110518	proton antiporter efflux pump [Mycobacterium smegmatis]	46	24	615
432	1	2663	1455	gi|1197634	orf4; putative transporter; Method: conceptual translation supplied by author [Mycobacterium smegmatis]	46	27	1209
458	1	2419	1211	gi|15870	portal protein [Bacteriophage SPP1]	46	30	1209
517	5	2477	4192	gi|1523412	orf5 [Bacteriophage A2]	46	23	1716
540	3	1512	1285	gi|215635	paca [Bacteriophage P1]	46	30	228
587	2	649	1242	gi|537148	ORF_f181 [Escherichia coli]	46	29	594
1218	1	747	391	gi|1205456	single-stranded-DNA-specific exonuclease [Haemophilus influenzae]	46	30	357

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3845	1	1	402	gi|450688	hsdM gene of EcoprII gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	46	33	402
4176	1	673	338	gi|951460	FIM-C 1 gene product [Xenopus laevis]	46	31	336
37	7	4813	5922	gi|606064	ORF_f408 [Escherichia coli]	45	24	1110
38	16	11699	12004	gi|452192	protein tyrosine phosphatase (PTP-BAS, type 2) [Homo sapiens]	45	24	106
87	2	1748	2407	gi|1064813	homologous to sp:PHOR_BACSU (Bacillus subtilis)	45	23	660
103	12	14182	13385	gi|1001307	hypothetical protein (Synechocystis sp.)	45	22	798
112	14	14791	13811	gi|1204389	H. influenzae predicted coding region HI0131 [Haemophilus influenzae]	45	23	981
145	4	4483	3461	gi|220578	open reading frame [Mus musculus]	45	20	1023
170	6	6329	4965	gi|238657	AppC=cytochrome d oxidase, subunit I homolog [Escherichia coli, K12, peptide, 514 aa]	45	27	1365
206	2	5230	4346	gi|222056	aminotransferase [Haemophilus influenzae]	45	27	885
228	1	60	716	gi|160299	glutamic acid-rich protein [Plasmodium falciparum] pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum	45	23	657
288	1	2	1015	gi|1255425	C33G8 2 gene product [Caenorhabditis elegans]	45	23	1014
313	3	4339	3128	gi|581140	NADH dehydrogenase [Escherichia coli]	45	30	1212
332	1	914	459	gi|870966	F4TA4.2 [Caenorhabditis elegans]	45	20	456
344	1	3	221	gi|171225	kinesin-related protein [Saccharomyces cerevisiae]	45	26	219
441	2	1501	1073	gi|142863	replication initiation protein [Bacillus subtilis] pir|B26580|B26580 replication initiation protein - Bacillus ubtilis	45	27	429
672	1	2	982	gi|1511334	M. jannaschii predicted coding region MJ1323 [Methanococcus jannaschii]	45	22	981
763	3	1145	851	gi|606180	ORF_f310 [Escherichia coli]	45	24	495
886	3	379	846	gi|726426	similar to protein kinases and C. elegans proteins F37C12.8 and 37C12.5 [Caenorhabditis elegans]	45	30	468
948	1	3	473	gi|156400	myosin heavy chain (isozyme unc-54) [Caenorhabditis elegans] pir|A93958|MHKW myosin heavy chain B - Caenorhabditis elegans sp|P02566|MYSB_CAEEL MYOSIN HEAVY CHAIN B (MHC B)	45	25	471
1158	1	2	376	gi|441155	transmission-blocking target antigen [Plasmodium falciparum]	45	35	375
2551	1	4	285	gi|1276705	ORF287 gene product [Porphyra purpurea]	45	28	282
1967	1	42	374	gi|976025	HrsA [Escherichia coli]	45	28	333

TABLE 2

TABLE 2

aureus - Putative coding regions of novel proteins similar to known proteins

contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
52	7	6931	5846	gi|467378	unknown [Bacillus subtilis]	44	22	1086
118	8	6475	6849	gi|173028	thioredoxin II [Saccharomyces cerevisiae]	44	28	375
221	5	7032	5617	gi|153490	tetracenomycin C resistance and export protein [Streptomyces laucescens]	44	21	1416
252	2	1331	1122	gi|1204989	hypothetical protein (GB:U00022_9) [Haemophilus influenzae]	44	30	210
261	2	3265	2093	gi|1136221	carboxypeptidase [Sulfolobus solfataricus]	44	26	1173
365	4	4963	3524	gi|296822	orf1 gene product [Lactobacillus helveticus]	44	31	1440
543	3	1315	1833	gi|Jb1250	low homology to P20 protein of Bacillus lichiniformis and bleomycin acetyltransferase of Streptomyces verticillus [Bacillus subtilis]	44	24	519
543	4	3942	4892	gi|951460	FIM-C.1 gene product [Xenopus laevis]	44	32	951
792	1	1224	613	gi|205680	high molecular weight neurofilament [Rattus norvegicus]	44	28	612
44	18	11303	11911	gi|1511614	molybdopterin-guanine dinucleotide biosynthesis protein A [Methanococcus jannaschii]	43	27	609
59	8	3665	5128	gi|153490	tetracenomycin C resistance and export protein [Streptomyces laucescens]	43	21	1464
59	10	5516	7527	gi|153022	lipase [Staphylococcus epidermidis]	43	22	1992
99	1	1346	681	gi|1419051	unknown [Mycobacterium tuberculosis]	43	21	666
310	8	9402	12134	gi|397526	clumping factor [Staphylococcus aureus]	43	21	2733
312	3	2782	2303	pir|A60540|A605	sporozoite surface protein 2 - Plasmodium yoelii (fragment)	43	29	480
519	3	2547	3122	sp|Q06530|DHSU_	SULFIDE DEHYDROGENASE (FLAVOCYTOCHROME C) FLAVOPROTEIN CHAIN PRECURSOR (EC 1.8.2.-) (FC) (FCSD).	43	21	576
4	13	12053	13121	gi|295671	selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]	42	18	1269
94	2	1766	1091	gi|501027	ORF2 [Trypanosoma brucei]	42	31	678
127	4	5791	4550	gi|42029	ORF1 gene product [Escherichia coli]	42	21	1242
297	3	1515	1036	gi|142790	ORF1; putative [Bacillus firmus]	42	25	480
144	6	4093	1525	ri|40320	ORF 2 (AA 1-203) [Bacillus thuringiensis]	42	30	573
512	1	2167	1115	gi|405957	lyeeF [Escherichia coli]	42	23	1053
631	1	2434	1223	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13484|TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS ROTEIN E).	42	24	1212

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
685	3	2359	1739	gi|1303784	YqeD [Bacillus subtilis]	42	19	621
4132	1	787	395	gi|1022910	protein tyrosine phosphatase [Dictyostelium discoideum]	42	25	393
A6	2	1375	884	gi|309506	spermidine/spermine N1-acetyltransferase [Mus saxicola] pir|S43430|S43430 spermidine/spermine N1-acetyltransferase - spiny ouse (Mus saxicola]	41	30	492
191	12	14797	14075	gi|124957	orf4 gene product [Methanosarcina barkeri]	41	22	723
212	6	2150	3127	gi|15873	observed 35.2Kd protein [Mycobacteriophage 15]	41	26	978
213	3	1261	2000	gi|633692	TrsA [Yersinia enterocolitica]	41	18	748
408	4	2625	3386	gi|1197634	orf4; putative transporter; Method: conceptual translation supplied by author [Mycobacterium smegmatis]	41	24	762
542	1	3	1103	gi|457146	rhoptry protein [Plasmodium yoelii]	41	21	1101
924	1	2	475	pir|JHO148|JH01	nucleolin - rat	41	30	474
1562	1	1	402	gi|552184	asparagine-rich antigen Pfa35-2 [Plasmodium falciparum] pir|S27826|S27826 asparagine-rich antigen Pfa35-2 - Plasmodium alciparum (fragment)	40	20	402
2395	1	518	261	pir|S42251|S422	hypothetical protein 5 - fowlpox virus	40	18	258
4077	1	3	305	gi|1055055	coded for by C. elegans cDNA yk37g1.5; coded for by C. elegans cDNA yk5c9.5; coded for by C. elegans cDNA yk1a9.5; alternatively spliced form of F52C9.8b [Caenorhabditis elegans]	39	21	303
948	1	1003	503	gi|1255425	C33G8.2 gene product [Caenorhabditis elegans]	37	25	501
59	12	8294	10636	gi|535260	STARP antigen [Plasmodium reichenowi]	36	24	2343
63	5	3550	8079	gi|298032	EF [Streptococcus suis]	36	19	4530
544	3	2507	3601	gi|1015903	ORF YJR151c [Saccharomyces cerevisiae]	35	22	1095
63	4	1949	3574	gi|552195	circumsporozoite protein [Plasmodium falciparum] sp|P05691|CSP_PLAFL CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT).	32	27	1626

TABLE 3

S. aureus : Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4	1	1234	692
4	3	1712	2278
4	4	3703	3032
4	14	13073	12585
5	2	2539	1601
5	3	1532	1771
5	7	4741	4550
5	9	7939	6422
5	12	8711	8547
6	4	2359	1982
8	1	349	176
11	8	5144	5983
11	9	5968	6498
11	10	6472	6284
11	16	10954	11271
12	5	5352	4942
12	6	4596	4862
15	3	1895	1650
16	10	11263	10835
18	2	1093	917
20	9	9125	7764
20	10	8571	8230
20	12	9201	8803
20	13	12158	10470
21	1	674	339
23	6	6138	5485
23	8	6376	5942

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
23	9	7651	6881
23	15	12618	12830
24	4	4556	4185
24	6	5642	5241
25	2	1824	2402
31	2	505	849
31	3	1177	1524
31	4	2454	3005
32	2	765	1388
32	9	7952	8575
32	10	8591	8728
32	11	9738	9379
32	12	10797	10087
34	2	1315	1049
36	7	5226	5801
36	11	7575	7261
36	12	7424	7621
37	4	3158	2964
38	2	1585	980
38	11	6425	6868
38	20	16982	16371
38	26	20253	20804
38	27	20722	21264
39	1	1	627
40	1	805	404
43	1	796	428
44	4	2674	2324

TABLE 3

S aureus Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
44	5	2484	3263
44	14	10587	10129
44	20	13724	13536
44	21	13596	13994
45	7	6575	6297
46	8	6365	6520
46	12	10449	10976
46	17	15032	15424
47	1	288	1079
48	9	7620	7778
50	1	1612	962
50	2	1621	1316
51	1	738	370
51	5	2520	2245
53	1	442	287
53	7	6705	6319
54	7	9014	8709
55	1	592	326
55	3	1052	786
56	1	1	261
56	3	1551	1228
56	4	1970	1560
56	17	19092	18712
57	4	3694	3521
57	8	5436	5822
58	9	8885	8553
59	3	1366	1509

TABLE 3

S aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
59	6	3026	2802
59	7	3770	3570
59	9	4946	4563
59	11	7518	8378
59	13	10401	16403
62	2	2696	1521
62	11	5440	5757
63	1	1	336
67	1	900	1781
67	2	1774	2610
67	3	2591	3904
67	8	7110	6955
68	1	78	326
70	6	6761	5199
70	11	8935	8645
77	3	1590	1192
79	2	1509	1228
79	3	1411	1791
83	1	2	403
85	9	8300	8653
85	10	8969	8781
86	3	1426	1232
87	8	9187	9366
88	3	1620	1922
89	1	3	161
89	7	5042	4878
91	1	1098	550

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
91	3	3938	3141
92	2	449	928
92	3	1958	1467
92	9	5638	6024
94	1	661	332
94	3	2445	1813
94	4	2583	2197
96	11	10601	11050
99	6	4672	4523
99	7	5014	4784
100	8	7658	7287
102	7	4697	4368
103	3	2496	2035
104	1	2	694
104	2	699	1277
105	1	1235	693
105	3	3233	2655
105	1	3	221
106	3	1209	1355
107	1	1081	542
109	4	4025	3651
109	13	11625	11996
109	14	11981	12268
109	20	17401	17688
110	1	2	760
114	10	8764	9384
116	1	1	309

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
116	3	6273	4462
116	8	11049	9976
116	9	10013	10158
120	5	3703	3320
120	6	4270	3869
120	13	9290	9844
121	2	417	569
126	3	1090	818
127	3	2648	3196
127	5	4084	4395
131	6	6773	6438
132	2	715	1695
134	1	2	667
135	2	512	258
135	3	1124	729
138	1	3	152
138	7	6008	6463
140	1	2060	1032
140	2	2019	1513
140	5	2387	2743
142	2	1360	2388
142	7	8830	7586
143	7	7290	6502
144	1	1227	640
146	1	2	511
146	3	502	1350
146	4	3673	2540

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
146	5	2874	3071
147	1	1	339
149	11	3956	3615
149	12	4036	3785
149	13	4507	4145
149	15	4807	4610
149	16	5495	5049
149	18	5739	5491
149	21	7416	7054
149	23	9216	8521
149	24	9681	9106
149	25	10679	9897
150	2	2303	1587
154	3	1795	1508
154	8	6586	6398
154	14	12704	12147
154	15	13531	12803
156	1	315	593
157	3	1183	2232
158	2	1471	1064
159	3	452	808
161	2	876	1808
161	6	4653	4279
161	7	4803	4540
161	8	4896	4717
161	11	5817	5638
163	2	1604	840

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
163	5	2796	2344
163	7	2952	2647
163	9	4905	5132
164	3	1338	1147
166	3	5213	4854
168	4	2500	2868
168	5	3595	4158
170	3	2517	2777
171	2	2277	1450
171	11	12576	11125
172	1	3	278
172	2	1940	1149
173	1	1289	708
173	5	7001	6114
174	2	593	1105
175	3	2552	2890
175	5	3820	3335
175	7	4342	4506
182	4	5477	4986
184	5	6043	5702
188	2	1210	1755
188	4	2647	2994
189	6	2614	3039
190	3	1998	2564
191	1	1	153
191	2	950	669
191	10	11786	13039

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
191	11	12902	12163
192	1	91	426
195	3	2306	1932
195	5	2899	2606
198	2	1016	1591
201	1	170	625
203	2	783	1466
206	6	8930	7815
206	12	13947	13636
206	21	28208	27960
212	2	170	817
212	3	796	1167
212	7	3128	1436
212	9	3749	4075
213	1	1	705
214	2	1076	570
214	6	4064	3738
214	9	6600	6995
214	10	7864	7469
217	1	1927	965
218	1	178	657
218	3	1776	2156
220	2	1851	1369
220	3	3251	2262
220	7	8275	7208
220	8	10244	8661
220	9	11796	10216

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
221	4	3095	2613
221	9	11428	10757
226	1	3	659
226	2	2196	1459
226	3	1476	1961
227	1	2	487
227	2	460	975
227	4	1855	2121
227	5	2052	2345
227	6	4760	3768
227	9	5591	6367
228	5	2503	2877
228	6	2846	3526
233	7	3944	3762
236	2	809	579
238	2	1975	1391
239	2	1417	905
241	5	4495	4334
242	2	1677	1363
243	1	127	576
244	1	1291	647
244	2	3035	1962
245	2	1614	1258
246	1	69	215
246	4	718	1733
249	3	3906	3712
250	1	494	249

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
254	1	1	156
256	2	956	1144
257	3	3700	3227
260	4	4906	4580
261	4	2196	2606
261	6	3214	3681
264	2	155	439
264	5	5252	4533
264	6	4739	5107
267	2	1323	931
268	4	5140	4700
272	1	862	446
272	3	1200	1439
272	9	4691	4909
272	10	6469	6035
276	4	1746	1901
278	1	224	553
278	5	3299	3448
278	7	4849	5127
285	2	551	736
288	3	1756	1950
288	5	2055	2276
289	1	2107	1055
290	2	2234	1932
291	2	332	622
291	5	1545	2051
295	3	1606	1349

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
295	4	2728	2141
295	5	2220	2762
297	2	788	465
298	1	2	205
300	2	2380	1928
301	7	2794	2624
304	1	3	194
306	1	109	654
306	5	4016	4257
307	1	674	339
307	8	3645	3995
308	1	1	654
308	2	1120	599
308	4	2643	2332
313	2	2314	1919
314	1	10	702
316	2	982	1341
316	6	2758	3165
317	1	2	1114
317	3	4570	3458
321	6	5645	5217
321	7	6319	6140
321	8	7450	6794
322	2	827	543
326	2	165	1112
326	3	1117	1467
328	1	936	469

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
128	5	3452	3276
329	1	3	719
329	2	781	1212
329	3	1471	1833
330	1	576	289
330	3	1447	1623
332	3	2353	2204
332	7	4971	5138
333	2	3295	3128
335	1	864	433
337	2	95	526
340	2	1658	1356
341	1	3	281
341	3	2476	3192
341	5	3618	3944
341	6	3929	4558
344	5	3197	2889
345	1	1532	768
346	2	221	592
350	3	1410	1598
352	2	2178	1765
352	3	7316	4596
352	7	7967	8404
352	8	8906	9247
352	9	10171	9854
359	1	1	546
362	1	3	656

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
364	2	2158	1808
364	8	10974	10714
365	2	1612	1313
365	5	4680	4090
365	7	4980	6239
366	1	520	1719
367	3	906	1085
368	1	748	494
375	1	2	136
380	3	1351	1097
389	1	1	276
390	1	2	877
390	2	1173	1549
391	2	751	560
395	1	391	197
396	1	2132	1068
398	3	1344	1141
399	1	176	669
401	3	566	847
402	2	100	465
404	8	5561	5370
408	2	3507	2269
408	3	2875	2672
408	5	3524	4423
410	3	2111	1890
413	1	880	488
416	1	607	320

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
416	2	578	847
416	3	2195	1590
417	1	3	179
417	2	161	616
420	2	788	513
422	2	357	677
431	2	856	1407
432	2	446	1084
433	1	1	417
433	3	2311	2033
434	1	942	535
434	2	2089	1235
440	1	1	450
442	2	1269	1320
443	3	1873	1520
444	1	1	696
444	7	6761	6366
451	1	940	614
453	2	896	636
453	8	3833	4786
453	9	4718	4512
453	10	4937	4731
455	1	434	219
455	2	472	930
459	1	265	687
462	1	2	247
466	2	1494	907

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
467	1	654	349
468	1	2	250
469	1	1488	925
469	3	2386	3372
469	4	3464	3706
470	1	77	538
470	6	4098	3694
470	7	6330	5686
470	9	7351	8181
470	10	8175	9773
471	1	940	500
471	2	1562	1017
476	1	70	267
477	1	2	760
477	3	1764	2081
477	4	2066	2332
480	5	4016	4261
481	2	956	480
486	3	613	774
487	6	1795	2112
488	1	715	359
492	1	127	675
493	1	2	520
493	2	496	1242
502	3	1149	1571
504	1	690	346
505	5	4566	4150

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
511	2	1741	1232
512	2	583	747
515	1	609	812
517	4	2179	2511
520	4	2097	2360
520	6	3908	3669
527	1	1	498
528	1	637	335
529	2	1679	1104
530	7	5298	5534
536	1	308	156
538	1	1362	736
53R	3	2203	2AA0
538	5	3531	3121
538	6	4348	3731
540	1	996	664
540	2	1495	1031
541	1	89	433
541	2	719	432
542	2	1048	1272
545	2	1012	734
551	1	2145	1129
555	2	892	704
558	3	1357	1154
558	4	1760	1458
558	5	2105	1821
558	6	2166	2020

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
558	7	2636	2322
558	8	3053	2802
558	9	3986	3453
560	1	475	921
565	3	1706	1485
571	1	308	156
571	3	994	1206
577	1	2	199
577	2	163	453
579	1	1	477
579	2	1784	1200
583	1	1988	996
585	1	946	539
587	1	22	573
588	2	1896	1372
588	3	1742	1554
590	1	47	334
592	2	1455	1141
593	1	2	775
593	2	817	1122
595	1	87	890
596	3	1593	1435
602	1	8	169
603	5	1071	1469
606	1	322	768
607	5	1444	1226
610	1	1029	541

TABLE 3

S aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
612	1	3	500
616	1	991	650
617	2	736	491
622	1	36	347
625	4	2046	2549
627	1	67	210
628	1	901	452
631	3	4789	4004
634	1	1448	759
636	1	189	368
636	2	1929	1053
637	2	2323	1994
638	1	227	1081
639	1	518	261
639	2	1377	611
641	1	118	444
642	3	1615	1331
642	4	2260	1847
643	1	3	608
645	4	1534	1758
645	6	2025	2321
645	7	2940	2488
648	1	2	1065
660	1	77	601
660	2	576	872
661	1	1725	961
664	2	89	304

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
667	1	3	413
668	1	1	330
671	2	812	516
673	1	3	338
674	2	865	584
679	1	1	237
679	3	1589	1906
688	1	1226	835
688	2	1352	1077
694	1	3	143
696	2	818	432
706	1	30?	224
709	3	1183	1449
711	1	3	908
715	1	3	167
716	1	2	637
721	1	133	570
722	1	763	383
723	1	1656	829
723	2	1498	1112
727	1	2	372
729	1	268	441
731	1	110	828
735	1	2	214
736	1	3	782
738	1	2	298
742	1	3	230

TABLE 3

5   Aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
745	3	1148	780
748	2	282	464
749	1	685	344
751	1	901	452
755	1	97	522
755	2	520	918
758	2	663	400
764	2	1013	746
767	1	1	405
768	1	2	373
771	1	1058	534
778	1	1735	902
785	1	1790	1023
787	1	1260	631
791	1	3	224
799	1	15	260
804	1	304	711
805	1	3	680
808	1	219	842
810	1	2221	1112
810	2	1774	1442
812	1	38	979
817	1	714	358
818	2	487	1104
819	2	1529	1032
819	3	1748	1419
820	1	195	1064

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
828	1	506	255
829	1	48	800
830	1	578	291
832	1	594	298
835	1	320	796
840	3	491	709
845	1	912	457
850	2	103	449
853	1	715	359
860	1	2	256
864	1	18	410
864	2	383	715
864	6	1676	1828
870	1	1	588
873	1	906	454
875	1	584	224
877	1	1661	1020
878	1	981	544
879	1	1567	785
881	1	1	243
882	1	389	604
890	1	2	508
905	1	793	398
906	1	852	544
912	1	373	188
913	1	3	290
913	2	1092	547

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
915	1	6	161
915	2	169	402
921	1	126	386
927	1	1578	808
928	1	2	385
929	1	2	400
932	1	2	400
934	1	1	384
936	1	1052	528
937	1	2	616
945	1	220	645
945	2	649	1242
946	1	1702	950
949	1	1	270
951	1	3	362
955	1	3	143
960	1	723	400
963	1	1	162
965	1	690	346
966	1	1079	606
969	1	3	302
971	1	12	170
974	1	319	161
976	1	692	348
977	1	2	211
982	1	1926	982
984	1	589	296

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
987	1	3	467
993	1	1	525
994	1	920	549
1004	1	557	318
1014	1	624	313
1015	1	2	463
1016	1	288	145
1019	1	1205	660
1022	1	839	474
1024	1	595	299
1024	2	276	431
1030	1	673	338
1032	1	355	179
1040	1	794	399
1043	1	3	269
1044	2	115	399
1047	1	1	159
1051	1	704	354
1051	2	1233	733
1063	1	2	400
1069	1	2	148
1069	2	769	533
1075	1	707	399
1077	1	97	405
1081	1	58	438
1086	1	1	384
1087	2	246	431

TABLE 3

S aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1088	1	3	374
1096	1	474	238
1098	1	1015	509
1100	1	1020	511
1100	2	1520	1158
1101	1	703	351
1102	1	385	194
1107	1	2	580
1114	1	3	422
1115	1	2	268
1119	1	22	267
1129	1	40	342
1132	1	360	181
1133	1	609	376
1144	1	446	225
1147	1	558	280
1153	1	1	153
1154	1	3	818
1159	1	1	330
1161	1	341	186
1164	1	427	254
1172	1	19	240
1174	2	108	299
1183	1	2	379
1195	1	355	179
1196	1	1	189
1200	1	33	197

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1203	2	129	464
1222	2	105	401
1232	1	1	387
1240	1	2	175
1247	1	520	311
1271	1	412	221
1286	1	2	595
1295	1	1	165
1306	1	367	185
1314	2	158	631
1316	1	58	570
1359	1	384	193
1370	1	1	402
1371	1	1	345
1374	1	710	357
1378	1	2	400
1392	1	3	413
1411	1	202	432
1433	1	311	167
1450	1	2	256
1453	1	295	149
1471	1	721	398
1477	1	869	639
1502	1	794	399
1518	1	126	449
1534	1	283	143
1546	1	3	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1547	1	506	255
1583	1	3	350
1587	1	3	563
1602	2	170	679
1629	1	1	402
1665	1	468	235
1760	1	625	314
1762	1	3	200
1876	1	119	286
1895	1	2	379
1931	1	798	400
1976	2	715	183
2055	2	252	401
2056	1	331	167
2150	1	523	263
2157	1	794	399
2164	1	564	283
2175	1	218	400
2212	1	492	331
2338	1	732	367
2342	1	3	167
2352	1	330	166
2352	2	622	398
2355	1	47	352
2356	1	679	341
2355	1	301	152
2421	1	296	150

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3046	1	367	185
3049	1	553	278
3050	1	3	314
3052	1	504	253
3065	1	2	157
3070	1	357	190
3075	1	440	222
3080	1	1	285
3092	1	320	162
3093	1	411	250
3100	1	52	237
3103	1	47	298
3118	1	344	174
3123	1	2	145
3127	1	1	147
3138	1	336	169
3142	1	388	203
3144	1	664	386
3151	1	337	170
3155	2	202	384
3164	1	12	176
3205	1	288	145
3282	1	1	150
3303	2	239	400
3371	2	211	399
3558	1	2	148
3558	2	36	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3046	1	367	185
3049	1	553	278
3050	1	3	314
3052	1	504	253
3065	1	2	157
3070	1	357	190
3075	1	440	222
3080	1	1	285
3092	1	320	162
3093	1	411	250
3100	1	52	237
3103	1	47	298
3118	1	344	174
3123	1	2	145
3127	1	1	147
3138	1	336	169
3142	1	388	203
3144	1	664	386
3151	1	337	170
3155	2	202	384
3168	1	12	176
3205	1	288	145
3282	1	1	150
3303	2	239	400
3371	2	211	399
3558	1	2	148
3558	2	36	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3568	1	751	377
3595	1	757	380
3618	1	2	238
3618	2	130	402
3622	1	86	358
3622	2	664	398
3642	1	876	439
3649	1	781	398
3651	1	625	314
3664	1	467	637
3674	1	55	311
3677	1	619	402
3704	1	1	402
3726	1	535	269
3765	1	510	256
3779	1	554	357
3794	1	266	135
3794	2	667	377
3796	2	638	375
3801	1	474	262
3806	1	453	298
3807	1	42	389
3815	1	798	400
3827	1	3	320
3842	1	781	392
3853	1	671	399
3855	1	1	324

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3857	1	2	235
3861	1	590	297
3865	1	695	399
3897	1	3	173
3897	2	141	400
3898	2	225	401
3921	2	103	342
3927	1	70	175
3930	1	76	234
3946	2	651	382
3951	2	105	377
3965	1	646	344
3970	1	795	400
3981	1	3	311
3998	1	3	356
4001	1	481	296
4003	1	90	335
4018	1	2	259
4018	2	186	401
4021	1	1	345
4043	1	3	344
4054	1	3	344
4066	1	1	150
4070	1	1	324
4072	2	187	390
4073	1	1	285
4077	2	127	372

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4083	1	3	359
4090	1	27	368
4101	1	103	297
4105	1	1	306
4107	1	570	286
4119	1	629	339
4121	1	740	372
4123	1	3	230
4127	1	3	341
4128	1	2	331
4130	1	768	415
4146	1	97	381
4157	1	3	206
4186	1	505	254
4224	1	510	256
4239	1	1	348
4242	2	709	356
4252	1	589	296
4253	1	1	174
4256	1	568	323
4258	2	498	334
4267	1	284	144
4271	1	2	304
4287	1	303	163
4289	1	471	319
4302	1	153	305
4304	1	1	186

TABLE 3

S. aureus Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4304	2	96	314
4306	1	2	151
4318	1	576	289
4322	1	5	148
4331	1	439	221
4331	2	528	364
4338	1	728	399
4346	1	671	277
4367	2	117	311
4373	1	2	268
4381	1	574	326
4384	1	614	309
4397	1	9	311
4402	1	1	249
4403	1	606	328
4406	1	3	317
4411	1	2	280
4411	2	697	398
4412	1	2	364
4418	1	3	230
4424	1	601	398
4443	1	427	215
4471	1	643	323
4478	1	540	271
4482	1	50	289
4489	1	601	302
4491	1	12	206

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4495	1	3	179
4496	1	500	252
4500	1	130	306
4511	1	493	248
4518	1	1	246
4526	1	480	241
4527	1	2	163
4532	1	3	239
4542	1	11	175
4567	1	36	200
4573	1	1	231
4578	1	642	322
4619	1	1	180
4620	1	349	176
4662	1	1	246
4669	1	2	157
4680	1	28	183
4690	1	344	174

Table 4

ORF	SEQ ID NO	BLAST HOMOLOG	Antigenic Regions			
			Region 1	Region 2	Region 3	Region 4
168_6	5192	lipoprotein	36-45	84-103	152-161	176-185
238_1	5193	chrA	21-39	48-58	84-95	232-249
51_2	5194	OppB gene product (B. sub)	20-36	70-79	100-112	121-131
278_3	5195	lipoprotein 1	20-29	59-73	85-97	162-171
276_2	5196	lipoprotein	21-33	65-74	177-186	211-220
45_4	5197	ProX	28-37	59-69	85-100	120-129
315_8	5198	hypothetical protein	45-54	88-97	182-192	243-253
154_15	5199	unknown	31-40	48-58	79-88	95-104
228_3	5200	unknown	25-38	40-52	64-74	80-89
228_6	5201	unknown	29-41	89-101	128-143	173-184
50_1	5202	unknown	21-33	52-61	168-182	197-206
112_7	5203	iron-binding periplasmic	21-31	58-67	92-101	111-120
442_1	5204	unknown	30-39	91-100	122-137	182-192
66_2	5205	unknown	50-59	104-116	127-136	167-182
304_2	5206	Q-binding periplasmic	19-28	48-57	75-84	103-116
44_i	5207	hypothetical protein	27-36	86-95	129-138	192-201
161_4	5208	SphX	27-44	149-161	166-175	201-210
46_5	5209	cmpC (permease)	21-33	61-70	83-92	100-109
942_1	5210	traH [Plasmid pSK41]	83-92	109-118	127-142	
5_4	5211	ORF (S. aureus)	12-22	87-96	111-120	151-160
20_4	5212	peptidoglycan hydrolase (S.	24-34	129-138	141-150	161-171
328_2	5213	lipoprotein (H. flu)	81-90	123-133	290-299	
520_2	5214	fibronectin binding protein	44-54	63-79	81-90	95-110
771_1	5215	emm1 gene product (S. pyo	30-39	65-82	96-106	112-121
999_1	5216	predicted trithorax prot. (D	7-16	120-129	157-166	
853_1	5217	ORF2136 (Marchantia polyr	43-52	88-97	102-111	
287_1	5218	psaA homolog	13-22	28-44	72-82	114-124
288_2	5219	cell wall enzyme	14-23	89-98		
596_2	5220	penicillin binding protein 2b	40-49	59-68	76-87	106-115
217_5	5221	fibronectin/fibrinogen bindi	28-37	40-49	62-71	93-111
217_6	5222	fibronectin/fibrinogen bp	10-19	31-40	54-62	73-92
528_3	5223	myosin cross reactive prote	4-13	29-47	60-73	90-99
171_11	5224	EF	20-31	91-110		
63_4	5225	penicillin binding protein 2b	12-21	59-68	95-104	
353_2	5226		46-55	62-71		
743_1	5227	29 kDa protein in fimA regi	23-32	68-79	94-103	175-184
342_4	5228	Twitching motility	10-19	48-60	83-92	111-121
69_3	5229	arabinogalactan protein	97-106	132-141	158-167	180-189
70_6	5230	nodulin	36-45	48-57	137-160	179-188
129_2	5231	glycerol diester phosphodie	8-17	41-50	55-74	97-106
58_5	5232	PBP (S. aureus)	26-35	70-79	117-126	152-161
188_3	5233	MHC class II analog (S. aure	72-81	94-103	115-124	136-145
236_6	5234	histidine kinase domain (Dic	24-33	52-67	81-94	106-121
310_8	5235	clumping factor (S. aureus)	59-71	77-86	93-102	118-127
601_1	5236	novel antigen/ORF2 (S. aur	45-54	91-104	108-117	186-195
544_3	5237	ORF YJR151c (S. cerevisae)	76-90	101-111	131-140	154-164
662_1	5238	MHC class II analog (S. aure	22-32	71-80	89-98	114-122
87_7	5239	5' nucleotidase precursor ('	29-45	62-71	105-114	125-137
	5240	R65G gene product (B. sub	102-111			

Table 4

ORF	Antigenic Regions (cont)					
	Region 5	Region 6	Region 7	Region 8	Region 9	Region 10
168_6	244-272	303-315				
238_1	260-269	291-301	308-317			
51_2	140-152	188-208	211-220	256-266	273-283	
278_3	198-209					
276_2	255-268					
45_4	177-199	221-230	234-243	268-279	284-293	304-313
316_8						
154_15	148-157	177-187	202-211			
228_3	101-119	139-154	166-181			
228_6						
50_1						
112_7	136-149	197-211	218-229	253-273		
442_1	199-210	247-257	264-277	287-309		
66_2						
304_2	178-187	250-259				
44_1						
161_4						
46_5	131-141	162-176	206-215	243-252	264-273	285-294
942_1						
5_4	189-205	230-239	246-264	301-318	340-354	378-387
20_4	202-212	217-234	260-275	314-336	366-373	380-391
328_2						
520_2						
771_1	145-154					
999_1						
853_1						
287_1	154-164					
288_2						
596_2	121-130					
217_5	244-253	259-268	288-297	302-311		
217_6	144-158	174-183	188-197	207-216	226-242	
528_3						
171_11						
63_4						
353_2						
743_1	197-207					
342_4						
69_3	195-211					
70_6	206-215	263-272	291-301	331-340	358-371	390-414
129_2	117-127	141-157	168-183	202-211	222-231	261-270
58_5	184-203	260-269	275-299	330-344	372-381	424-433
188_3						
236_6	138-147	163-172	187-198	244-261	268-278	308-317
310_8	131-140	144-153	177-186	190-199	204-213	216-227
601_1	208-218					
544_3	170-179	184-193	224-235	274-287	327-336	352-361
662_1						
87_7						
120_1						

Table 4

| ORF | Antigenic Regions | | | (cont) | | |
	Region 11	Region 12	Region 13	Region 14	Region 15	Region 16
168_6						
238_1						
51_2						
278_3						
276_2						
45_4						
316_8						
154_15						
228_3						
228_6						
50_1						
112_7						
442_1						
66_2						
304_2						
44_1						
161_4						
46_5	306-315					
942_1						
5_4	393-407	416-426	456-465			
20_4	396-405	410-419	461-481			
328_2						
520_2						
771_1						
999_1						
853_1						
287_1						
288_2						
596_2						
217_5						
217_6						
528_3						
171_11						
63_4						
353_2						
743_1						
342_4						
69_3						
70_6	453-471	506-515				
129_2	296-315					
58_5						
188_3						
236_6	358-377	410-423	428-439	442-457	467-476	480-493
310_8	238-251	256-275	281-290	296-310	314-333	338-347
601_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 17	Region 18	Region 19	Region 20	Region 21	Region 22
168_6						
238_1						
51_2						
278_3						
276_2						
45_4						
316_8						
154_15						
228_3						
228_6						
50_1						
112_7						
442_1						
66_2						
304_2						
44_1						
161_4						
46_5						
942_1						
5_4						
20_4						
328_2						
520_2						
771_1						
999_1						
853_1						
287_1						
288_2						
596_2						
217_5						
217_6						
528_3						
171_11						
63_4						
353_2						
743_1						
342_4						
69_3						
70_6						
129_2						
58_5						
188_3						
236_6						
310_8	357-366	370-379	429-438	443-452	478-487	551-560
601_1						
544_3						
662_1						
87_7						
120_1						

Table 4

ORF	Antigenic Regions	(cont)				
	Region 23	Region 24	Region 25	Region 26	Region 27	Region 28
168_6						
238_1						
51_2						
278_3						
276_2						
45_4						
316_8						
154_15						
228_3						
228_6						
50_1						
112_7						
442_1						
66_2						
304_2						
44_1						
161_4						
46_5						
942_1						
5_1						
20_4						
328_2						
520_2						
771_1						
999_1						
853_1						
287_1						
288_2						
596_2						
217_5						
217_6						
528_3						
171_11						
63_4						
353_2						
743_1						
342_4						
69_3						
70_6						
129_2						
58_5						
188_3						
236_6						
310_8	622-632	670-685	708-718	823-836	858-867	877-886
601_1						
544_3						

Table 4

ORF	Antigenic Regions		(cont)
	Region 29	Region 30	
168_6			
238_1			
51_2			
278_3			
276_2			
45_4			
316_8			
154_15			
228_3			
228_6			
50_1			
112_7			
442_1			
66_2			
304_2			
44_1			
161_4			
46_5			
942_1			
5_4			
20_4			
328_2			
520_2			
771_1			
999_1			
853_1			
287_1			
288_2			
596_2			
217_5			
217_6			
528_3			
171_11			
63_4			
353_2			
743_1			
342_4			
69_3			
70_6			
129_2			
58_5			
188_3			
236_6			
310_8			
601_1			
544_3			
662_1			
87_7			
120_1			

Table 4

ORF		BLAST HOMOLOG	Antigenic Regions Region 1	Region 2	Region 3	Region 4
46_1	5241	aldehyde dehydrogenase	8-17	36-52	83-96	112-121
63_4	5242	glycerol ester hydrolase (P.	9-26	57-73	93-107	123-133
174_6	5243	ketopantoate hydroxymeth	71-80	203-212	242-254	265-274
206_16	5244	ornithine acetyltransferase	1-10	34-43	54-63	194-210
267_1	5245	NaH-antiporter protein (E.	120-129	332-347	398-408	
322_1	5246	acriflavin resistance protein	58-75	153-164	203-231	264-284
415_2	5247	transport ATP-binding prot	108-126	218-227	298-308	315-334
214_3	5248	2-nitropropane dioxygenase	123-136	216-233	283-292	297-306
587_3	5249	clumping factor	5-14	43-54	59-68	76-95
685_1	5250	signal peptidase	59-68	72-81	86-95	99-108
54_3	5251	fibronectin binding protein I	23-32	37-46	50-59	89-98
54_4	5252	fibronectin binding protein I	43-52	66-75	95-104	147-156
54_5	5253	fibronectin binding protein I	49-60	81-90		
54_6	5254	fibronectin binding protein I	55-71	82-97	139-158	175-186
328_1	5255	lipoprotein (H. flu)	11-20	61-70	96-105	

Table 4

ORF	Antigenic Regions Region 5	Region 6	Region 7 (cont)	Region 8	Region 9	Region 10
46_1	215-242	333-352	376-385	416-432	471-487	
63_4	145-154	191-202	212-223	245-265	274-283	291-300
174_6						
206_16	239-259	275-284				
267_1						
322_1	298-319	350-359				
415_2	344-353	371-380	395-404	456-465	486-495	518-527
214_3	318-337	365-375				
587_3	106-115	142-151	156-166	173-182	186-198	204-213
685_1	113-122	130-145				
54_3	128-138	185-194	217-226	251-260	268-277	295-305
54_4	175-188	191-200	203-212	220-229		
54_5						
54_6	220-230	287-304	317-326	344-353	364-373	378-387
328_1						

Table 4

ORF	Antigenic Regions			(cont)		
	Region 11	Region 12	Region 13	Region 14	Region 15	Region 17
46_1						
63_4	306-315	319-328	366-376	395-420	453-462	467-476
174_6						
206_16						
267_1						
322_1						
415_2	539-555					
214_3						
587_3	217-226	278-287	318-327	332-342	351-360	377-386
685_1						
54_3	316-325	329-345	355-372	387-396	416-425	438-448
54_4						
54_5						
54_6	396-407	427-436	514-531	541-550	569-578	612-622
328_1						

Table 4

ORF	Antigenic Regions			(cont)		
	Region 18	Region 19	Region 20	Region 21	Region 22	Region 23
46_1						
63_4	485-500	513-525				
174_6						
206_16						
267_1						
322_1						
415_2						
214_3						
587_3	396-405	426-442	459-470	485-494	505-514	531-562
685_1						
54_3	455-462	472-491	517-536			
54_4						
54_5						
54_6	639-648	673-681	703-715	723-732	749-760	772-788
328_1						

Table 4

ORF	Antigenic Regions			(cont)		
	Region 24	Region 25	Region 26	Region 27	Region 28	Region 29
46_1						
63_4						
174_6						
206_16						
267_1						
322_1						
415_2						
214_3						
587_3	567-578	584-601	607-840	844-854	858-870	877-886
685_1						
54_3						
54_4						
54_5						
54_6	793-802	811-826	834-848	866-876	893-903	907-918
328_1						

Table 4

ORF	Antigenic Regions		(cont)
	Region 30	Region 31	
46_1			
63_4			
174_6			
206_16			
267_1			
322_1			
415_2			
214_3			
587_3	889-911	927-936	
685_1			
54_3			
54_4			
54_5			
54_6	925-944	951-997	
328_1			

SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: Human Genome Sciences, Inc.
        (B) STREET: 9410 Key West Avenue
        (C) CITY: Rockville
        (D) STATE: Maryland
        (E) COUNTRY: US
        (F) POSTAL CODE: 20850

    (ii) TITLE OF INVENTION: Staphylococcus aureus Poly-
               nucleotides and Sequences

   (iii) NUMBER OF SEQUENCES: 5255

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
        (B) COMPUTER: HP Vectra 486/33
        (C) OPERATING SYSTEM: MSDOS version 6.2
        (D) SOFTWARE: ASCII Text

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:

   (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 60/009,861
        (B) FILING DATE: 05-JAN-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 5895 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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aaataGGTAA TAATGTAATA GCTTCTATTA TGATGCCTAA TTGAATGAAT TGGGCAAATG    180
GCTCTTTGAT GATAAGTGTG ATAATGAAAA GGGTTAAACT AACAATAATC GCATAATATT    240
TTTTTCGTTT AATAAGTCGC ACAGGAATGG GCTTCTTTTT AGTTGCTGCA GGAGCATATA    300
CTCACATTAC ACCTAAAGAA ATAACTGTTA AAATAATCAT AATTAAAAAG TTAATATGAA    360
AATTTACTAT TACTAAAGGT AAAAGTATAA ATAGTATAAT ACTTTCTACA TAACACCAAA    420
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TAATTAACGT AAACAGAAAA ATGTTTAAAA TATAGGCAAT AGTATACATA ACAATTAATT    540
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CTAAGTTATT TCTCTTTTGA AGATACGTGG CAAACTGGTC AATTTTATTA TCAAAATAAT    660
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GTACTAAAAG TATGAGTTAT TAAGCCATCC CAACTTAATA ACCATGTAAA ATTAGCAAGT   1140
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TTACGAAAAT TTCAAGAATA TTAATATTCA TTTTCAAATT CCAAATATAA ATGCATTTTC        3540

AACGCATATT TATTATACTT AGATTAATAC TTACATGAAA AAGGGAGGTG TCTCGTGAAA        3600

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ATCCAAAACC AGACCCTAAT AAGCCAAATC CTAACCCGTC ACCAGATCCC GATCAACCTG        4200

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TACAACAGCA ATCGAATTAC TTTAGATTCC aATATTTCAA TCCATTGAAA TCAGAAAGGT        4560

ACTATCGTAA TTTAGATGAA CAAGTACTCG CATTAATTAC TGGTGAAATT GGATCAATGC        4620

CAGATTTGAA AAAGCCCGAA GATAAGCCGG ATTCAAAACA ACGCTCATTT GAACCGCATG        4680

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TGTTAAGTGC TAAACTTTAG GTTTTTTAAG GAGGAACAAT CATGCTAAAA CCAATTGGAA    5820

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TGATAGTGCT AAAGA                                                    5895
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(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6796 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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ACCTTCAAGT ACTATGCGTA CGCCAGATGA TATGAAGTCA TTTTTGACGA AAGACCAATA     240

CCGATTATAC AAATTAATTT GGGAACGATT TGTTGCTAGT CAAATGGCTC CAGCAATACT     300

TGATACAGTC TCATTAGACA TAACACAAGG TGACATTAAA TTTAGAGCGA ATGGTCAAAC     360

AATCAAGTTT AAAGGATTTA TGACACTTTA TGTAGAAACT AAAGATGATA GTGATAGCGA     420

AAAGGAAAAT AAACTGCCTA AATTAGAGCA AGGTGATAAA GTCACAGCAA CTCAAATTGA     480

ACCAGCTCAA CACTATACAC AACCACCTCC AAGATATACT GAGGCGAGAT TAGTAAAAAC     540
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CGGTTTCTTT AGTAGCTTTA AACAAGATGT TGAACGTGCT GAAGAAGAGA TGGAAAAGAT        840

TGAAATCAAA GATGAGCCAG CCGGTGAAGA CTGTGAAATT TGTGGTTCTC CTATGGTTAT        900

AAAAATGGGA CGCTATGGTA AGTTCATGGC TTGCTCAAAC TTCCCGGATT GTCGTAATAC        960

AAAAGCGATA GTTAAGTCTA TTGGTGTTAA ATGTCCAAAA TGTAATGaTG GTGACGTCGT       1020

AGAAAGAAAA TCTAAAAAGA ATCGTGTCTT TTATGGATGT TCGAAATATC CTGAATGCGA       1080

CTTTATCTCT TGGGATAAGC CGATTGGAAG AGATTGTCCA AAATGTAACC AATATCTTGT       1140

TGAAAATAAA AAAGGCAAGA CAACACAAGT AATATGTTCA AATTGCGATT ATAAAGAGGC       1200

AGCGCAGAAA TAATATTTTT ATTTCCTACA TACATTTTAA GATTGTTAAA TAGAATCATT       1260

AGTGAATCTT ATTTTAAAGA TAGTAAAGGA TTAATCTAAA TAAGTGCGGA TAATATAAAC       1320

ATAACAACAT AATTAAmAGA CATAAATGAC aATAAAAGGA GTATAGAAAT GACTCAAACT       1380

GTAAATGTAA TAGGTGCTGG TCTTGCCGGT TCAGAAGCGG CATATCAATT AGCTGAAAGA       1440

GGAATTAAAG TTAATCTAAT AGAGATGAGA CCTGTTAAAC AAACACCAGC GCACCATACT       1500

GATAAATTTG CGGAACTTGT ATGTTCCAAT TCATTACGCG GAAATGCTTT AACTAATGGT       1560

GTGGGTGTTT TAAAAGAAGA AATGAGAAGA TTGAATTCTA TAATTATTGA AGCGGCTGAT       1620

AAGGCACGAG TTCCAGCTGG TGGTGCATTA GCAGTTGATA GACACGATTT TTCAGGTTAT       1680

ATTACTGAAA CACTTAAAAA TCATGAAAAT ATCACAGTTA TTAATGAAGA AATTAATGCC       1740

ATTCCAGATG GATACACAAT TATCGCAACA GGACCACTTA CTACAGAAAC CCTTGCGCAA       1800

GAAATAGTGG ACATTACTGG TAAAGATCAA CTTTATTTCT ATGATGCGGC TGCTCCAATT       1860

ATTGAAAAAG AATCTATTGA TATGGATAAA GTTTACTTAA AGTCCCGTTA TGATAAAGGT       1920

GAAGCTGCAT ATTTAAACTG TCCTATGACT GAGGATGAAT TTAATCGCTT TTATGATGCA       1980

GTATTAGAAG CTGAAGTTGC GCCTGTAAAT TCATTTGAAA AAGAAAAATA TTTCGAGGGT       2040

TGTATGCCTT TTGAAGTAAT GGCAGAACGC GGACGCAAGA CATTACTATT TGGACCAATG       2100

AAACCAGTAG GATTAGAAGA TCCAAAGACT GGGAAACGTC CTTATGCGGT GGTTCAATTA       2160

AGACAAGATG ACGCTGCTGG TACACTCTAC AATATTGTTG GCTTCCAAAC GCATTTAAAA       2220

------CCTC ------GAAGT CATTAAATTA ATTCCAGGCT TAGAAAATGT TGATATTGTT       2280
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TATGTAGAAA GCGCAgcTAG CGGCTTAGTT GCAGGTATCA ATCTTGCGCA TAAAATATTA    2460

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TCTCATGCTA AAAACAATAA GAATTTCCAA CCTATGAATG CTAACTTCGG GTTATTACCA    2580

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TATTCATTCT TAAGTCATCA ACGAGTAAGT AATGACTTTC TAAATGGAAA ATACTTATCC    2760

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ACAAGTCATC ATGAAACAAA CGGCAAGAAA AGTGCGACGT TTATATGAAG GTAAAGTGTT    4140
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ATTACAACAG TTTAGTGGTA ACTTAGAAAG AGCTGCTGTT GAATTGGCAC AAGAATGGCG   4260

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ATCAGGAGGC AACTACGCAT TAAGCGCAGG ACGTGCATTG AAACGCCATG CATCGCATTT   4440

GTCTGCTGAA GAAATGGCAT ATGAGAGCTT GAAAGTAGCG GCTGATATTT GTGTCTTTAC   4500

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CGTAAAGTGG CAATTGCCCT ACGTAATCGA TACAGAAGAA GTTTATTAGA TGAGGAATCA   4740

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CAAACGAATA ATCCTTTAGA GTCACTTTTC GGAGGTGCAA TTCCAAATTT CGGACAAAAT   5100

AACGAAGATG AAGAAGAACC ACCTACTGAG GAAATTAAAA CAAAACGTTC TGAAATTAAG   5160

AGACAGCTAG AAGAAGGCAA ACTTGAAAAA GAAAAGGTAA GAATTAAAGT CGAACAAGAT   5220

CCTGGTGCTT TAGGTATGCT AGGTACAAAT CAAAATCAGC AAATGCAAGA GATGATGAAT   5280

CAATTAATGC CTAAAAAGAA AGTTGAGCGA GAAGTTGCTG TTGAGACGGC AAGGAAAATC   5340

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GAATTAGCAG AACAAATGGG TATCATCTTT ATAGATGAAA TCGACAAAGT TGCGACGAAT   5460

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ACTGTAAACT TTACCGATGA AGCAATTACT CGCTTAGCTG AGATTGCTTA TCAAGTAAAT   5820

AAAATACAG AGAACATTGG TGCAGGTCGA CTTCATACAA TTTTAGAAAA GATGCTAGAA   5880

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AAATATACAA AAGGAGAAAA ATTCATGAGC TTATTATCTA AAACGAGAGA GTTAAACACG      6060

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AGCGTAACTG TAACAAATGT ATTTATTGTA TCGCGTCGAG GTAAAATTTT AGGATCGAGT      6180

CTAAATGAAT TATTAAAAAG TCAAAGAATT ATTCAAATGT TGGAAGAAAG ACATATTCCA      6240

AGTGAATATA CAGAACGATT AATGGAAGTT AAACAAACAG AATCAAATAT TGATATCGAC      6300

AATGTATTAA CAGTATTCCC ACCTGAAAAC AGAGAATTAT TCATAGATAG TCGTACAACT      6360

ATCTTCCCAA TTTTAGGTGG AGGGGAAAGA TTAGGTACAT TAGTACTTGG TCnAGTACAT      6420

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GAAaTCTTAC GTGAGAAGCA TAGTGAAGTA GAAAnAGAAG CGCGCGATAA AGCTGCTATT      6540

ACAATGGCAA TTAATTCATT ATCTTATTCT GAAAAAGAAG CGATTGAACA TATCTTTGAA      6600

GAACTTGGCG GTACGGAAGG CCTATTAATC GCATCAAAAG TTGCAGATAG AGTTGGTATT      6660

ACTAGATCTG TAATTGTAAA TGCACTACGT AAATTAGAAA GTGCTGGTGT AATTGAATCA      6720

CGTTCTTTAG GAATGAAAGG TACTTTCATT AAAGTTAAAA AAGAAAAATT CTTAGATGAA      6780

TTAGAAAAAA GTAAAT                                                       6796
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(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2073 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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ATCCTAAAAT TnAAAATTAT CACGCCTTTT GaACAGCTTT GTAACCaTCt GGACGATCAT        60

kAAATTCCaA TGTAAATCCT GGTTTAAaGT TGATCTTTAA CCTTATTTAA AyCACCAATT       120

GTACGTATAT TATGTTGTTT AGCAAAATCA CGTTTTACAG CTAAAGCATA CGTATTGTTA       180

TACTTCATTG GTTTTAACAT AGTCATTTGA TATTTCTTTT CAAGACTTTG CTTAGCTTGT       240

TCATAAACTT TTTTCTCTTC TTTTGACTTC AATGGTTCTT TTGTTAATTC ACCTAAAACT       300

GTTCCAGTAA ATTCTAAATA CCCATCTATA TCGTCAGATT TTAAAGCATT AAATAAAAAT       360

GCTGTTTTGC CCATACCATC TTTCACTTCT ACAGTATTTT TGGTCTCTTC TTCTATTAAA       420

ATTTTATACA TATTTGTAAT AATCGATGGC TCGGAGCCAA GCTTTCCAGC TAACGTAATT       480

TTATCACCTT TTTGTGCAAA CATAGGAATA GCGATAGCCA GTATAATAAT CATCACTATA       540
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TCAAATATAA TTGCCAATAA GGCTGCTGGA ATTGCACCTA ATAATATCAA CGATGCATTG        660

TTACGGTCTA TACCTAATAA AATTAAATCT CCTAGTCCGC CTGCACCAAT TAATGCTGCT        720

AGTGTTGCTG TACCTATAAT TAATACCATA GCCGTTCTTA CACCAGCCAT TATAACAGGC        780

ATTGCTATCG GAAGTTCGAC TTTAGTTAAA CGTCTAAATG GTTTCATACC TATACCTTTA        840

GCCGCTTCAA TGAGTGATGG ATCAACTTCT TTAATTCCAG TATACGTATT CCTTAAAATT        900

GGTAACAACG CATACACTAC AAGTGCAATA ATTGCTGGCA CACGACCGAT ACCAAATAAA        960

GGAATCATTA AACCTAATAA TGCCAACGAT GGTATGGTTT GAAGAATTGC CGCAATATTC       1020

ATTACGATTT CAGATATCGT TTTAGTCTTC GTTAATAAAA TACCTAATGG TACCGCAATA       1080

GCAGTTGCAA TCAATAATGC GATAAATGAT ATTTGAATAT GTTCTATCAT TGTCGAAAAG       1140

AGTTGCCCCT TACGTTCACT CAATATGTCg AAAAAGTTAG TCATGTTGAG CTACCTCCTT       1200

TTTCTGGGAC AAATATTTGA AGATATCTTT CCTATCAATA ACATATTGAC CTACGCTATC       1260

TTCTTGCATG ACAATGACAC GCTCGCTCTC TGATAAAAGT TGATACAATA CTTCAATTGG       1320

TTGATTGTCA TAAACAATTG GATAAGCGCT CATAGATGTA ACCTCATCGA TTGGTTTCAT       1380

AATATCCAAG TCACGGATAA TTGCGTTCTC TTCAACACAT GGCGCATCAT CTTCTAAATG       1440

ACTACCCATA AATTGTTTAA CAAATTCACT TTGAGGATTA TTTTTAAATC CTTCTGGTGT       1500

GTCAATTTGT TCAATATGCC CTTCATTCAA AAGACAAATC TTATCACCAA GTTTCATCGC       1560

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TAAATCATCT TGAAGTTTTT CTCGGCTGAT TGGGTCTAAT GCACTAAACG GTTCATCCAT       1680

TAAAATAACT GGTGGATCAG CTGCTAACGC ACGTATAACT CCTACACGTT GTCGTTGCCC       1740

CCCTGACAAT TCATCAGGTT TTCTGTTTTT ATATTTTTCA GGTTCTAATC CAACCATTTC       1800

AAGTAATTCA TCTACTCTTT TATCTATATC TTTTTCTTTC CACTTTTTCA TTTGTGGCAC       1860

TTGTGCAAtA TTTTCTTTGa wTGTCaTATG TGGGAATAAT GCAATCTGCT GcAATACGTA       1920

TCCAATATCC CAACkCATTT CGTATACTGG ATAATCACTT ATTGGTTTAT CTTTAAAATA       1980

AATATAACCT TCACTTAAGT GAATGAGTCG ATTAATCATT TTTAATGTCG TAGTTTTTCC       2040

ACAACCTGAA GGTCCAATTA GCACAAAAAA TTC                                    2073
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(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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ACTATTCTAG CTTCATCAGT TATCATATAT TCTTTGAAAC ACTTGTAAGA AAATATAATG      60

AGTATTTACT ACATAATGAT ATTTCAAATT AGAAAAAAGG AAGTTATGAT TTAATGGCCT     120

TGAGCCTATC ATAACTTCCT TTTATCATTT TATTGTTGTG TTGATGTTTC GATAACGTGG     180

TACATCTTAT CAAACATCAA TTCGAAACCA TGCACCATGG CATCATGATA TTCTTTTTTC     240

TTTTGCTTGT ATTCTAAATT AGTAAATCGT CTTTCTTTTT CAACTAATGA ACGATAATAA     300

AATAGCATTT GGGTGCCACC TGTTTCACGT TCAAAAAATT CTACCTCAAT GACATCTTGC     360

GTTTCACTTA GTCCAGGCAT ACCGATAGTC ATCTTAACGT ATTCATCCAT AACTAAAGAT     420

TCATAAATGC CTTCAATCAC ATTTACTTTG CCATTACGTT GTTGATCTAC AATACGATAT     480

TTACCGCCTT CTTTAACGTC CGCTTCAATC TCTTTATTCG TTCTGGCTGA TGTCATAAAC     540

CATTGTTTCA ACAAATCTTT CTTTGTCCAA GCTTCGTATA CTAACTCTGG AGAAAATTTA     600

TAAAGCTTTT CAATTTCAAC TTCGACATGT TCATTCTCTA CATTAAATTT TGCCACTGTT     660

GTCCACCCAC TTTCGCTCTT ACTTTTATTT TAACGTATTT TTGCTCAGTT CCAAACATAG     720

ATGATCATCA TTTTTAAAAG ATTAGCGTTA TACGGTGAGT ACAACATGAT CTGTTAATAT     780

AACAAGCCAC CTTACTTGGC TACATCGATA TATTGTTAAG CATTAATGTT TCATTTCTTG     840

ACTAGTGTTC TTTTTTAGCT TTGGAAAATT AAATAAAATC GCAATAAGTC CGCATACACC     900

TAATAATATA GGATAAATGC TGTATGGGAA TAACATTAAC GGTGAAATAC CAGCTACACC     960

AGCCGCTGaA ATGACTTGCG GGCTATATGG TAATAAACCT TGGAAGCAGC CTCCAAATAT    1020

ATCAAGAATA CTTGCTGATT TCCTTGAATC TACATCATAT TCATCTGCAA TATTTTTAGC    1080

TAAAGGACCT GACATAATAA TAGAGATGGT GTTGTTTGCC GTGGCAATAT CTGCGACACT    1140

TACCAAACTA GCAATTCCTA ATTCTGCGCC ACGCTTTGAT TTCACTTTAG AGCGAACAAA    1200

TTGCAACAAC CATTCAATAC CACCATTGTG TTGAATAATA CCGACTAAAC CACCAATTAG    1260

CAACGCAATC ATAGCAATAT CTTCCATGCT TATAATACCT TTGGACACTG CATCTAGTAG    1320

CCCCATCCAA CCGAATGAAC CATCTATGAG ACCAATGATT CCGGCTAATA ATGTTCCGCC    1380

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TACAACTTTA ATTAGATTAT AATCATAGTt TTTAGCATGA TTTAAAGAAA TGCCATTCGT    1500

TAAGAAATAC AGAATAATAA TCGTTAAAAT AGCACCTGGC AATACAATTT TAAAGTTTAC    1560

TCTGAATTTA TCTTTCATTT TCGTATGTTG TGTTCTAACC GCAGCAATTG TTGTATCTGA    1620

AATCATTGAT AGATTATCGC CGAACATTGC ACCTCCAACA ACTGTAGCCa tTGctAGCGC    1680
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TCCTACAGAC GTCCCCATAG ATATAGAAAC AAACATACAA ATCACAAACA ATCCTACAAT      1800

AATTAAATTT TCTGGGATTA ATGATAGTCC TAAATTAACT GTCGACTTTA CGCCACCCAT      1860

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GTTTGAATGG CCTGCACCTT TCGTGAAGAC CTCAACTTTT TTAGCAAATG ATTCTTTTCG      1980

ATTCATTAAT AACGCCACAA TTACCGTTAT CGTAATTGCA ACATTTAATG GCATTGAAGT      2040

AAAATCACCT GTGATAATAC CTACGCCTAA AAACAACGCC ACAAATAATA ACAAGGGGAA      2100

TAATGCCCAA GCATTGCTCT TTTTATGTAC TTCCATCCTT TTTACCTGCT TTCCAATTAA      2160

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TTCAAACCAT TACGGTTACT GGAATTGGCA CATTCGAGAT GTTGCCGAGG CTTCATAGGG      2280

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ATTAATGCAA TAAAAATGAA CACGATAGAC ACACTTACTA ATATTAATGA TATGACTTTA      2520

AATTGCTGAA CACGTTGCTT GGAGATGACT TTCAACTGTT TGTTTGATAG ACGCGTATTT      2580

TTTATACTGA TTCCCAGTAT ATTTTCTAAT ATTTGAACCA ATACGATACT TATTGCAAAT      2640

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          TAACTAAATT AATATTATGT TGTTCAATTA AAAGCTTCAT ACAAACCTAA      3420
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GACCAGAATG GACCAGGCGC TACACAGTTC ACTCTAATTC CTTTTGGTCC TAATTCTTCT      3660

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GGACTAGGAT TATAACCTTG TACAGATGAT GTCGTTGTAA TTGACGCACC CGGTTTTAAA      3780

TATTCCAATG CTTTTTGAAC TGTCCAAAAT AGCGGATAGA CATTCGTTTC AAATGTTTCT      3840

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CTTTTAATGC ATGTGTTTCA ATAATTTTAA AAGCGCCATG TCCTAGTTCT TCTGCTGATT      5160

GAAAAATGAA TTTAACACGC CCAGTAAGAG TGCCCTCAAT TTCTTTTAAT TTTACAGCTG      5220

TAGCCAAAAT ACTAGCCATG TGAATATCAT GACCACACGC ATGCATAACA CCTTCATTTT      5280
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CTAATATTCT AATATGATGT TCTGTTAAAA TATCTTTAAT TTTTTGTGTA GTCTTAAATT       5460

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AATGATAGAC AGTTGTTTAA TAATATCGTA ACACTGTTGT CAAACTATTC TAACTTTTAT       5700

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CAAAATGATA TGGAATATAT TCATGATTTG GTGCATCCCA AATTACTAAA TTAGCCTTAT       5940

CACCTGTGTT AATTGTACCC GCGTTAATGT CTATTGCTTT AGCAGCATTG ACCGTAACAG       6000

CATTCCAAAC TTCATTAGGT GATAGCTTTA ATTTCAAGGC TGCAATCGCC ATAACAAGTT       6060

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CATAACCACT CTTACTTTCA ACTGCAAGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT       6660

GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATTA ACGGTAGATA       6720

ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTTGACGT TTTAATGACA       6780

TCTCATGTTC TCGAGATCCA CCAAATGTTA AATGGGTATG TGCATCTACT AATGCTGGGG       6840

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CAGCATATAC AATTTTGCCA TCTTTAATGA CAACTGTACC ATTTTTCACA ACATTTAATT       6960

.......... ..TAGCCTTC AAAGGCTTAT CTGTTGATCT CGGTAAAATT AATTCTGCTA       7020
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GTGATGGAAT GAAATCCATG AACCACCTGC AGCTGTGTTA ATGAGTGCAT TCAATACAGC   7320

CCAATCACCA ACCGCGTCAC TACCATCTTT CATACTTTCT GTTTCACGGT TAGGACTAGC   7380

AACTGAACCA GCATCTAAAT GGTCTCGTCC AATAACAATT GGTGCTGAAA TTTCACCGTC   7440

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TCTCATAAAA TTCGCTCCTG TTCTTTTAAG AAGTTAATTC CACTAAATTT AAAACGCTTA   8760

CATTATTATC TTCAATATTC ATTATAGTAT GTTAAAATAT AGCCAACAAA TATAAATAAA   8820

CTAATTATCC ATAGCTTGAA TCTATAAATA AAAGGAGCAA AACACATGAA AATTATTCAG   8880

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TTTGTTCATC TCGGCTTAGG TTACGCTATC ATTCCGACAT TTTATTACCA ATCATTTCAC      9600

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TATGTACAGC TTTAATACAT TTGCAGATAG CTTTATTTTA TTACAATCAA CAGGCTTATC   12420

AGTACCTATT ACACACATTC TGATTGGACA TATTCTGATG GCGTTCGTAG TAGAATTCGG   12480

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GACTAAAGGA CGTACAATTT ATATTGCAAC GACATTCCAT GCTTCAATGA CATTCGGACT    12720

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TGAAGATGAA ATAGAGCAAT CATTAnAAGA ACCTGCGACT TATAAAGAAG ACAGACGTnC    13260

ATCAGTTGTA ATTGATGCAG AAAAACATAT CGAAAAAGCT GAAGAnCAAT CTTCAGATAA    13320

A                                                                    13321
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(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8549 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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ATGTGTTGTA AACTTTTATG TTGAAAAAGC TACTTATCTC AATGAAAACA AGTAGCATTT      60

AATAAATTAA TTAGTATACA GCTAGTTTTT CTAATTGTTC TTTAACTTGA ATTAAGTTTG     120

ACCGTATTAG AGAGGCAGAT TGATCCATCG TTTGAATTGC TTGTCCTTCA TTTTCGTTCA     180

AGCCATTACA AACAACTTCA AACTGTTGTG CCATTTGATC AAGACGCGCA TGAGCTTGTG     240

TGTTTAAAAT AAACATATCG TCATAATGTG ATGGCGAATA GATAATTCGT CGTTGTATAC     300

AAACGTATAA AAACCTTGTC ATATCAACGG TTTTGGCATT TTTAAACCTC TGTGTTTTCC     360

ACGCATGTTT GCCCTTATTT AAATAATTTG CCCTTTTTTC GCCCCGAAAA AAAAACACAA     420

. . . . . . . . . AGAGTCGTAA ATTAATAGGT GGTGTGGTTT TGTTGATTGT AGGGGTATAA     480
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GGGACCAACA GTCAGATATA TGGCCTCTGC CGGGCTATAT AGTTCACTCC TACTATATAA         1740

AAGTAAGTAT AACATAAAAA GCACCCCGTA AACTGTTATA CGGGAATGCT AAAGTCATAT         1800

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CCAAATAGTT ATTTAATAAC TGTAAGATTC CCTATAATTA ATGTAGCaAA ATTTTTATTC         2100

TAAGTAAATA CTAAATCGTG CTAAACTTAC CAAAACTACT TATTCTATTA CCTGCCTTGT         2160

CTACCTCTCC TGTCGCTATA TAACGACGTT GTCCACTATT AGCAATATAA GTAATCCATC         2220

TATAGCCATT GATGCAATAT GCGCCGTCAT ATTTAATTGT TGCGTTATTA GGTAATACAC         2280

CTGTAATTCT TGAATTAGTT GAATAGCCGT CCCTTACGTT ATTACCTTTA ACATTGGCAA         2340
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CACCTATAGG CTTACCATGA ATCGCACCGG CTATTAATTT AGAATACAAG TCATAGTTTT        2520

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TCAAAAATAG TTTTTAACAA GGCTATAACA AATGTACTTA GAATCGTCCC TATTAATCCT        4080
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CCATTTTTTA TAGCCTCGTC CATTGCTTTC GCACGATCCA TAATAGTTTT TTCTAATTCC      5940
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CTACCATTAT AATAAATTTG CTCAGCGAAG TGTTGAATTG TTTTAGCTyT CTGATGCAAC   8160

TTAAACTCTG TTGTCAAGCC AAGCGCAAAT TGCTCTATTC TTTGTAAGTT TTGTATTTCC   8220

TTAGCTCTAT AATCTCGACC TGCTAAAGCT CCCAAATCCT TTATTAAATA CAAATTTTCC   8280

ATAATGCACC TTCCTTTCTA ATAAAATAGC ACTGTACCAA GTTTCCCACT ATCGTCAACT   8340

GTTATTTTCC ACAATTTACC GTTTGGGGAT TTCTGTACAA TGCTATTTTG AATAATTgcC   8400

TGctTCGCCT ATTTTTAAAT TATCTAATTT ATTTkTATCA TTTACCGAAA TGATACCGTC   8460

TTGAGGCAAT CCATCAATAn CACTACTGCC TGCATAAGGT ATCCCATTTA TAGCTTTCCA   8520

ATGTGTAGCT GGAAAGTACT GTTTATCGT   8549

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3601 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGGCGTGTAG TGACTTACGG nTAGGAAACT ATGTATCCGA ATGATTTATT GAGACCAAAA   60

AGGCATTAAA GTCCATTGAA ATATCnGGTA GCGmGTTGGT ACgTGGACGT GGGGGCCCTA   120

GATGTATGAG TCAACCATTA TTCAGAGAGG ACATTTAACG TAATAAATTA TAGAmACGAG   180

GGTGAAAATA ATGACAGAAA TTCAAAAACC GTATGATTTA AAAGGCAGAT CATTATTAAA   240

AGAAAGTGAT TTTACCAAAG CAGAATTCGA AGGACTTATT GATTTTGCAA TTACATTAAA   300

AGAGTATAAG AAAAACGGTA TTAAGCATCA CTACTTATCT GGAAAAAATA TTGCACTACT   360

ATTCGAAAAG AATTCGACGA GAACGCGTGC TGCGTTTACA GTTGCGTCTA TTGATTTAGG   420

TGCGCATCCA GAATTTTTAG GAAAAAATGA TATTCAATTA GGCAAAAAAG AATCTGTAGA   480

GGATACTGCG AAAGTATTAG GTAGAATGTT CGATGGTATT GAATTCCGTG GTTTTTCACA   540

ACAAGCTGTT GAAGATTTAG CGAAGTTCTC TGGTGTACCG GTGTGGAATG GATTAACAGA   600

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TCTAGAAGGA ATAAACTTAA CTTACGTTGG AGATGGACGT AATAATATTG CGCATTCATT        720

AATGGTAGCA GGTGCTATGT TAGGTGTTAA TGTAAGAATT TGTACACCTA AATCATTAAA        780

TCCAAAAGAG GCATATGTTG ATATTGcAAA rGAAAAaGCG AGTCAaTATG GTGGTyCAGT        840

CATGATTACG GATAATATTG CAGArcCAGT TGAAAaTwCm GATGCTATAT ATmCAGATGT        900

TTGGGTATCG ATGGGTGAAG AAAGTGAATT TGAACAcGTA TTAATTTATT AAAAGACTAT        960

CAAGTGAATC AACAGATGTT TGATTTAACA GGTAAAGATT CAACGATATT CTTACATTGT       1020

TTACCAGCAT TCCATGATAC AAATACACTT TATGGACAAG AAATTTATGA AAAATATGGA       1080

TTAGCTGAAA TGGAAGTTAC AGACCAAATC TTTAGAAGTG AACATTCAAA AGTGTTTGAT       1140

CAAGCTGAAA ATAGAATGCA TACAATTAAG GCAGTAATGG CAGCAACATT GGGGAGTTAA       1200

TCACTAAATG GAACGATATG AATATGATGT GTCTGATGAT ATAAGTGTCA TGTACAGACA       1260

CCTCATATTG GTATTAAAGG AGAAATGAAT ATGAACGAAT CAGGAGATAA CAAACTCAGT       1320

AAATCTTCTT TAATTGGACT AGTTATAGGA TCCATGATTG GTGGCGGTGC GTTCAATATA       1380

ATGTCTGATA TGGGCGGTAA AGCCGGTGGA TTAGCCATTA TTATTGGTTG GATTATTACA       1440

GCTATAGGAA TGATTTCATT AGCGTTCGTA TTTCAAAATT TAACCAATGA ACGGCCGGAG       1500

CTAGACGGTG GTATTTATAG TTATGmTCAA GCAGGATTTG GCGATTTTGT AGGATTTATC       1560

AGTGmTTGGG GATATTGGTT CTCAGCGTTT TTAGGCAATG TTGCCTATGC AACACTATTG       1620

ATGTCAGCAG TAGGTAACTT TTTCCCGATT TTTAAAGGAG GCAACACATT ACCAAGTGTT       1680

ATTGTCGCCT CGTTACTACT CTGGGGTGTC CATTCTTGA TTTTAAAAGG CGTTGAAACA       1740

GCAGCATTTA TCAATAGTAT TGTTACTGTT GCAAAGTTAA TACCGATTTT ACTTGTAATC       1800

ATATGCATGA TAATTGCATT CAATTTTGAC ACTTTTAAAA CAGGCTTTTT CAGTATGACG       1860

TCAGAGGGTG TATTGCCATT TAGTTGGGCG AGCACAATGA GCCaaGTtAA AAGTACGrTG       1920

CTAGTGACAG TTTGGGTGTT TATCGGTATC GAAGGTGCAG TAATTTTTTC TAGTAGAGCT       1980

nAAAATGAGA AAGATGTAGG TAGTGCCACG GTTATAGGAC TTATATCAGT TTTAATTATC       2040

TATyTCTTAT TAACTGTATT AGCTCAAGGC GTGATTTTGC AAAATCATAT TTCGCAATTA       2100

GATTCGCCAA GTATGGCACA GGTGCTTGCA ACTATTGTAG GTGGTTGGGG ATCTACACTT       2160

GTAAATATTG GTTTAATTAT TTCGGTACTA GGTGCATGGT TAGGATGGAC ACTGCTTGCT       2220

GGTGAATTAC CTTTCATTGT TGCAAAAGAT GGATTATTTC CAAAATGGTT TGCTAAAGAA       2280

uAuvAAAATG GAGCACCTGT AAATGCACTG CTTATTACCA ATATATTAGT ACAATTATTT       2340
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CGACAGCAAG CAACTACTAA ACAATGGACG ATTGGTATCA TAGCCTCAAT TTATGCTATA      2520

TGGCTTATAT ATGCAGCAGG TATCAATTAC TTATTATTGA CGATGTTACT TTATATTCCA      2580

GCTCTTCTTG TTTATACaAT CGkTCmAAAG rATwATCAGa CACGTTTGAT TAAATCAGrC      2640

TATATTCtTT TTATGATTAT tATCGTACTT GCAGTTATCG GGTTAATTAA GTTATTGATG      2700

GGAACGATAA ATGTTTTTTA AAAGGAGCGA CAAAAATATG AAAGAGAAAA TTGTCATTGC      2760

ATTAGGCGGT AATGCGATAC AGACAACAGA AGCAACAGCT GAAGCACAAC AAACAGCTAT      2820

TAGATGTGCG ATGCAAAACC TTAAACCTTT ATTTGATTCA CCAGCGCGTA TTGTCATTTC      2880

ACATGGTAAT GGTCCACAAA TTGGAAGTTT ATTAATCCAA CAAGCTAAAT CGAACAGTGA      2940

CACAACGCCG GCAATGCCAT TGGATACTTG TGGTGCAATG TCACAGGGTA TGATAGGCTA      3000

TTGGTTGGAA ACTGAAATCA ATCGCATTTT AACTGAAATG AATAGTGATA GAACTGTAGG      3060

CACAATCGTT ACACGTGTGG AAGTAGATAA AGATGATCCA CGATTTGATa ACCCAACTAA      3120

AcCAaTTGGT CCTTTTTATA CGAAAGAAGA AGTTGAAGAA TTACAAAAAG AACAGCCAGA      3180

CTCAGTCTTT aAAGAAGATG CAGGACGTGG TTATAGAAAA GTAGTTGcGT CACCACTACC      3240

TCaATCTATA CTAGAACACC AGTTAATTCG AACTTTAGCA GACGGTAAAA ATATTGTCAT      3300

TGCATGCGGT GGTGGCGGTA TTCCAGTTAT AAAAAAAGAA AATACCTATG AAGGTGTTGA      3360

AGCGGTTATA GATAAAGATT TTGCTAGTGA GAAATTAGCA ACGCTGATTG AAGCAGATAC      3420

CTTAATGATT CTTACGAATG TAGAAAATGT ATTTATTAAC TTTAATGAAC CTAATCAACA      3480

ACAAATCGAT GATATTGATG TAGCAACACT GAAAAAAtAC GCGGCACAAG GTAAGTTTGT      3540

GGAAGGATCG tGTTGCCAAA AATAGAAGCT GCGtACgtTT GTTGAaAGtG GGGaAACCAA      3600

A                                                                      3601
```

(2) INFORMATION FOR SEQ ID NO: 7:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 573 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
CGACACTATT AAATGAATTA GAGCACAATC TAACAAATCA AATTCATTTT TCAAAAGATG        60

AACGACTCAC ACATATCGCT TTAAAGTTAT TCGAAACAAC CGATCCTGTT TCAACAAAGC       120

AACTTGCGCA AGATGTTAAT GTTTCGCGTC GGACAATTGC AGATGATATT AAAATGATTC       180
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TTATTGGTGA GGAAGATCAT TATCGTAAAG CGTATGCACA CTTTATACAT CAATATATGA      300

AACAAGCTGC ACCTTTTATA GAGGCGGATA TCTTTAATTC AGAATCAATC GCATTGGTTC      360

GCCGTGCCAT TATTAAGACA TTAAATAGTG AAAATTATCA TTTAGTTCAG TCGGCTATCG      420

ATGGCTTAAT CTATCATATA CTCATTGCCA TTCAGCGTTT AAATGAAAAT TTTTCGTTCG      480

ATATACCTAT CAATGAAATT GATAAATGGC GACATACTAA TCAGTATGCn ATTGCTTCAA      540

AAATGATAGA AAACTTAGAA CGCAGTGTAA TGT                                   573
```

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1221 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
TTGATATTTA TAACGTTATA TTTTAATAGT TCACCTGGAT TATTAAATAA ATAGTCCGCC       60

AAATTTTCTT TTTCTTTATC AATCTGaTkG TAATTAACaC TTTCGaCTTC TGTAGGAATT      120

CTAATGTCAA CAGAAGCATT GATATAAGCT TGATGTTGCA TGCAATCACA CTCCTAATCC      180

TTCATmTmAA ACGGAGAAGT AAACCCGTCA CTATTCAAAT TCAATCCTTT TGCCCAATCA      240

ACAGGCTTAT TCATGATAGT TTCGATTTCC TTAAGTCCAT TTGAACCTCT AGGTATTTCT      300

ACAATTACTT CATCATGGAC ATGGCCAACT ATTTTAAAAC CTAATGCTTC AAGCCTTGCT      360

ATAGAAATCG CAAGTAAATC CCTTGCAGTT GCTTGAACAA TATTCTCGAC TAACTTCCCA      420

CCATACGTTT TTAACTTTGA CCATTTACGG TTAAGATCTA ACCCCATAAA TTCAACAACT      480

TGACTACCCC AACTATTTTC ACCAACTAAA GCTTTTGGAT AAGCTAAAGC TCTTCCACTA      540

GGCAGTTCAA TCATTAGAAA ACCTTTTTTC ATATAAAATC TAAGTCCATG TGTATGATGC      600

GTCTTTCGGG ATTTTACAGT ATTAATTGCA GCCTCTTGGC AAGCCTTCCA AAAATTAACT      660

ATGTTAGGAT TTGCGTTACG CCAACTATCA ACTAAACCTT GTAACTCGTT TTCTTCAATG      720

CCCATTTCCA ATGCACCCAT TGCTTTTAAA GCTCCAGCGC CACCTTGATA GCCTAAAGCT      780

AATTCGGACA CTTTTCCTTT TTGTCTGAGA GGGTCGCCTT TAGTTATGCT TTCTACCGGT      840

ACATTAAACA TTTGAGAAGC CGATGCTTCA TATATCTTTC CGTGTGTGTT GAATACATCT      900

AAACGCCATT GTTCTTTTGC ATACCATGCT ATGACTCTTG CCTCTATTGC AGAAAAATCA      960
```

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AGATCTCTTG CTATTTCTAA TTCAGTATCT GAAATATAAT GCTTTGTTAA ATTCTGAAGT      1140

TGTACACCTC TACCTGCCCA TCTTCCAGTA CCGGCACCGT AAAATTGAAA CAGACCTCTT      1200

ACCCGTTCAT CACTGCACAT C                                               1221
```

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1090 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
TTTTGTTTGG TATGAGGTAG CAATGACGAC GTGTCATTGG TGGAGATTGT AAAAATACAT        60

AATAAAAAGA AGCGGCAATG TATACCGCTC CTTTTTTATA CTACATACCG ATTTTCAACC       120

ATCTCTTTCT ACTTAGTAAT AAGACAATAG TATTAACTAT AAATAGAAGA ACGAAGAATG       180

ATACTATATT TATAATTTCA GTAGGACACA TAAATGTTGA CTCGTTATTC AATATTTTTT       240

CTACGGCACG ATACATCGTA TTGCTCGCCT CAAATGGAGC AACGATACCA AATATATTTT       300

TATTAATGGC AACTAAGATG ACTGAACCAA TCCAATATAC AATGCTGATA CCTAAGCTGA       360

TTAAAATGTT AGGTGAAACC ATACTAATCG TTCCAACAAC TAAGATATAT TGTAAGATAA       420

CGAGTGAAAA TAAGATTATT AATAGTAAGT AATGTGAGAA ATCCGAATAT ATAATTGAAA       480

TAATAGTGAT ACTTAGAATT ATGAACACTA AACATTCAAA AAATAACACT GCTACCTTTT       540

TATAGAAGAA GGTAAAGATA TTATCGCCAA TCAATTTATA AAACAGGATA TTTTTATTCG       600

AATACTCTTT ATTAATAAAA TATGCAATAA CAAATGAAAA TAGTAAGAAC CCTAATTGCG       660

TTGCAACAGT ATATGAACTG AAGAAAAACT GGCTATAGCT TAAACTTTTA ACTTTGTCTA       720

TACCTATTGG TAAAAAATAC CCAAGTAAGA AAAGGAATGT GAATAGCACA ACAAGCGTGT       780

AAATAATTTT ATTGGAAATA CTTTTTTTAA ATTCTAATTT CAAAGTGGAC ACCTCAATTA       840

TAAATTAATG TAATCATTTA TGACTTCTTC TTTTGATTGG TACTCTTCTA TTTGAAGGTC       900

TTTAAAAATA AAGTATTTAC CCGGCAAAGC ACTTAAATCG GATAAATTaT GTGTAATATT       960

GATAATAGTT TTAGTTTGAT GGCTTTGAAT AAAATCATTT AAAAATTCAT AAATTTCATT      1020

AACTGTTTTC TTGTCTAAAG CGTTTGTAAC TTCATCTAAT ATGATTAAAT CATGATCTTC      1080

CAATAAGAAA                                                            1090
```

(2) INFORMATION FOR SEQ ID NO: 10:

```
        (A)  LENGTH: 904 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: double
        (D)  TOPOLOGY: linear
```

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      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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TTAGGACTAT TTTATCATAT TCATTTAAAT TACGGCTAAA AATTTTAAAA ACGGGGATTA      60

ATATATGGAA TTAAGCTATG AAAGTTAATT GATACTTGCA TTTTACGCTG ATTTATATAA     120

GAATAACTAT TGTATAGTTT TAAAAACGAA CGTACGTTTG CAGGAGGCGA AATCATTGGC     180

AATGAATAAA CAAAATAATT ATTCAGATGA TTCAATACAG GTTTTAGAGG GGTTAGAAGC     240

AGTTCGTAAA AGACCTGGTA TGTATATTGG ATCAACTGAT AAACGGGGAT TACATCATCT     300

AGTATATGAA ATTGTCGATA ACTCCGTCGA TGAAGTATTG AATGGTTACG GTAACGAAAT     360

AGATGTAACA ATTAATAAAG ATGGTAGTAT TTCTATAGAA GATAATGGAC GTGGTATGCC     420

AACAGGTATA CATAAATCAG GTAAACCGAC AGTCGAAGTT ATCTTTACTG TTTTACATGC     480

AGGAGGTAAA TTTGGACAAG GCGGCTATAA AACTTCAGGT GGTCTTCACG GTGTTGGTGC     540

TTCAGTTGTA AATGCATTGA GTGAATGGCT TGAAGTTGAA ATCCATCGAG ATGGTAATAT     600

ATATCATCAA AGTTTTAAAA ACGGTGGTTC GCCATCTTCT GGTTTAGTGA AAAAAGGTAA     660

AACTAAGAAA ACAGGTACCA AAGTAACATT TAAACCTGAT GACACAATTT TTAAAGCATC     720

TACATCATTT AATTTTGATG TTTTAAGTGA ACGACTACAA GAGTCTGCGT TCTTATTGAA     780

AAATTTAAAA ATAACGCTTA ATGATTTACG CnwGGgTAAA GAGCGTCAAG AGCATTACCA     840

TTATGAAGAA GGGAtCaAAG rGTTgTTAGT atGTCCAaTG ArGGAAAAGA AGTTTTGCCT     900

GACG                                                                 904
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(2) INFORMATION FOR SEQ ID NO: 11:

```
        (i)  SEQUENCE CHARACTERISTICS:
             (A)  LENGTH: 11271 base pairs
             (B)  TYPE: nucleic acid
             (C)  STRANDEDNESS: double
             (D)  TOPOLOGY: linear
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      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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GATTTCTAAA TCAAGATCTG TTTTACGATA ACCATTCAAA CCTTGACGTT CATCTTCTTC      60
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TTAATAAGAC GATTCAGCAA GTTTTAAAGT ATTATTTGAC TATGTTGGAT TAGGCATCTA    300

GTCCTATAAT ATCACTGACA TTGTCAAAAT GATGATCTTT TAAGTAACGT GCGATGCCTT    360

TGTTCATTTT CTTAGTTAAA CCTGGGCCTT CAATAACAAG TGATGAATAA ATTTGAATAA    420

GTGACGCACC GTGACGCATC ATTTTGATTG CATCTTCAGT ACTGAATACG CCGCCTGTAC    480

CTATAATTAA AAATTCACCA TTTGTTTGCT GATAAgCATa CTTAATCAAT TTTAAATTAC    540

GTTCAAATAA TGGACGACCA CTCAAACCGC CTTCTTCGAC TTTATTAGCA GAAGTTAAAC    600

CATCTCGTTG TCGCGTTGTG TTTGCTAAGA TGATACCGTC AAATGTCTCA GTAATCGCTG    660

GTAATAGTGC TTTTAAGCCA TCGAAATCCA TATCAGACGT TAGTTTTAAA TAAATTGGCA    720

CTGTTACATC ATGTTGTTTT TTAAATGCTG TTAAAGCTTG GCATAACATT GAAAATTCAT    780

CTTTATCATG GAAGTTTTGA AGATTTTCAG TATTTGGAGA ACTGATGTTG ACTGTGAAAA    840

ATGAAACGTC GTGTTTAAAC GTATCAATAA CCTTTATATA ATCTTGATAA CGCGCTTCAT    900

AAGGTGTCAT TTTATTCACA CCAACATTGA TACCAACAGG TACTTGATAA GCATTTTTAC    960

GCAAATGACT TAGTGCTTTG TTCATACCAA TATTATTGAA GCCCATTCGA TTTATCAAGG   1020

CGTCATCTTC TAATAATCTA AACATGCGTG GTTGAGGGTT ACCCGGTTGA GGTTTAGGTG   1080

TGATACCACC TAATTCTAAA GCACCGAATC CAAGGTGTTC CAATGCTTTT GGTACTTCGC   1140

AAGATTTGTC GAAACCAGCT GCTAAgCCAA TTGGATTGTC GTACGTATTA CCTTGTATCG   1200

TTTGTGATAA CGTTGGATTC TTATAAGTAA ATAGTTTATC GACGACTGGG AATAAAACCG   1260

GaAACTTTTG TaACGTTTTT AATGCATCGA TAGTTAGTCC GTGTGCTTTT TCGGGTTCGA   1320

TTTTGAATAA GAAAGGTTTA ATTAATTTGT ACATGAGTAT GCTCCTATTT CATTATATTT   1380

GAGGCTTACT ATCCTCAACT TAATATATGT GAAATATATT CTTTTAATAG ACTAGCATTT   1440

CCATĂCATAA TTTCCTAGTT AAAACTAAAA AGTTTTGAAA ATTGACGCAA gTTTGAATAA   1500

CGTTTTTAAG ATTAAATCAT CCTAATTAGG CAATATTATA GTATAAAGTA AGTAGATTGG   1560

AAGGTGTTTG TATGAATGAA CAATGGTTAG AGCATTTACC TTTAAAAGAT ATTAAAGAGA   1620

TTTCACCAGT GAGTGGTGGT GATGTAAACG AAGCATATCG AGTCGAAACA GATACGGATA   1680

CATTTTTCTT ACTTGTCCAA CGTGGACGTA AAGAATCATT TTATGCTGCA GAAATTGCAG   1740

GTTTAAATGA ATTTGAACGT GCAGGTATCA CGGCACCTAG AGTAATTGCA AGTGGCGAGG   1800

TTAACGGTGA TGCGTATTTA GTGATGACGT ATTTAGAAGA AGGGGCTTCA GGGAGTCAAC   1860

GCCAATTAGG GCAACTCGTA GCTCAATTAC ACAGTCAGCA ACAAGAAGAA GGCAAATTTG   1920

GCTTCTCATT ACCTTATGAA GGTGGCGATA TTTCTTTTGA TAATCATTGG CAAGACGATT   1980
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GGCTATGGGA TGCCAACGAT ATCAAAGTAT ATGACAAAGT GCGACGTCAA ATTGTGGCGG        2100

AATTAGAAAA GCATCAAAGT AAACCGTCTT TATTACATGG TGACCTATGG GGTGGTAATT        2160

ATATGTTCTT ACAAGATGGT CGTCCGGCGT TATTTGATCC AGCGCCATTA TATGGTGACA        2220

GAGAATTCGA TATCGGTATT ACAACGGTAT TTGGTGGTTT TACGAGCGAA TTTTATGATG        2280

CGTATAATAA ACATTATCCA CTCGCAAAAG GTGCATCCTA TAGACTTGAA TTTTATCGTT        2340

TATATTTATT GATGGTCCAT TTATTGAAAT TTGGTGAGAT GTACCGTGAT AGTGTTGCGC        2400

ATTCTATGGA TAAGATTTTA CAAGATACAA CAAGTTAGTT AAGACGTTAG ATTGAGATAA        2460

ATAGATAATA TGCACAGATA TTTTTACAAT GAGAAGCGAT ACAGCTGCCT CAATAAAAAT        2520

ATTTGTGCGT TTTTATTGTT GGAAAATAAA ATTTTAATCG CTATTGTTAA TTTCTGTAAT        2580

GTAAAACAAG GTTGAGTTAC AATAAAAGTG ATTTTATAAC TTTTTGTTCA ATAAAATTCT        2640

AGGAATGATA CATATTTATT GATACAATAA TTTTGAATAT AATCATAAAA CAATATTTAA        2700

GTATAATTGA ATGTTTGAAT ATCATATATT GATACAGTTT CTAATAATTT TAAAATAATT        2760

TAAATGGAGA GAGGTGTAAA TGATGAGTAC AGTTCAAAGT GATATTTTTA AGACCAATAG        2820

TGCATCATCA TCTATTAAAA GCGCTGTTGA AACATGTAAT AATGTGTCGA AACCGGATAA        2880

AGATGAAAGT ACAACAGTAA GTGGAAATAA TAATGCTCAT AGTGTGATAG ATGATTTGAT        2940

GAGTAAGAAT CAATCTGTTG CTGAAGCAAT ACGAACTGCG AGCGATAATA TACAAAAAGT        3000

TGGTGAGGCT TTTGACCAAA CTGACGTAAT GATTGGTAAT GAAATTGGTA AAAATTAAAA        3060

CGTGGTGAAA TGATGTCGAA TAAACTGGAT GAAATCAATA AAATAATCAC AGCGAAACAT        3120

GAGCAAATGG ATGACTTATA TGATGAAAAG CGAGAGGTTA AAGCATTGAT AGATGAAAGT        3180

GATGCGCTTA ATCATTCGAT AGATCAATTA TATCAACATT TAGGTGAGCG TTATTATAGT        3240

AGCAATATGG CTAGTCGTAT GGAACAGTTC CGCGATGAAT TTCATTTTGC GAAACGACGT        3300

TCAACGGAAG CGTTATACGA GCAGCAACAG CAAATTCAAC ATGGCATTCG TAAAGTGGAA        3360

GAAGAGATGA TTGACTTGGA AATGCGAAGG AATGTTGAAA TTGAGACGGT GACAAAGGAG        3420

GAAAATAAAT GGAAACAATA GGAAGCATTA TTTATTTAAA AGAAGGTTCG CAAAAGTTAA        3480

TGATTATTAA TAGAGGmCCA aTTGTAGAAA TTGAAAATCA AAAGTATATG TTTGACTATT        3540

CTGCATGTAA ATATCCGATT GGTGTTGTAG AAGATGAAAT TTATTATTTT AACGAGGAAA        3600

ATATAGATTC AGTTATTTTT AAAGGTTATT CTGATCAAGA TGAGGTTAGA TTTCAAGAGT        3660

TGTTTGAAAA TATGAAACAA AATTTGGATA GTGAAATACA ACGTGGAGAA GTTACACAAC        3720
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ATGTCATTCA TAATCATTTG AACTAAACGT AGCAGCCTTA AATTTTAAAA AAAGACACAT   3900

ACCAACTTCC GAAATGTAGA TGAATTCTCT ACAATAACGG AAGTTTTTCT TTTAATATTG   3960

AAATTTCTCA AGGATAGGTC TATACTTTAT AAATCGTAAT TATTACGATT TATAATCAAA   4020

AACAATAACT TGAAATAGAT CATTGAGGGA GTGTTAATAT GCAACATCAT AAAGTGGCTA   4080

TTATcGGTGC CGGTGCTGCA GGTATAGGTA TGGCCATTAC CTTAAAAGAT TTCGGTATAA   4140

CAGATGTCAT TATTTTAGAA AAAGGAACAG TAGGACATTC ATTTAAACAT TGGCCGAAAT   4200

CGACCCGTAC GATCACGCCA TCATTTACGT CTAATGGATT TGGCATGCCT GATATGAATG   4260

CAATTTCCAT GGATACTTCA CCAGCATTTA CATTTAATGA AGAACATATT TCCGGAGAAA   4320

CATATGCTGA ATATTTACAA GTGGTTGCCA ACCATTACGA GCTGAATATC TTTGAAAATA   4380

CAGTTGTCAC AAATATATCT GTAGATGATG CATATTATAC GATTGCAACG ACAACAGAGA   4440

TATATCACGC GGATTATATC TTTGTCGCAA CAGGTGATTA TAATTTCCCT AAAAAgCCAT   4500

TTAAATATGG TATTCATTAT AGTGAAATTG AAGACTTTGA TAACTTTAAT AAGGGGCaAT   4560

ATGTGGTTAT CGGAGGTAAT GAAAGTGGCT TTGATGCTGC ATATCAACTT GCAAAAAATG   4620

GCTCTGACAT CGCACTTTAT ACTAGCACAA CCGGTTTAAA TGATCCGGAT GCTGATCCTA   4680

GTGTTAGATT GTCACCTTAT ACACGTCAGC GACTAGGTAA TGTCATTAAG CAAGGTGCTC   4740

GCATCGAAAT GAATGTACAT TATACAGTTA AAGATATTGA TTTTAACAAT GGACAGTATC   4800

ATATCAGTTT TGATAGCGGA CAAAGTGTGC TTACACCTCA TGAACCAATA CTAGCAACTG   4860

GCTTTGATGC AACAAAAAAT CCAATCGTTC AACAATTATT TGTGACAACA AATCAAGATA   4920

TTAAATTAAC AACACATGAT GAATCGACAC GTTATCCGAA TATTTTTATG ATTGGTGCAA   4980

CAGTTGAAAA TGATAATGCC AAATTATGCT ATATCTATAA ATTTAGAGCG CGATTTGCAG   5040

TACtTGCACA TCTTTTAACA CAGCGGGAAG GcTTACCAGC TAAACAAGAT GTCATTGAAA   5100

ATTATCAAAA AAATCAAATG TATTTAGATG ATTATTCATG TTGTGAAGTG TCATGCACAT   5160

GTTAGAAGTG AAATATGATA TGAGAACTGG GCATTATACG CCCATACCTA ATGAACCTCA   5220

TTATTTGGTT ATTAGTCATG CGGATAAACT TACCGCAACA GAAAAAGCGA AATTAAGATT   5280

ATTAATCATA AAACAGAAAT TAGATATTTC ATTGGCAGAA AGTGTAGTTT CTTcGCCTAT   5340

AGCGAGTGAA CATGTGATAG AACAATTGAC ACTATTTCAA CATGAGCGAC GACATTTAAG   5400

ACCTAAAATA AGTGCGACAT TTTTAGCCTG GTTGTTGATA TTTTTAATGT TTGCATTGCC   5460

AATCGGTATC GCTTATCAAT TTTCAGATTG GTTTCAAAAT CAGTATGTGT CAGCATGGAT   5520

AGAATATTTA ACTCAAACAA CATTGCTCAA TCACGATATA TTACAGCATA TATTATTTGG   5580

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ATTGATTAGT TTATCAACTG CTATAATTGA TCAAACAGGA CTCAAATCAT GGATGATATG        5700

GGCAATTGAA CCGTCAATGT TATGGATAGG ATTACAAGGT AATGATATCG TGCCACTATT        5760

AGAAGGGTTT GGATGTAATG CAGCAGCTAT TTCACAAGCA GCACACCAAT GCCATACCTG        5820

CACGAAGACA CAGTGTATGA GTTTAATAAG CTTTGGTAGT TCTTGTAGTT ATCAAATAGG        5880

TGCGACATTA TCTATTTTTA GTGTAGCTGG AAAGTCATGG CTATTTATGC CGTACTTAAT        5940

ATTAGTACTT TTAGGTGGCA TCTTACATAA AGGATATGGT TGAAAAGAA TGATCAACAA         6000

CTTAGCGTTC CGCTACCTTA TGATAGGCAA TTACATATGC CAAATATACG TCAAATGTTG        6060

CTACAAATGT GGCAAAATAT ACAAATGTTT ATCGTTCAAG CGCTACCTAT TTTTATCACA        6120

ATCTGTCTTA TTGTTAGTAT TTTATCACTA ACGCCAATTT TGAATGTTTT ATCACAAATA        6180

TTTACACCTA TATTATCGTT ATTAGGCATC TCGTCAGAAT TGTCACCAGG GATTTTATTT        6240

TCAATGATTC GAAAAGACGG CATGCTCTTG TTTAATTTGC ATCAGGGCGC CTTATTACAA        6300

GGAATGACAG CAACACAGTT ACTACTACTT GTGTTTTTTA GTTCAACATT TACAGCGTGC        6360

TCGGTCACAA TGACGATGCT TTTGAAACAT TTAGGTGGTC AGTCAGCACT AAAATTAATT        6420

GGAAAGCAAA TGGTGACATC ATTGTCTTTA GTTATTGGTG TAGGCATCAT TGTTAAAATA        6480

GTAATGCTGA TTATTTAAAA AAAATGAACT ATAACTGAAT ATAGAGTCAT GTCAGTCAAT        6540

AGGAGATCTA TCTTGGAATA TGCTATTCAT ATGAAGTATA AGAGGAGAGT CGCAGATGAA        6600

AATAGTTATT ATAGGTGGGT TTTTAGGTGG CGGTAAAACG ACTGTCTTAA ATCATTTGCT        6660

CGCTGAATCA TTAAAGGAAT CGCTGAAACC AGCAGTCATC ATGAATGAAT TTGGGAAAAT        6720

GAGTGTTGAT GGTGCCTTAG TATCTGAAGA CATACCTTTA AGTGAACTGA CAGAGGGGTG        6780

TATCTGTTGT GCAATGAAAG CAGATGTATC AGAACAGTTA CATCAATTAT ATTTAAAAGA        6840

GCAACCAGAC ATTGTATTTA TTGAATGTAG TGGGATTGCA GAACCGGTCT CTGTCTTAGA        6900

TGCTTGTTTA ACGCCTATTT TAGCTCCGTT TACAACAATT ACACATATGA TTGGTGTAAT        6960

AGACGCAAGC ATGTATAAAC ACATTAAATC ATTCCCTAAA GACATCCAAG GCTTATTTTA        7020

TGAGCAATTA GCATATTGTT CTGTCTTATT TGTTAATAAA ATAGATTCAG CAGATGTTGA        7080

AACAACGAGC AAACTATTGA AAGATTTAGA AGTTATTAAC CCAGAGGCCG ATATACAAGT        7140

CGGTATGCAT GGCAGCGTCA CTTTGCCAAT ATCAGTTAGA CAAATGACAG CAACTTCTGA        7200

CAATAAACAT AAGTCTTTAC ATCAAATGAT TAATCATCAA TTTGTGCAAT CACCAGTCAA        7260

ATGTACTAAA GCAGAGTTTA TAAAACGTTT AGCATGCCTT CCGTCTCATA TTTATAGGTT        7320
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CGGAAAGGGT ATTTCAAAAG AAGACTATCA ATGTTTGGAA CAGTAGTGTT TTCAGTGGAA   7500

GAGAATGGTT AACATGCCTT CATGTATAAT AACGAGTTGA TTTGAACGTT TAAGCGTAAA   7560

TAAAAATAAG CTTGGTCAGC CATCAAATAT AATTTGAAAA CTGTCCAAGC TGTTTTATTA   7620

GAGAACAATC AATTAACCCC ACATATTTAA TAATACATCA GCAAAGCCTT CAGGTTTTTG   7680

AATATAACCT AAGTGACCGC CTGGAATATC TACAATAGGT ATGCCAGTTT CTTTATTTAT   7740

ATAAAGTTA ACATCTTGTG GGAAGGAGCC TCTAGAATCT GTCCCATTTA GTAGGGTGAT   7800

TTTATCGCTG TATTTTGTGA AATCATCCAA AGTAATATCT GAATGCGTAT ATTGTCTAAT   7860

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AGCAGGTTGA GACATCATTT TTGCATCAAT TGGTGCGATA TTTAATGTTT CGCCAAATGT   7980

TTTCATGCCT TTTTCTAAGC CTTCTGTTAA AATTTGATGC ACAATGTCAT CATTTTTATC   8040

TTTCCAATAA GTACTGTCTG GTAAAAATGT ATTAATTGGT GGTTCGTGAA ATGCAATCTT   8100

TTTAACGACT TCAGGGTAAT CTTTTAACAC ATGCATCGCA ACGATTGAAC CTGAACTTGA   8160

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCCTGTGC   8220

GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT   8280

TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA   8340

CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG   8400

CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC   8460

CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT   8520

TTGTATAACT TATTTTCTCT TTTTCTTCAT CTGTTAAACC CAGTTCATCT AAAAATACAC   8580

CTAATTTTTC AGGCTCAATA TATGGATAAT CAGCAGCATA AAGAATTCTA TCAATACCTA   8640

CTTCTTTCTT GACTAAATCA AACTGTGGCT TCGTTAACAT GCCACTCGGT GTGATATAAA   8700

AATTATTTTT AAAGTAATAG CTTACAGGGT GGTTCAAATG TTCAGCGAAT AAAGCTTCAT   8760

CCATACGTTC TAAGAAGAAT GGGATAAACT CACCCCAATG TCCAATAATC ATATTTAACT   8820

TTGGATAACG ATCAAAAATA CCAGATAATA CTAGATGTAT TGTATGAATG CCGACATCAA   8880

TGTGCCAACC ATAACCAAAA CAAGCAAATG TTGCCGCAGT TACTTCAGGA TAATTTCCTT   8940

TATAGTATGA TTGATAAATG TCACTGTTAA CTGGCGCGGG ATGTAGATAA ATCGGTACGT   9000

CTAAATTTTC AGCTGTTTTG AAAATAATGT CATATTTGTC TTGATCAAGA AAACCATCTT   9060

GTGCACGTCC CATAATGAGC GCACCTTTGA ATCCTAAATC ATTGATGCAA CGTTCGAATT   9120

CTCGCGCTGC GGCTTCAGGC TCATTGATAG GTAAAGTTGC AAAGCCTACA AAGCGATTGG   9180

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TCTGACCAAC CAAATTTGAA GGAGAACCAT TTCCATAAGA TAAGACTTGA ATTTGAACGT    9300

CTTGATTATT CATAAATTGG ATACGTTCAT CATGATGTGA TAATTCGTCG GCATTTGTAA    9360

AACCTGTCTT TTTTTcAAGG CCTTCTAACA TTACTTTCAT CGGTACACCT TTAGGATCTG    9420

CTGATATCGC ATTCATCGTT TCTTTTTGAA TATCTTCAAT GACATAATGT TCTTCAAACG    9480

TAATACTTTT CATTTACTTC GCCTCCATAT TGTATTGCAT GTTTATTGCA TCTATTGCAG    9540

AAGCATTTTT TATATACCTC TAATTTCAAT GTTTGTAACA TAAAATTGAT CTACCAAGGC    9600

ATCTCTCCAT CGCCATTAAT AAATGTACCT GTTGGGCCAT CTGCACCAAT CGTTGCTAAT    9660

TGAATGATTG GCTTGATTCC TTCAGAAACG TGTTTGGAAT TATTACTAAA ATCACCAACT    9720

AAATCAGTAT TTGTAGCGCC TGGATCAGCA GCATTGATTT GCATGTTAGG TAATCCTTTA    9780

GCGTATTGTA GCGTTAGCAT TGTTACTGCC GATTTAGACG AACAATAAGC TAATGAATTC    9840

ACTTTAGATT CAGCTGTTTC GGGGTTTGTA ACCATTCCAA ATGAACCTAA ACCACTTGAT    9900

ACGTTGACGA CAACAGGTTG TTCAGATTTT TCTAAGAGAG GGACGAATGT ATTCATCATT    9960

CGTACGATAC CGAATACATT CGTTTGATAT ACTTCTTCAA CGTCACGAGG TGTCAATTTG   10020

GAAGGTGCTG AAAAATTGACC AGATATACCT GCATTGTTAA TGAGGATATC AAGACGGCCT   10080

TCTTTTTCAG CAATCATGTT ATAAGCATTT TTGACTGAGT AGTCACTTGT AACATCTAAT   10140

TGTACATAAT GAACACCTAA TTTTTGTGAT GCTTGTTGTC CTCTTACATC ATTCCGAGAA   10200

CCTATATAAA CTTTGTAACC CAATGCTTTA AGTGCCTCTG CACTTGCATA GCCTAACCCT   10260

TTATTGCCTC CTGTGATTAA CACAATTTTA GTCATTACGT CCCACCTCAT CTAAATAAAT   10320

GTTTAATAAA TAATTTCTGT ACGCTTCAAT TGAAATATGG CGATGCTCTA TTTGGAAGGC   10380

AAATACACTA GTTGATAATG ATTGCAACAG CATATCTGTT TTGAAtTCGT GTAAGTGTCG   10440

TCATCGCTTT TAAATAAGTC ATAATAAAAA TCAAATAATT CTTGATAAAA TGCGCTTTGG   10500

TAAAAACGTA ATTTATTGTT GCCTGCTTCA ATACATTGCA GTAGTGCCTT ATTATCGATT   10560

TTAAATTGTA AAAGATAATC TAACGACACT TGCATAACCT CATAATTAGA ATGATAGTCA   10620

TCTTTAATTT GCTTAAAATG AGTGATAAAA ATATCAAGGT CTCTTTGTAT GACGTAGTAG   10680

CATAAATCGC TTTTATCTTT GAAATGTCGA TACAATGTCC CCATACCGAT ACCTAGTTCT   10740

TTAGCAATAC GATTCATACT AATGTTTTCA ACGCCTTCTT CATCAAAAAG TTTGTGCGCT   10800

ATTTCTTCAA TTCGTTGCCT ATTCTCTTTT GCATCTTTTC GCATGATTAC ACCTACTTAA   10860

AATTCTCTAA AATTGACAAA CGGATAACTC TCCGTTTATT ATAAAACGTG TTAAGAAAGT   10920
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ACCTTATCGG TTCAAATGAT TGCTGAAAAA CTGAATGTCA CTACAGAAGA TGTGGAAAAA    11100

GTATTAGCTA TGACAGCGCC ACTAGGCATT TTTAGTCATC AATTACAACG ATTTATTCAT    11160

TTAGTATGGG ATGTCAGAGA TGTAATAAAC GACAATATTA AAGGAAATGG ACAAACACCA    11220

GAACCATATA CGTATTTAAA AGGTGAAAAA GAGGACTATT GGTTTTTAAG A             11271
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(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6261 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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CAACCCGTTC AGAACAAAAT AAAAACCGTA CAATTTTATC ATCTTAATGA TTATTGTACG      60

GAAAAACTTT TTTACATCAT ATCTGCATGT GCATAATCGA TATCGGTAAA TTTATTATAT     120

TGTTTCATAA AATGTAACTT AACTGTGCCT GTTGGACCGT TACGTTGCTT AGCAATGATA     180

ATTTCAATTT CACCGTTTTC ATCATTCGTT TGTGGCTCGA AACCACCATC ATCGTCATCA     240

TCTTCATCGC CGCCACGGTT ATAGTAATCA TCACGGTATA AGAATGCAAC GATATCGGCA     300

TCTTGCTCAA TCGAACCAGA TTCACGAATA TCACTCATCA TTGGACGTTT ATCTTGTCGT     360

TGTTCAACAC CACGAGATAA CTGACTTAAT GCGATAACTG GACATTTTAA TTCACGGGCT     420

AATGCTTTTA ATGTACGAGA GATTTCAGAA ACTTCCTGTT GTCTGTTATC GGACGCACGT     480

GAACCACTAC CTTGAATCAA CTGTAAGTAG TCAATCACAA TCATGTCTAA GCCATGTTCT     540

TGCTTTAATC GACGACATTT AGAACGTAAA TCATTAATTC GAATACCCGG TGTATCATCA     600

ATAAAAATCT TCGTACGTGA TAATTTACCT ACCGCTATAG TAAAACGACT CCAATCTTCC     660

TCAGTCATAG TACCCGTTCT TAAGCGGTTT GAGTCAACAT TTCCAGAACT ACAAATCATA     720

CGTGTGGCTA ACTGATCAGC ACCCATCTCT AGCGAGAAAA TACCAACTGT ATACATATCT     780

TCATGCGTTG CAACTTTTTG TGCAATATTA AGTGCGAACG CAGTCTTACC TACAGATGGA     840

CGCGCTGCAA GGATAATTAA ATCATTTCGG TTGAACCCTG CTGTCATTTG GTCTAAATCT     900

CGATATCCTG TAGGTATACC TGGTGTTTGA CCACTATTTT GATCAAGCTC TTCAGCTGTT     960

TCATACACTT GTCCTAAGAC GTCTCGAATG TCTTTAAAGC CATCGCTTTC ACGAGAAGAT    1020

GATAGCTCTA AAATTCGACG TTCTGCATCA CTTAAAATCG CATCTAGTTC AAGTTCATCA    1080

TTATATCCAT CATTGGCAAT ACTATCTGCA GTTTGAATCA ATCTACGTTT TAATGCATGC    1140
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TCTGCAAGAT ATTGCGGGCC ACCCGCTTcA TTCAACGTAC CTTCCGTCGA TAATTGATCC      1260

ATCAATGTTA CAACATCAAT TTCTTTATTA TCTTCATTTA AGTGCATCAT TGCACGGAAA      1320

ATATGTTGAT GGGCACCCCT ATAAAACGAC TCAGGAAGCA AAACTTCCTG AGTAGTATTA      1380

ATCAATTCTG GATCTATAAT AATTGAACCT AAGACAGACT GTTCAGCTTC ATTGTTATGC      1440

GGCATTTGAT TTTGCTCATA CATTCTATCC ATGAATGGTT ACACCTCTTA TTTCAATCCA      1500

ACTTTATTGT TCAACTGTGT GTACGCGAAT TGTACCTTCA ACTTCTTTAT CTAATTTAAC      1560

AGGTACATTC GTATATCCTA GGGAATGAAT TCCATTTGGT AAATCCATTT TACGTTTATC      1620

AATTTTAATA TCATGTTGTG CTTTTAGTGC TTCGGCAATT TGTTTTGTAC TTACTGACCC      1680

AAACAATTTA CCACCTTCAC CAGTTTTTGC TGaTACTTCA ACTTCAATGT TTGATAACGT      1740

TTCTTTTAAT GCTTTAgCAT CTTCAATTTC TTGTTGGCGT TCTTGTTTTG CACGTTTTTT      1800

CTGTAACTCT AATTGTTTAA GGTTACCTGG TGTTGCTTCT ACAGCATAAT TCTTTTTCAA      1860

TAAGAAGTTA TTTGCATAAC CTACTGGTAC TTCTTTAACT TCACCTTTTT TACCTTTACC      1920

TTTACCTTTA ACATCTTGTG TAAAAATTAC TTTCATGCAT CTTCACTCCT ACTTAATTGT      1980

TCTGTAATTG CTTGTTGTAA TTGTGCTATC GCCTCTTCGA CTGTCACACC TTTAAGTTGT      2040

GTTGCCGCAT TGGTTAAATG TCCACCGCCA CCAAGTGCTT CCATTGTTAA CTGGACATTT      2100

ACTGAACCGA GTGAACGCGC AGATATACCA ATCAGATTAT CTTCACGTCT CGCAACAACA      2160

TATGATGCTT CAATACCTTC TAAACTTAAC AGTTCATCTG CTGCTTGTGC AACTGTTACT      2220

GGATGATAAA TTTTATCGTC TGAACCATGC GcAATGGCTA TGCCATTATC TTCAACTTTT      2280

ACAGTTCGAA TTAATTCAGA TCGATTAATG TAAGTATCCA CATCATCTTT TAAGAAATGT      2340

TGCGTTAAAA TCGTATCTGC ACCATGTGCA CGTAAATAAC TCGCTGCATC GAATGTTCTT      2400

GATCCTGTTC GTAATGTAAA GTTTCTTGTA TCTACAATAA TACCTGCATA CATCACTGTT      2460

GATTCAAGAC GTGTTAAACG TTGTTCTGTT GGTTGATATT CCAGTAACTC TGTTACCAAT      2520

TCAGCTGTCG AACTTGCGTA TGGTTCCATA TATATCAACA ATGGATTAGA GATGAAGCTT      2580

TCACCACGTC TATGATGATC GATAACAACT TTACGGTTTG CTTTATTTAA GACATTTTCA      2640

TCTAAAACCA GTTCCGGTTT ATGCGTATCA ACAATCACTA CGGTTGTCTT AGATGTCATC      2700

ATATCCCAAG CATCATCTGA TGTAATAAAT CGCTCTCTTA ACTCTGGCTT TTTATCTATT      2760

TCGTTCATCA CGCGTCGTAA TGTTGGATCA ATGTCAGTCT CATTTAATAC GATGTATGCT      2820

TCTAAATTAT TCATCATTGC AAATCTAGAC ACACCGATTG CTGCACCAAT TGCATCTAAG      2880
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CCATAGAAAC GCACATTACC ATTAATACTT TTAATTGCAA CTTGGTCGCC ACCGCGTCCT   3060

AATGCTAAGT CTAGGCCTGA TTGTGATAAT TCACCTAAGT CGATTAAATT TTCAGTACCT   3120

TCACCAACAC CGATACTTAA TGTTAATTGG GCACGATAAC CAACACTTTT TTCACGTAAT   3180

TGACTCAAGA TATCAAATTT AGATTCTTCT AAGTCAGCTA ATATTTTTG ATTTAAATAG   3240

GCTACGAATT GATCGGAACT GTATCTTTTG AAAAATATAT TATACTCAGT TGCCCATCGA   3300

CTAATGACAC GCGTTACCAT TGAGTTGATT TCCGAACGCT GCGTATCATT CATATTTTGC   3360

GTAATCTCAT CGTAGTTATC TAAAAATAAT GTCGCAATGA TTGGTTTAGA ATTTTCATAT   3420

AGTTCATTTG TTTGTACTTG TTCAGTTATA TCAAAGAAAT AGAGGCAGTG ATCATTCTCA   3480

GAATAACGTA CTTGGAAATG ATACTGATTA TATTCTATTT cAACGGATTT CACTCTATCT   3540

AATTGCTTTA AAATGTTTGG AAATACTTCA TTTACAGATT CAGAAATGAC ATTCGCTTCC   3600

ATATGATCTG TCATAAATTG GTTAACCCAT TCGATGTGAT CATTTTCATC TAAAACAATG   3660

ATACCAATTG GTAAATGTTT GATTGCTTTA TTATTTGTTG TTGAAATTTG AGCACTCAAA   3720

CCATCTACAT AACTATCCAT TTTCATTAAA GCTTGTCTGA ATAAAATGAT GCTAACAATA   3780

ATCATCACGA CAAGAACGAT AGATGCAATT AGTGCTATAA GACTATTAAA GATAAACCAT   3840

ACACCCATTA AAACAATTGC TGTGATGATC ATGATGACAA ATGGTATTAG TAAAGCTTTC   3900

TTAGTGGACT GCCGATTCAT TATTCCACCT CTATTCACTT TTTAGAATTA TTTTTCATGA   3960

TTCGCTTCAA ATTCAAACTT AAATCGATAA CACCAAGTAG TCCTACAATA TGTGTCGTAG   4020

GTGTCAGTAT TGTACCGATA ACCAATAGTA AAATCGTTAC TGCATTCGGC AAACCTTTCG   4080

CTTTACCAAA GAAATGAATA ACACTTAAAC CTTGAATATA CATTACTAAT GATAACACAA   4140

GTTGGAAGTT TAAAAGAATG CTCTGGAACA CACTCGGTTG ACCTGTAAAT AATAAACATA   4200

TGATAACAAT AATGTATATC CATAATAAAA TACCGCTCAT TTGCCACGCG AAAAGTGGCT   4260

TAAATACAGG TGTAGCGATT TTAAATTTTC GTAAAATCGG AAATGTAACG ATTAAGTTAA   4320

TTAAGACGAT TAAAAATGTA ATGATAATGA TGAAACCTGG TAATTGAACG GTCGCTTGTC   4380

TAAACCCTTC TTCTAATATT TGGGTCATAT TCGCATCGGC ACCGCTCATC GTAATCGCTT   4440

CATGTAATGT TTGCTTGAAA GGTTTTACTA TGCTCGCTGA TGGTGGAATC CTTCCGAATG   4500

TTTGTAGTAA CATAAAAGCG ATTAATGAAA TTnArCTCAT CGCTACTGTT GTTACGTATA   4560

ATATTCTTTC TTTAGACGTT CTTTCTTTGA GCAATTGACC AATAATTAAA CTTGCAATTA   4620

AGACTAATAT GATGGCACTT AAAACGAAAG TATTACCTAA AACAGTTGTT ATAATTACTG   4680

TAATAAGTGC ACTAATCCCG AAAGATTGTA TTGATTTATT CCATAAAACG ATACCTGGTA   4740

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CAAATACCAA CGCAATCGTT GCAATTATTG TTGCTTTAGG TTGTATTTTT GAAAACACAT        4860

AAGCCACTCC CATATTTTTA ACTATAGCTA TTATTTTAAC CTCTTTAATG AAAATTAACA        4920

ATTTATAGAT TGTATGCTTC TATTTCATTT AATTGAATAA TAACTTTCAT GTTTTATAAG        4980

TAATTAACAT ACTCATTTGA ATCGCTTTTG TGTGCTTTCA TTTTCAACAT GATTATTTAA        5040

TCCCACTACA TAGCAATCAA GCTTGATTTA GATTTACAAT ACATTCCAC TCTCATGTAC         5100

TCTAGATGTT TTTGAATATG ATAACTGTGA TTTAGTGGCT TCATTCTTTG AAAATATATA        5160

TTATTACTTA CGCTTAAAAT GCTTTAAATT TAAGAAATGA TATAAGTTAG GTGCCCAGGT        5220

ACTAAAGTTT AGTAGGaATC CATCATGCCC AACATTATCA GGCACGAAGA AATGACGATG        5280

ATATTTAAAA CGTTCACCTA ATGCACGAAC TTGATCATCC GGATATAGCA AATCATCTAT        5340

GAACCCCATC GTTAACACTT TTGTTTCTAA ATTTTTAAAA ACATGCGTTA CGTCTGTGCG        5400

ACCTCGGTCA ATGTTGTGAC TATCCAATAC ATCTAGCAGT GTCAGATAAC AATTCAAATC        5460

AAAATGTTCT TTAAATTTAT TACCTTGATG TTGTTGGTAT GCGACTACTT CATCCGGCGT        5520

AAAACGTTCA TCATAACTTT TTGATGATCG ATATGTCAAA AAACCTAATT GGCGTGCAAT        5580

ACTTAGACCT TCCTTACCAC CAAGATGAAT GGCTTGCCTT GCAATTTCAT TGAAAGCTCT        5640

ACTATAAGAT GATGTTCGAC TTGTTGCAGC AAGGATAATG GCTTTATCTA CTTCAAACTG        5700

TTGATTGTAG AGTAGTTCCA TTGCTTGCAT ACCTCCAAGA CTTCCCCCTA TTAAAATATT        5760

AATCTTATCA TAACCAAGGG CTTGTATACC TCGTTCATTC GCTCTGACTA TATCTCTTAA        5820

TGTTAATTTT TTAGGAAAAT GAGGGTCGTT TAAAGGTGAA CTTGAACCGA AAGGACTACC        5880

AATAACATCA AATGTTAAAA ATTGATAATC GTGAATGGGT ATATATCCCC CATCAATAAT        5940

TTCTCGCCAC CAACCCGGAT AATCATCTGT TCCATATGTT AAATGATTGC CAGTTAATGC        6000

ATGAGAAACT ACAACTAATG GTTGTCCATG ATAACCGACA TGCTCATATC TCAAACGCAA        6060

GTnATCTATG ACTTCCCCAG ATTCTGTAAT AAATTCCCCT AAATTTAAAG TATCTACTGT        6120

GTAATTTGTC ATTGTTCTTT CCTCCTTAAA CAAAAAAACT TCTCACCCTA TTGAAAAGTA        6180

AGAAGTCTTT ATACTTATCA TTCGAGTAAC TCGTTGGTTT TAGCACCGTG CTATAAAGTC        6240

GGTTGCTGAA GTATCACAGG G                                                  6261
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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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ATGCGATTAA CTCTGGAAAT ATCTTTTCCA TATTTACGTn TTAAATTATT CAGCAAATTC       60

ATACGAGaTT CATACTCGTT yAACACTTGT TCGTCGAATT CTGTATTAGC CATTTCATCA      120

TATAACTCAT GTTTTGCATC TTCTAAAATG TAGTAAAATT GATCAATATC TTCTTTTAAT      180

TTGTCATATT TGTTTGGAAC TATATCGTTT ATTGTTAACA AATGGTTGCT TAGTTCATAT      240

AAACGATCAG TGATAGCATT TTCATCCGTT AATGTCATAT ATGCGTTATT AAGCGCTAAG      300

CTTAATTTTT CAGAGTTTTG AATGCGTTTA ATATCTATTT CAAGTTGCTC TATTTCGCCT      360

TCTTTTAGAT GTGCTTCAGA CAATTCTTCT AATTGGAATT TCATTAAATC TAAACGCTGT      420

AGCAATGCTT GGTCTGCTGA TTCTAAATCT TCTAACTCTT GCTTTTTGGC TTTATAATTT      480

TGAAAAGTTT GGTGATATTT ATCCAACAAA TCTTGATAAC GTGATTCTGC GTAATTATCC      540

AATAATGTTA AATGGTATTT TTGTTTCAAC AAAGACTGCG TTTCATGTTG GCCATGAATA      600

TCTAATAATT CTTGCATAAC TTTTCGTAAA TCTTGTAAAG TAACTGTTTG ATTATTAATT      660

TTACAAAGAC TTTTACCAGA GCTGAAAATT TCCCGTTTAA CTAATAAAAA ATCTTCATCT      720

ACATCAATAT CCATATTTTT CAATATATGT ATAGCATCTT TACTCTCGTC AATATCAAAT      780

ATACCTTCGA TGACAGCCTT TTTTTCACCA TGTCTTACAA AATCAGATGA AGCTCTCATT      840

CCAATTAATT GTCCAATTGC ATCTATAATA ATTGACTTAC CTGAACCCGT TTCACCACTT      900

AAAACAGTTA AACCATCAGA AAATTGAATT TCTAATTCTT CAATAATAGC AAATTGCTTG      960

ATTGATAAGG TTTGTAACAT AAACTCATCG CATCCTTATA ACAAATTGAA AATTCTTGAC     1020

TTGATTTCAT CACTTGCCTC TTTGCTTCGA CAAATAATTA AACAAGTATC ATCACCACAA     1080

ATTGTGCCTA GTACTTCTTC CCAATTGATT TGGTCTAATA TAGCTCCAAT AGATTGTGCA     1140

TTACeAGGTA TGTTTTTAGA ACAAGTAAAT TATCAGTACC ATCTATATTA ACAAAGGAAT     1200

CCATTAAATA ACGTCCCAAT TT                                              1222
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(2) INFORMATION FOR SEQ ID NO: 14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1021 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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TTTGTTATTA TTACnTnAAA TAATTGCATT ACTTTTTACT GATGGTACAA CTTTCCATCC       60
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TTCTTTTGGC ACGACATAAT TGTCTTTATC TTGAACTAAA TATCCGCCAG ATACTGAAAC      180

AAACTCTTCT TCGTTACTGT CTATAGTCAT ATCAATTTCT AATAATCTTA CATTCTTCTT      240

TTGTTTTAAA ATATCTAATG CTTCATCTGT AAATTTTGGT GCAATAATGA CTTCCAAAAA      300

GATACTATGC AATTGCTCTG CTAACTCAGG TGTTACAGCT CGGTTTAATG CAACAATTCC      360

ACCAAATATT GATTGACTAT CCGCTTCATA CGCATGTTGA AATGCTTGTT CTATCGTGTC      420

ACCGATACCA ACACCACATG GATTCATGTG TTTAACCGCA ACTGTAGCAG GTGTATCAAA      480

CTTTTTAACT AAAGCTAGTG TAGCATCTGC ATCTTTAATA TTGTTATAGC TTAATTGTTT      540

CCCATGTAAT TGTTTAGCGC CTGCAATCGT GTGCTTAGCA TTCGAAGTTC TCACAAAATA      600

CGCTGATTGT TGTGGATTTT CTCCATATCT TAAAGTTTCT TTATCCCCTT TAAAGAAACG      660

TACAATCGCT TCATCATATT CTGCAGTATG CTCAAAAACT TTAATCATTA ATGATTGTCT      720

ATATGACTCA TCTAACGAAT CGTTTCTTAA TCGCGTCAAT ACTTCTTGAT AATCTGCCGG      780

ATGTACAATT GTTGTTACAT GTTTATAGTT TTTAGCTGCA GCACGTAACA TTGTTGGACC      840

ACCAATATCA ATATTTTCAA TTGCTTCGTC CATCGTCACA TCAGGGTTTG CAACAGTTTG      900

TTGGAATGGA TATAAATTAA CTACTACCAT ATCAATTAAA TCTATATGTT GTTCTGATAA      960

TTCATTTAAA TGCTGCGGTT TATTTCGATC AGCTAAAATG CCACCATGAA CAGCCGGATG     1020

T                                                                     1021
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(2) INFORMATION FOR SEQ ID NO: 15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3759 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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TCATTCACTC CTAAATTGTT ATTACACTAT TACACaTAGC TAATCATCAA TGTGAAATCA       60

CCTTCAAAGA CACTATCCAA ATCTTCAGAA GTCAAAATAA AGTTTGTACC AGTAGTCAGT      120

TTGAAAATTT CACCATCGAC AATCATTTGC CCTTCGCCTT CCAACACTGT AACTAAACAG      180

AACTCTCTAG GCTTCATATA ATTTAACGTG CCAGAAATTT CCCATTTAAC CAATGTAAAG      240

AAATCATTCG ATACAATGTG TGTACACTTA TGGTTTTCAA TAATTTCGCT TTCAGGCAAA      300

ATATTAGGTA ATGGTGCATT GTACTGAATA ACGTCTAAAG CTTTTTCAAT ATTTAACGGT      360
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ATAAAAtAGa ATTCyCCAGG kTTTACtTTA AtatATCyAA gTAtCGaCtC tATCGTTCCG        540

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GCATCTTCTT CTGCATCTAT AATATACCAA CATTCAGATT TGCCATATTG CCCgTTTTCA        660

TGCTCATAAG CATAAGAATT ATCAGGGTGC ACATGAATAG AAAGTGATTC TCTTGCATCC        720

ACTATTTTAG TTAGAAGCGG AAAATCTTTG CTTGGGAAAT CACCAAACAA TTCACGATGT        780

TCTGACCAAA TACGGTCTAA TGTTTGACCT TGATATGGTC CATTAATAAT CTCGCTCGTA        840

CCATTTGGAT GTGCTGACAC ACACCAACAT TCCCCCAGTT GTATCATTGT CTAATTGATA        900

TCCAAACTCA CTTAGACGTT GACCGCCCCA TAATTTTGTT TTTAAAATTG GTTGTAAAAA        960

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TCCATTATAT TTTGATTTTG TTCTCATTTA CATCGTATTA TTAACTTCCA CATTTCAAAT       1080

TAACTATTAG TGATTGTACC ATATTTACTA ACATTGCAGT ACTGCCAATT AAAAGnGCTT       1140

CACTTAAATT TACAGTACTT TAACATTTTC AAAAATTTAT AGCATAGAGA TTATATCTCT       1200

CTTACATTTG TACATATTTC CCTTTAAATT TACTCGCCCA TTATACCAAT TAATAaACAA       1260

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TTCAAATCAT ATTTACTATC CTTATTAATC CGTTTCATTT TCAAATTGAG TTAAAGCATC       1440

TTTAATGTCC TGATCACCAC TAATAATTTG AAACTCTTGG TGATTAAAAT GATTGGATGT       1500

GACAATTTCT TTTAATACTG TCGCAACATC TTCTCTAGGA ATTTCACCTT TACCATCAAA       1560

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CTAAATCGAC AATAATTGTT TTATCTGCAC CCGTGTTCCC TCCAGAACCT ACTGAAAAGA       1860

TAACTTTATC GAATGGTTTA AACGTCTCAG TTAAAGTCTC TATTGAATCA TTTTCAACAT       1920

CAACAAGAAT TGCTTTCATA CCTTGTGATT TTAACGCATT AAGTTGATCT GATTGCCTAA       1980

CACCAGCAGT AAATGGTACA TTTTCTTTTG CTAATTGTTG CACTAGTAAC GAACCTACAC       2040

CGCCATTAGC ACCTATAACC AAAATATTCA TTTACAACAC TCTCCTATkT ATTATTCTCT       2100

ATGCCATACC ACTTTATGAG ATATGTAAAA CTTGTTACAA CTATAAAAAT CAATTGACAT       2160

ACTACTGGGA ACGTATTAAA TTAATATATG AACAAATATT CATATGAAAG GATTGTCATA       2220
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tCaAGGCATT AGcGATTACA ATCGAATACG TATCaTGGAA TTGTTATCaG TCAGCGAAgC      2340

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TCCTAAAGAA AGTGGGTTAT AATATGTCTC ATTCACATCA TCATCATGAC CATATGCATA      2580

GTCATGTAAC TACAAATAAT AAGAAAGTAT TGTTTATATC GTTTTTAATA ATCGGTCTAT      2640

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CCATTGCATC GATTAAACTT TTCAATGGCA GTAGGTTTTT TATGTCTTTA TGGCGACTTG      3600

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TCATATTTTT GACAATTTAC TATTATAATT CTCTAACTTT AGTCACTTTA ATTAATTTTT      3720

ATTAGATATT AATATGAAAA TAACGTGTTT TTTGTTATT                            3759
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(2) INFORMATION FOR SEQ ID NO: 16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13086 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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TAATTATCGC GCATAACAAA ACATTAGCAG GACAATTATA TAGTGAGTTT AAAGAATTTT        60
TTCCTGAAAA CAGGGTGGAA TACTTTGTAA GTtACTATGA TTATTATCAn CCAGAGGCAT       120
ACGTACCGTC TACTGACACT TTTATTGAAA nAGATGCCTC AATCAnTGAT GAAATTGATC       180
AACTACGACA TTCTGCTACA AGTGCATTAT TTGAACGCGA TGATGTAATT ATTATTGCTA       240
GTGTAAGTTG TATATATGGT TTAGGTAATC CTGAAGAATA TAAAGATTTA GTAGTAAGTG       300
TTCGAGTTGG TATGGAAATG GATAGAAGTG AATTACTTAG AAAACTTGTc AGATGTGCAA       360
TATACACGAA ATGACATCgA TTTcCAACGA GGAACGTTTC GAGTGCGTGG TGATGTAGTG       420
GAAATATTCC CAGCCTCTAA AGAAGAACTT TGTATAAGGG TTGAGTTTTT CGGCGATGAG       480
ATTGACCGTA TCCGAGAAGT TAACTACCTA ACAGGTGAAG TGTTGAAAGA AAGAGAACAT       540
TTTGCGATAT TCCCAGCTTC TCACTTCGTA ACACGTGAAG AAAAGTTGAA AGTTGCGATT       600
GAACGTATTG AAAAAGAATT GGAAGAACGA TTGAAAGAAT TACGAGATGA GAATAAATTA       660
CTAGAAGCGC AAAGGTTAGA ACAGCGTACC AACTATGATT TAGAAATGAT GCGAGAGATG       720
GGATTCTGTT CAGGAATTGA AAACTATTCC GTACATTTAA CTTTGCGACC ACTGGGTTCG       780
ACACCATATA CTTTATTGGA TTACTTTGGC GATGATTGGT TAGTAATGAT TGATGAATCA       840
CATGTGACAT TACCGCAAGT TCGAGGCATG TATAACGGAG ACAGAGCGCG TAAACAAGTT       900
TTGGTGGATC ATGGGTTTAG ATTACCGAGT GCATTAGATA ACCGTCCACT TAAATTTGAA       960
GAATTTGAAG mAAAGACAAA ACAACTTGTG TATGTATCTG CAACGCCTGG ACCATACGAA      1020
ATTGAACATA CGGATAAGAT GGTTGAACAA ATTATTCGTC CTACTGGTTT ACTGGATCCT      1080
AAGATTGAGG TTAGACCTAC TGAAAATCAA ATTGACGATT TATTAAGTGA AATTCAAACA      1140
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TGCGCGTAAC GATAAaGGTG AAGTCATTAT GTATGCCGAT AAAATGACTG ATTCGATGAA      1500
GTATGCAATT GATGAGACAC AACGTCGTCG AGAAATACAG ATGAAACATA ATGAAAAACA      1560
TGGTATTACA CCTAAAACAA TTAATAAAAA AATACATGAT TTAATTAGTG CTACTGTTGA      1620
AAATGACGAA AATAATGACA AAGCACAAAC TGTGATACCT AAGAAGATGA CGAAAAAAGA      1680
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      AGTAAATGAA AGAACCATCC ATAGTAGTAA AAGGTGCTCG TGCGCATAAC TTGAAAGATA        1860

 5    TTGATATCGA ACTACCTAAA AaTAAATTAA TTGTTATGAC AGGTTTATCT GGGTCAGGTA        1920

      AATCGTCATT AGCATTCGAT ACTATATATG CTGAAGGACA ACGACGTTAT GTTGAATCAT        1980

      TAAGTGCCTA TGCGCGTCAA TTTTTAGGCC AAATGGACAA ACCAGATGTT GATACAATTG        2040

 10   AAGGATTATC GCCAGCAATT TCAATAGATC AAAAAACAAC AAGTAAAAAT CCAAGATCAA        2100

      CTGTAGCAAC AGTAACAGAA ATATATGATT ATATACGTTT GTTATATGCA CGTGTTGGTA        2160

 15   AACCTTACTG TCCAAATCAC AATATAGAAA TTGAATCGCA AACAGTACAA CAAATGGTTG        2220

      ACCGCATTAT GGAATTAGAG GCACGTACAA AGATTCAATT ATTAGCACCT GTCATCGCTC        2280

      ATCGTAAAGG TAGTCATGAA AAGCTAATCG AAGATATTGG TAAAAAAGGT TATGTACGTT        2340

 20   TAAGAATCGA TGGCGAAATT GTTGATGTAA ATGATGTACC TACTTTAGAT AAGAACAAGA        2400

      ATCATACAAT AGAAGTTGTT GTAGACCGAT TAGTTGTTAA AGATGGAATT GAAACACGAC        2460

      TAGCTGACTC TATAGAAACT GCCTTAGAGC TTTCAGAAGG ACAATTAACA GTCGATGTCA        2520

 25   TTGACGGGGA AGACCTTAAG TTTTCAGAAA GCCATGCTTG TCCTATATGT GGATTTTCAA        2580

      TCGGAGAGTT AGAACCAAGA ATGTTTAGCT TTAACAGTCC TTTTGGTGCT TGTCCGACAT        2640

      GTGATGGCTT AGGCCAAAAG TTAACAGTCG ATGTAGACTT GGTTGTTCCC GACAAAGATA        2700

 30   AGACGCTAAA CGAAGGTGCA ATAGAACCTT GGATACCGAC GAGTTCTGAT TTTTATCCAA        2760

      CATTGTTAAA ACGTGTTTGT GAAGTTTATA AAATCAATAT GGATAAACCT TTTAAAAAGT        2820

      TAACAGAACG TCAACGTGAT ATTTTATTGT ATGGTTCTGG TGACAAAGAA ATTGAATTTA        2880

 35   CATTTACACA ACGTCAAGGT GGTACTAGAA AACGAACAAT GGTTTTCGAG GGTGTAGTTC        2940

      CTAATATAAG TAGACGATTC CATGAATCTC CTTCAGAATA TACACGTGAA ATGATGAGTA        3000

      AATATATGAC TGAACTACCT TGCGAAACTT GTCATGGAAA GCGATTGAGT CGTGAAGCkT        3060

 40   TATCTGTTTA TGTAGGTGGT TTAAATATTG GTGAAGTAGT CGAATATTCA ATCAGTCAAG        3120

      CGCTGAACTA TTATAAAAAC ATTGATTTGT CAGAACAAGA TCAAGCGATT GCAAATCAAA        3180

 45   TATTGAAAGA AATTATTTCC CGACTCACTT TTTTAAATAA TGTGGGACTT GAATATTTAA        3240

      CGTTAAACAG AGCTTCAGGT ACACTTTCAG GTGGTGAAGC ACAACGTATT CGATTAGCAA        3300

      CGCAAATTGG GTCGCGTTTG ACTGGTGTCT TATATGTATT AGATGAGCCA TCAATTGGAC        3360

 50   TGCATCAAAG AGATAATGAT CGATTAATTA ATACACTTAA AGAAATGAGA GATTTAGGAA        3420

      ATACTTTAAT TGTAGTTGAA CACGATGATG ATACAATGCG TGCGGCTGAT TACTTAGTGG        3480
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GCAACAATCT TAAAGGGGTT GATGTGGACA TACCACTATC AATCATGACG GTTGTTACAG      3720

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TTTATTTTAG CTTTTCAATG TAGATTGGTG TTATATTTTT GATATGATAA GAAGAGATGT      5280
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TGCGCATAAT GATTAATAAT GAGGAGGCGT TAATAAAATG ACTGAAATAG ATTTTGATAT        9120

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GCCCCGCCAA CTTGCACATT ATTGTAAGCT GACTTTTCGT CAGCTTCTGT GTTGGGGCCC       10560

CGCCAACTTG CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTATGTTG GGGCCCACAC       10620

CCCAACTCGC ATTGCCTGTA GAATTTCTTT TCGAAATTCT CTGTGTTGGG GCCCACACCC       10680
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TAGACCCTAG GACATTGATT TATGTCCCAA GCTCCTTTTA AATGATGTAT ATTTTTAGAA   10920

ATTTAATCTA GACATAGTTG GAAATAAATA TAAAACATCG TTGCTTAATT TTGTCATAGA   10980

ACATTTAAAT TAACATCATG AAATTCGTTT TGGCGGTGAA AAAATAATGG ATAATAATGA   11040

AAAAGAAAAA AGTAAAAGTG AACTATTAGT TGTAACAGGT TTATCTGGCG CAGGTAAATC   11100

TTTGGTTATT CAATGTTTAG AAGACATGGG ATATTTTTGT GTAGATAATC TACCACCAGT   11160

GTTATTGCCT AAATTTGTAG AGTTGATGGA ACAAGGAAAT CCATCCTTAA GAAAAGTGGC   11220

AATTGCAATT GATTTAAGAG GTAAGGAACT ATTTAATTCA TTAGTTGCAG TAGTGGATAA   11280

AGTCAAAAGT GAAAGTGACG TCATCATTGA TGTTATGTTT TTAGAAGCAA GTACTGAAAA   11340

ATTAATTTCA AGATATAAGG AAACGCGTCG TGCACATCCT TTGATGGAAC AAGGTAAAAG   11400

ATCGTTAATC AATGCAATTA ATGATGAGCG AGAGCATTTG TCTCAAATTA GAAGTATAGC   11460

TAATTTTGTT ATAGATACTA CAAAGTTATC ACCTAAAGAA TTAAAAGAAC GCATTCGTCG   11520

ATACTATGAA GATGAAGAGT TTGAAACTTT TACAATTAAT GTCACAAGTT TCGGTTTTAA   11580

ACATGGGATT CAGATGGATG CAGATTTAGT ATTTGATGTA CGATTTTTAC CAAATCCATA   11640

TTATGTAGTA GATTTAAGAC CTTTAACAGG ATTAGATAAA GACGTTTATA ATTATGTTAT   11700

GAAATGGAAA GAGACGGAGA TTTTCTTTGA AAAATTAACT GATTGTTAG ATTTTATGAT    11760

ACCCGGGTAT AAAAAGAAG GGAAATCTCA ATTAGTAATT GCCATCGGTT GTACGGGTGG    11820

ACAACATCGA TCTGTAGCAT TAGCAGAACG ACTAGGTAAT TATCTAAATG AAGTATTTGA   11880

ATATAATGTT TATGTGCATC ATAGGGACGC ACATATTGAA AGTGGCGAGA AAAAATGAGA   11940

CAAATAAAAG TTGTACTTAT CGGTGGTGGC ACTGGCTTAT CAGTTATGGC TAGGGGATTA   12000

AGAGAATTCC CAATTGATAT TACGGCGATT GTAACAGTTG CTGATAATGG TGGGAGTACA   12060

GGGAAAATCa GAGATGAAAT GGATATACCA GCACCAGGAG ACATCAGAAA TGTGATTGCA   12120

GCTTTAAGTG ATTCTGAGTC AGTTTTAAGC CAACTTTTTC AGTATCGCTT TGAAGAAAAT   12180

CAAATTAGCG GTCACTCATT AGGTAATTTA TTAATCGCAG GTATGACTAA TATTACGAAT   12240

GATTTCGGAC ATGCCATTAA AGCATTAAGT AAAATTTTAA ATATTAAAGG TAGAGTCATT   12300

CCATCTACAA ATACAAGTGT GCAATTAAAT GCTGTTATGG AAGATGGAGA AATTGTTTTT   12360

GGAGAAACAA ATATTCCTAA AAAACATAAA AAAATTGATC GTGTGTTTTT AGAACCTAAC   12420

GATGTGCAAC CAATGGAAGA AGCAATCGAT GCTTTAAGGG AAGCAGATTT AATCGTTCTT   12480
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GCGTTAATTC ATTCTGATGC GCCTAAGCTA TATGTTTCTA ATGTGATGAC GCAACCTGGG      12600

GAAACAGATG GTTATAGCGT GAAAGATyAT ATCGATGCGA TTCATAGACA AGCTGGACAA      12660

CCGTTTATTG ATTATGTCAT TTGTAGTACA CAAACTTTCA ATGCTCAAGT TTTGAAAAAA      12720

TATGAAGAAA AACATTCTAA ACCAGTTGAA GTTAATAAGG CTGAACTTGA AAAAGAAAGC      12780

ATAAATGTAA AAACATCTTC AAATTTAGTT GAAATTTCTG AAAATCATTT AGTAAGACAT      12840

AATACTAAAG TGTTATCGAC AATGATTTAT GACATAGCTT TAGAATTAAT TAGTACTATT      12900

CCTTTCGTAC CAAGTGATAA ACGTnAATAA TATAGAACGT AATCATATTA TGATATGATA      12960

ATAGAGCTGT GAAAAAAATG AAnATAGACA GTGGTTCTAA GGTGAATCAT GTTTTAAATA      13020

AGAAAGGAAT GACTGTACGA TGAGCTTTGC ATCAGAAATG AAAAATGAAT TAACTAGAAT      13080

AGACGT                                                                13086
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(2) INFORMATION FOR SEQ ID NO: 17:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1350 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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CATTAGTCAT GAAAATAGCC GACAACTTCA TCTGTGAAAT CACCGGCCTT TTATTTTAGC        60

TAACTTTATT TCTGATTTTA CGATTTTAAT TGATCATACA GAGAAAGTGA TCTTTTTACA       120

ATTTCTAAAA ACTCATGATC TATATTGGAC ATTTGATGAA AATAAGACAA AATGTTTTCT       180

GTTAGCTTCT CTTGTTTTGG GAATGAATCA TCTTCTTTAA TCCAAATCGC TAATTCGCCT       240

AATGGTGTTT TATCATCTTT AAATGTTTGT ATATATTCGT AAAAGCTCAT AGTATTCCTT       300

CTCTCAATTT ACTTATATAA ATCCTACCAC GAAAGCTTTC AAGAAAACAC AATTAAATGT       360

CTATTTAGTG AACTTTTTAA GGTTGTGCAC TCTTTTAATG TCTGCCAATT AGGTCAATTA       420

ATCATCACAA TGTACAATTA ACTCTATTTT CAGTTCATAT ACTCACACAC CGTTTTTGAA       480

CAACACATTA ACTTCTCATT TAGATAAAAC GCAAAAAAGC CTGGCACCAA TACAATAGAT       540

GCCAGACTAA GAGTCTACTA TATAAATTTA TTTAGCGTAT GGTTTTACTT CGATTGCACC       600

TTCATTTTCA TCATGAACAC CATGCTTATA ATAATCAATA TATTGTGGCT CTAAAGGCTT       660

TCTGCCACGT ATAATGTCTG CTGCTTTTTC AGCTAACATT AAAACAGGTG CGTGTATATT       720

CCCATTTGTC GTACGTGGCA TAGCTGATGC ATCAACTACA CGTAAATTTT CCATACCGTG       780
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ACTACAAGAT GGGTGTAATG CTGTTTCACC ATCTCTACGA ACCCAATCAA GAATTTCTTC   900

GTCTGTTTGC ACTTCTGGTC CTGGTGAAAT TTCTCCACCA TTGAATGGAT CCATTGCTTT   960

TTGAGATAAG ATATTTCTTG CTACACGAAT TGCTTCTACC CATTCTTTTT TATCTTCTTC   1020

TGTTGATAAA TAATTAAAGC GGATACTTGG TTTTTCGAAT GGATCTTTAG ATTTGATTTT   1080

CAAGCTACCA CGAGAGTTTG AATACATTGG TCCTACGTGA ACTTGATAAC CATGTGCGAC   1140

CGCTGCCTTT TGACCATCAT ATCTTACAGC TATTGGTAAG AAATGGAACA TTAAGTTAGG   1200

ATAAtCAACT TCGTTATTTG AACGTACAAA TCCGCCACCT TCAAAATGGT TAGATGCTGC   1260

TGCACCTGTA CGTGTGAAAA TCCATTGTAA ACCAATAAAT GGcATGCGCT TGAtATCTAA   1320

GCTTGGCtGt AATGATACAG GTTCCTTACA   1350

(2) INFORMATION FOR SEQ ID NO: 18:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1376 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAATGCTATT GGCAACACCA TATATGAAAn CTCCAAACGA TCCTAAACCG ACTATAGATT   60

CACCAAATTT nACAATCCAT GAATAAAGTA GTGGCCATAA GAATAACAAT ATGACAACTA   120

AAAATGTACA GTAAAATGCA GTCATAATTG GAACTAGACG TTTACCACTA AAAAATGATA   180

ATGCTAATGG TAATTCTGTT TCACTAAACT TATTGTATGC ATAAGCTGCT ATTAAACCTA   240

TTACAATACC AACAAAGACA TTGCCATTAT TCATCTTTTC AAAAGCTGAA TTTATTTCCG   300

ArGCTTTCAT TCCTAATAAA GGCGCTAATT TCATTGGTGA TAATACAACT GTAACTAAAA   360

AATATCCTAA CGTrGCTGCA rGCGsGACTG CACCATCATT TTTCTTTGCC ATTCCTATAG   420

CTACACCAAT TGCAAATAAA ATACCTAATT GCTCTAAAAT CGTAGTACCT ACCGTAGTAA   480

AGAACATTGC GATTTTCGGC GTCGCATGAA GTGCATTTAA CGTATTACCA ATTCCGGCAA   540

TAATTGCTGC AGCCGGTAAA ATGGCAACTG GTAACATTAA CGAACGCCCT AAATTTTGGA   600

AAAATTTATA CATTGAATGT CATCCTTCTT AAAATAATGT AGAAATATAA AGATTACTAA   660

TGTAACTAGA ATAACTACTT CGATACTCCG TTATAGTCAC CTAGGCTTAC TAACCAGCTA   720

TATTTCTACC TCAAGTTATT TTATAAACTT TTTACAATTT CATGCAATTC TTGTTGTAAC   780

TTTGCTGTTC GTGTTTCAAT CTCTTTTGTA ATATAATCGA TACGCTCGTT TCGTTTTAAA   840

AAAGACCGTG AATCTTAGTA GGACCAACAT AAGCAACAGG TAATATTGGT GACTTACTTA   960

ACATTGCAAT TGTTGAAGCA CCaCGTTTCA AAGGTGCACC TTCTTGCGAT GTGCGAGAAC   1020

CTGTTGGGAA GATACCAACT GTCTTATTAT CTTTCAACAA ATTGATTGGG CGTTTTAAAG   1080

TACTAGGTCC TGGATTTTCA CGATCTACAG GAAATGCATT TAAAGACGTT AAAAATTTAC   1140

CAATCCATTT ATTTTTGAAT AATTCTTTTT TAGCCATATA ATGAATTTGA TTAGGATATA   1200

ATGCCATACC TAGCATAATG ACTTCGTTAT AACTTTCATG CGTACAAGTT ACGACATATT   1260

TACTATCCTT AGGAATATTA TCTTTACCGA TTACGTATAA TGATTTTGAC ATTTTAACTA   1320

AAATGAAATT CAAAATCTTA CTAATCACTG AATACATTGT GCCACCTACT TAACTT   1376

(2) INFORMATION FOR SEQ ID NO: 19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7363 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTGTCATACC AATATTTTGT AAAATATGGA ACACAAGTAA AGTGACGAAA CCAACGATAA   60

AGATTTTGTT AAATTGATCT TCAATTTTCG CAGCTAATCT TATTAGATGG AAGATTAAAA   120

ATAAAAATAT TAAGATCAAT ATGACAGAAC CGATAAAGCC AAGTTCCTCT CCAATCACTG   180

AAAAGATAAA GTCAGTATGA TTTTCAGGTA TATAAACTTC ACCGTGATTG TATCCTTTAC   240

CTAGTAACTG TCCAGAACCG ATAGCTTTAA GTGATTCAGT TAAATGaTAG CCATCACCAC   300

TACTATATGT ATAGGGGTCA AGCCATGAAT TGATTCGTCC CATTTGATAC AGTTGGaCAC   360

CTAATAAATT TTCAATTAAT GCGGGTGCAT ATAGaATACC TAAAATGACT GTCATTGCAC   420

CAACaATACC TGTAATAAAG ATAGGTGCTA AGATACGCCA TGTTATACCA CTTACTAACA   480

TCACACCTGC AATAATAGCA GCTAATACTA ATGTAGTTCC TAGGTCATTT TGCAGTAATA   540

TTAAAATACT TGGTACTAAC GAGACACCAA TAATTTTGAA AAATAATAAC AAATCACTTT   600

GGAATGATTT ATTGAATGTG AATTGATTAT GTCTAGAAAC GACACGCGCT AATGCTAAAA   660

TTAAAATAAT TTTCATGAAT TCAGATGGCT GAATACTGAT AGGGCCAAAC GTGTACCAAC   720

TTTTGGCACC ATTGATAATA GGTGTAATAG GTGACTCAGG AATAACGAGC AAGCCTATTA   780

ATAATAGACA GATTAAGAAA TACAATAAAT ATGTATAATG TTTAATCTTT TTAGGTGAAA   840

TAAACATGAT GATACCTGCA AAAATTGCAC CTAAAATGTA ATAAAAAATT TGTCTGATAC   900

TTGCTAAAAC AGCTATAGTG GCTACTAATA CCCAGTCTAC TTTGCGAAnC aATGCTTATC   1020

CGGCTGTTGA CGAGATGAAT AATTCATTGC AAACTCCTTT TATACTCACT AATGTTTATA   1080

TCAATTTTAC ATGACTTTTT AAAAATTAGC TAGAATATCA CAGTGATATC AGCTATAGAT   1140

TTCAATTTGA ATTAGGAATA AAATAGAAGG GAATATTGTT CTGATTATAA ATGAATCAAC   1200

ATAGATACAG ACACATAAGT CCTCGTTTTT AAAATGCAAA ATAGCATTAA AATGTGATAC   1260

TATTAAGATT CAAAGATGCG AATAAATCAA TTAACAATAG GACyAAATCA ATATTAATTT   1320

ATATTAAGGT AGCAAACCCT GATATATCAT TGGAGGAAAA CGAAATGACA AAAGAAAATA   1380

TTTGTATCGT TTTTGGAGGG AAAAGTGCAG AACACGAAGT ATCGATTCTG ACAGCACAAA   1440

ATGTATTAAA TGCAATAGAT AAAGACAAAT ATCATGTTGA TATCATTTAT ATTACCAATG   1500

ATGGTGATTG GAGAAAGCAA AATAATATTA CAGCTGAAAT TAAATCTACT GATGAGCTTC   1560

ATTTAGAAAA TGGAGAGGCG CTTGAGATTT CACAGCTATT GAAAGAAAGT AGTTCAGGAC   1620

AACCATACGA TGCAGTATTC CCATTATTAC ATGGTCCTAA TGGTGAAGAT GGCACGATTC   1680

AAGGGCTTTT TGAAGTTTTG GATGTACCAT ATGTAGGAAA TGGTGTATTG TCAGCTGCAA   1740

GTTCTATGGA CAAACTTGTA ATGAAACAAT TATTTGAACA TCGAGGGTTA CCACAGTTAC   1800

CTTATATTAG TTTCTTACGT TCTGAATATG AAAAATATGA ACATAACATT TTAAAATTAG   1860

TAAATGATAA ATTAAATTAC CCAGTCTTTG TTAAACCTGC TAACTTAGGG TCAAGTGTAG   1920

GTATCAGTAA ATGTAATAAT GAAGCGGAAC TTAAAGAAGG TATTAAAGAA GCATTCCAAT   1980

TTGACCGTAA GCTTGTTATA GAACAAGGCG TTAACGCACG TGAAATTGAA GTAGCAGTTT   2040

TAGGAAATGA CTATCCTGAA GCGACATGGC CAGGTGAAGT CGTAAAAGAT GTCGCGTTTT   2100

ACGATTACAA ATCAAAATAT AAAGATGGTA AGGTTCAATT ACAAATTCCA GCTGACTTAG   2160

ACGAĀGATGT TCAATTAACG CTTAGAAATA TGGCATTAGA GGCATTCAAA GCGACAGATT   2220

GTTCTGGTTT AGTCCGTGCT GATTTCTTTG TAACAGAAGA CAACCAAATA TATATTAATG   2280

AAACAAATGC AATGCCTGGA TTTACGGCTT TCAGTATGTA TCCAAAGTTA TGGGAAAATA   2340

TGGGCTTATC TTATCCAGAA TTGATTACAA AACTTATCGA GCTTGCTAAA GAACGTCACC   2400

AGGATAAACA GAAAAATAAA TACAAAATTG ACTAACTGAG GTTGTTATTA TGATTAATGT   2460

TACATTAAAG CAAATTCAAT CATGGATTCC TTGTGAAATT GAAGATCAAT TTTTAAATCA   2520

AGAGATAAAT GGAGTCACAA TTGATTCACG AGCAATTTCT AAAAATATGT TATTTATACC   2580

ATTTAAAGGT GAAAATGTTG ACGGTCATCG CTTTGTCTCT AAAGCATTAC AAGATGGTGC   2640

TGGGGCTGCT TTTTATCAAA GAGGGACACC TATAGATGAA AATGTAAGCG GGCCTATTAT   2700

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AAACCCTAAA GTAATTGCCG TCACAGGGTC TAATGGTAAA ACAACGACTA AAGATATGAT        2820

TGAAAGTGTA TTGCATACCG AATTTAAAGT TAAGAAAACG CAAGGTAATT ACAATAATGA        2880

AATTGGTTTA CCTTTAACTA TTTTGGAATT AGATAATGAT ACTGAAATAT CAATATTGGA        2940

GATGGGGATG TCAGGTTTCC ATGAAATTGA ATTTCTGTCA AACCTCGCTC AACCAGATAT        3000

TGCAGTTATA ACTAATATTG GTGAGTCACA TATGCAAGAT TTAGGTTCGC GCGAGGGGAT        3060

TGCTAAAGCT AAATCTGAAA TTACAATAGG TCTAAAAGAT AATGGTACGT TTATATATGA        3120

TGGCGATGAA CCATTATTGA AACCACATGT TAAAGAAGTT GAAAATGCAA AATGTATTAG        3180

TATTGGTGTT GCTACTGATA ATGCATTAGT TTGTTCTGTT GATGATAGAG ATACTACAGG        3240

TATTTCATTT ACGATTAATA ATAAAGAACA TTACGATCTG CCAATATTAG GAAAGCATAA        3300

TATGAAAAAT GCGACGATTG CCATTGCGGT TGGTCATGAA TTAGGTTTGA CATATAACAC        3360

AATCTATCAA AATTTAAAAA ATGTCAGCTT AACTGGTATG CGTATGGAAC AACATACATT        3420

AGAAAATGAT ATTACTGTGA TAAATGATGC CTATAATGCA AGTCCTACAA GTATGAGAGC        3480

AGCTATTGAT ACACTGAGTA CTTTGACAGG GCGTCGCATT CTAATTTTAG GAGATGTTTT        3540

AGAATTAGGT GAAAATAGCA AAGAAATGCA TATCGGTGTA GGTAATTATT TAGAAGAAAA        3600

GCATATAGAT GTGTTGTATA CGTTTGGTAA TGAAGCGAAG TATATTTATG ATTCGGGCCA        3660

GCAACATGTC GAAAAAGCAC AACACTTCAA TTCTAAAGAC GATATGATAG AAGTTTTAAT        3720

AAACGATTTA AAAGCGCATG ACCGTGTATT AGTTAAAGGA TCACGTGGTA TGAAATTAGA        3780

AGAAGTGGTA AATGCTTTAA TTTCATAGAG ATTAGTCGAG GGACCTTTTA CTTATAAAAA        3840

TGATTTGAAT TAATACTAAA AGATTACAAA GAAGAGGTGG TTTTGTGTGT AAATACAAAA        3900

TTGCCTTTTT CTTTTTATGT TAAATCTATA AATTTGAAAC TAAATCAAGG TTAATTCTAT        3960

GTACACACTT TATATAGGAA GTAGTTTGAA TGTTTATATA ATGTTTTACA AAAAGATGTA        4020

GTATTATAAT GTCTAATTTC ACATGTGTTT CAGTAAAATT TGTTGTGGAA TGTTAACGAT        4080

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CTTATCTAAT GCTAGCTTTT TGACAAAAAT ATGACAATCA ATTAATGTGA TTCTAATAAA        4200

TATTCGCAAA TTGCTTTATT GCGATTAAAT TTTTTTGGTG GTACTATATA GAAGTTGATG        4260

AAATATTAAT GAACTTATAT GCAAAGTAT ATTGAGAAAT AAACAGGTAA AAAGGAGAAT        4320

TATTTTGCAA AATTTTAAAG AACTAGGGAT TTCGGATAAT ACGGTTCAGT CACTTGAATC        4380

AATGGGATTT AAAGAGCCGA CACCTATCCA AAAAGACAGT ATCCCTTATG CGTTACAAGG        4440

AATTGATATC CTTGGGCAAG CTCAAACCGG TACAGGTAAA ACAGGAGCAT TCGGTATTCC        4500
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AGAATTGGCA ATGCAGGTAG CTGAACAATT AAGAGAATTT AGCCGTGGAC AAGGTGTCCA      4620

AGTTGTTACT GTATTCGGTG GTATGCCTAT CGAACGCCAA ATTAAAGCCT TGAAAAAAGG      4680

CCCACAAATC GTAGTCGGAA CACCTGGGCG TGTTATCGAC CATTTAAATC GTCGCACATT      4740

AAAAACGGAC GGAATTCATA CTTTGATTTT AGATGAAGCT GATGAAATGA TGAATATGGG      4800

ATTCATCGAT GATATGAGAT TTATTATGGA TAAAAATTCCA GCAGTACAAC GTCAAACAAT      4860

GTTGTTCTCA GCTACAATGC CTAAAGCAAT CCAAGCTTTA GTACAACAAT TTATGAAATC      4920

ACCAAAAATC ATTAAGACAA TGAATAATGA AATGTCTGAT CCACAAATCG AAGAATTCTA      4980

TACAATTGTT AAAGAATTAG AGAAATTTGA TACATTTACA AATTTCCTAG ATGTTCATCA      5040

ACCTGAATTA GCAATCGTAT TCGGACGTAC AAAACGTCGT GTTGATGAAT TAACAAGTGC      5100

TTTGATTTCT AAAGGATATA AAGCTGAAGG TTTACATGGT GATATTACAC AAGCGAAACg      5160

TTtAGAAGTA TTanAGAAAT TTAAAAATGA CCAAATTAAT ATTTTAGTCG CTACTGATGT      5220

AGCAGCaAGA GGACTAGATA TTTCTGGTGT GAGTCATGTT TATAACTTTG ATATACCTCA      5280

AGATACTGAA AGCTATACAC ACCGTATTGG TCGTACGGGT CGTGCTGGTA AAGAAGGTAT      5340

CGCTGTAACG TTTGTTAATC CAATCGAAAT GGATTATATC AGACAAATTG AAGATGCAAA      5400

CGGTAGAAAA ATGAGTGCAy TcGTCCACCA CATCGTAAAG AAGTACTTCA AGCACGTGAA      5460

GATGACATCA AAGAAAAAGT TGAAAACTGG ATGTCTAAAG AGTCAGAATC ACGCTTGAAA      5520

CGCATTTCTA CAGAGTTGTT AAATGAATAT AACGATGTTG ATTTAGTTGC TGCACTTTTA      5580

CAAGAGTTAG TAGAAGCAAA CGATGAAGTT GAAGTTCAAT TAACTTTTGA AAAACCATTA      5640

TCTCGCAAAG GCCGTAACGG TAAACCAAGT GGTTCTCGTA ACAGAAATAG TAAGCGTGGT      5700

AATCCTAAAT TTGACAGTAA GAGTAAACGT TCAAAGGAT ACTCAAGTAA GAAGAAAAGT      5760

ACAĀAAAAAT TCGACCGTAA AGAGAAGAGC AGCGGTGGAA GCAGACCTAT GAAAGGTCGC      5820

ACATTTGCTG ACCATCAAAA ATAATTTATA GATTAAGAGC TTAAAGATGT AATGTCTTGA      5880

GCTCTTTTTT GTTTTCAATA ATTGATTCTC TGTAGATATC aAAGTaCTAA CGTTTTAAAG      5940

GTTAAATATT TAATTGGATT GAGATCTGTA TGCGGTTATA TCaTTCTGTG TAAATATGGT      6000

TCTCCACCAA ATGTGGTGAG TATATAATTT AAAGAACTAT TTTTAAATTA AGAATAATCG      6060

AACATAAATA AACTTATGA AATTTCAGTA TCATGTTCTT ATAAAAAACA ATAGGGCTTT      6120

TTGCtGACGC TAGTGCGCGA TAAATAATAA GTTGAATATA AAAAAGATCA CTGCCAATCA      6180

TTCGTTTAAT GGCAGCGATC TTTTTTATTT AATTATTTCT CTTTCCACTG CAACATTTGA      6240

TAACCAATGC GTGGATGTGT TTTAATAATA TCTTTTGCGT CCTCATGACA TTGTGAAAGT      6300
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CCATATATTC GTTTTAATAT CATCTCATAA GTGAGTACTT TTCCTTTATG ATTTGACAAT      6420

AGTTCTAACA AGCTAAATTC ATTTGGCGTC AAATGTACCT CCTGATTATT AATAACAACA      6480

GATTTGGAGC CAAAGTCGAT GCTTAGCAAA CCGTTAGTAA ATACAATGTT AGTTTCTTGA      6540

TGTGACTTAG CGATTCTCTC GATGACTCGT ATTCGTGCCC GAAGCTCATC AACATTAAAA      6600

GGTTTAGTCA TATAGTCATT CGCACCGTTA TCTAAAGCTT GAATAATTGT TTGTTCTTCT      6660

TGTCTTGCAC TTATTACAAT GATAGGAATG TCAGTATGTT GCCTGATTTC TGAAATCAAA      6720

CATAATCCAT CTTTATCTGG TAAACCTAAA TCTAATAAAA TGACATCTGG TTTATCAATT      6780

TGAATTTTAA AGTGTGCTTG TGTGGCATTG TCGGCTGTAG TTACATTGTA ATAATCTAAA      6840

GTTAATGCAA CATCAAGTAA ATGTGTGATT GCGTGATCAT CTTCAATTAT CAATATTTTA      6900

GATTGCATTA TACGTCTCCT TCGTTAAAGT CTGTATATAT ATTGAAATAG AATATACTGC      6960

CGTGTGGTTG GTTCGGTTTA TATTGTAAGT TTGATTGATG TTTGTGTAGG ATAGTCTGTA      7020

CTAAATATAA GCCTAGTCCC ATGCTTTCTT TTTGGTTATC TTTAAAATAT TTATTTGATC      7080

CTGTGTAAAA AGGCTCGAAT ATCTTTTGTt GTTCTTCTAA ACTAATTCCA GGTCCTTCGT      7140

CTATAACGGC AAATTCGATT TGTTCATAGC TAGCATAACG AATAGATAAA TTGATTTTGG      7200

TGTCAGTAGA AGTGTGTTTA ACTGCATTTT CAATCAAATT GAAtAAAgCT TGTAAAATCA      7260

ACTTACTGTC AATGTGTATA AACtGTAAAT TTACTGAGGA TGATACAGTT ATACGCTTTT      7320

TTAAATGGCG ACGTTCTAAA ATACATATCG ATTTCTTATA CTA                       7363
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(2) INFORMATION FOR SEQ ID NO: 20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10470 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

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TTAACAATCG ATAACCACAA TACTTCTATT GTAATTGTTT AACGATTTCn CGATTAAAAT       60

CATCTAAATC GTCTGGTACT CGACTTGTTA CAATATTGTT GTCTACACTa CTGACTCATC      120

AACTACATGT GCGCCTGCAT TTGATAAATC TTTGCGTACA TTTAATACTG CTGTTAACGT      180

ACGACCTTTT AAATCGTCTG TATCTATTAG TATTTGTGGC CCATGACAAA TGGCAAATGT      240

TGGTACATCA TTTTTAGTAA AGTATTTAGC AAATGTGCCA TATCGACCTT CTGTATCTCC      300

ACCTAAATGA TCTGGTGAAA ATCCTCCAGG AATTAATAAT GCATCATAAT CTTCTGGTTT      360
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ATTTGCAGTA TCTCCAATCA CTACAGTATT AAAGCCTGCA TTCTCTAATG CCTCTTTAGG      480

GCTTGAATAT TCTATATCTT CAAATTCGTT TGCTAGAATA ATTGCTACTT TTTTAGTCAT      540

TGAAAATCAC CTTTCTATAT ATCATTGATA TAATTACTAT AGACAAGTAA ATCAGTGATT      600

AAACATACAA GATATAAAAA ATATTAAGCG ACTGTCGCGA TATCTAACCC TAACACATCT      660

TATGTGGCAT TTACTTAGAT ACTAATTTAA CCTTTTCTTC AAGCTGATCT AACAATCCAA      720

TCCATTCATC TATATCTTCA ACACGTACTT CATCAGGATT TACATGATCG ATATCCTCAA      780

TAAACTTATT TAAACGCGCT TTTATCTGTT CGATTGTTTG CTGTTCATTC ATAAAAAGTT      840

AACTCCTTTT ATTTTGTTTT CTTTTTCATT ATTATCCTAA CAGAAATTGC GTTAAAGCGA      900

TATAATCTTA GCTATATTTA TGACATTCAA ATTATTTTGA CTTTTAAAAA TCCCCTTTTC      960

AATTAACTAA AATTAAGAGA TAATTTGTTA CGAGTGATAA TACGAaGkGG TaTCATACCG     1020

ATATGAACCA AATAGAAAGA AGGAAGTTTA AGACGATGAA TAGCGTCAAA TTGAAGCAAC     1080

CTGTTAGCAT TTACAATGAT CCATGGGAAG TGAAATTTAT ATACATTTAA ATTTCATGAG     1140

ACAATAAACG TTGATTTAAT GCGTTTTTTT GCCTTTTTTA TTTTCCTTAT TTTTTCTGTT     1200

TTACAACAAA ATGGTATCAA AAATGGTATC ATTTGTAGTT ATTTTAGCTT CACATATTAA     1260

AACAACCACA CTCCTAAATT AATAGGTGGT GTGGTTTTGT TGGTTGTGTG GGGATAAAAA     1320

TAACCGCATC AGTTAAGATG CGGTTATCTA GCAAGGGCCA CGTATTTATA AATACGTTTA     1380

GAATCTCTTC GGCAACTTTG CTATAGACAG TCTATGCTGT TACTAAATTA TACCACCACA     1440

CAAACCTACT CCCATTCAGG AACACAGAGC TTTGTCGCTC GTCAGCAACG TCATATGAAT     1500

TCTCAGTTCA TGTTGTGGTG ACACTTTAAA CGGTCTGTGC CAGTAGCGAC CGAGTCATTT     1560

CAAGAATGAC CATTTCACAT TTATATTATA ACACTTGTCG TGCGTAACTG TATAGTTTTT     1620

CAGTTGTATT TAAAGTTAAG TTATCTACTT CGCGCTTTCC TTGCCTTAAT TGTGAAATTA     1680

CATATTGCGC TACGCCAGTT TGTTTGTGAA TTTGGTAACC TGTTATATCA CTTTTGATCA     1740

ATTCAATTAT TTTTAATTTA TAATCACTCA TATTATCTAC GTCCATTCTT TTTATCTAAA     1800

CAATAAAAAT GTGTCTTTCT CCCGATAAAT AATAACAATG GTAGGCTTAA TAAAAACAAT     1860

ATTAAATACA TTTGTTCTGT CATAATTGAA AACCTCCAAA TAATATTATA TTATATAAGT     1920

GTAAGGAGGA GCCATCAGGC TCCAAGCATA ATGTTAATCT TTGTTGTTTG GCTTTCGGTC     1980

TAGGTAGCCG AGATGCCaTT CTCTAAGTTG TTTTAACACT TCTGGAATTA TCAGTACTGC     2040

CAATACTTGA TGTTCTAGAA GTGTTTTTAT TATGTCTAGC ATGAGGCTTT TCACCTCCTT     2100

ACACATAATT TGTAAGTCAT CAACTAACCT ACAAATATAA TTATACTAAA CAAATGTTTA     2160
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GTTATCTACA TTTAAATCTT GAGAGAAATG TTAAAAAGTT CTAGTAAAAT AATAGCACAT        2280

TTTATCTTTA AATGTAAATA GAAAGCAGGT ATGTAACGCA CCTGCTTAAA TAGaCATGAC        2340

TATGTCATTC TAACTGATTT CTCCCCATAA GTCACCTAAT ATCTGATTAG GTGGGGCAGA        2400

ACCATTCCAT GTTCTAATAG GCAAGTAATA ACGTTGCCCC TCCCATGTAT ATCCTACCCA        2460

AACATGACCA TCTTGTAACA TCACTTCTGT ATAATCACAA TACCCACCAG GTTGGAACTG        2520

ATAACCCACT GGACAAGATA AGAATGGCCC CACTTTTCTT ACTGTGATTG GTTGATTGCC        2580

GTTTGTGAAT CTAGCACTTT CTTCCATGTA GTAAGTACCA TATTTATTAC GTTTCCATGC        2640

ACTTGCAACT GGTTTAACTG TATTACTTGA AGCGCTTGAC TCATTAGAGA CAGTGGCAAC        2700

CGGTATTTTA CCATCCATGT ACGCCCTAAT CTGCTTGATA AGTAGTCTT TAAGTTGCAA        2760

CCGCTTGTCT TCTGGCAATA GACCGCGAGT TACTGGGTCA AAACCAGTGT GTAAAACCGA        2820

ACTTCTATGA GGGCATGATG TTGAAGTAAA TTCATTGTGC AATCTGATTG TATTTCTGTT        2880

TGCTGGTAAT CCCCATTTTT TCAACAATCT AGCGCATTCT TGGAAAGTTG CCTGTTCATT        2940

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGATTGACAT ACTTCAATAC CGTAATAATA        3000

TTTATTACCT ATTTGATTAG CGGTATGCCA ACCTACTTGT GATTCATCTA AGGCTTGCCA        3060

AACTGTGTTG CCTGATACGT AACTATGCGC AATGCCCGCT TCTAATCTTG ATAAAGGTGC        3120

ATTTACTAAT CCGTTACGAT ATGCTTCAGC AGTCGCCCCT TTGCTCCCTG CGTCGTTGTG        3180

TATAACTATA CCTTTAGGGT TACTACCACG CTTAGGTAGG TCATAACCTT TAACCACATC        3240

TTTGATGATT TTAAGTTCTA CTGCTTTAGG TTGTGGCTTA GCTGTTTCTT TTTTAGGTGC        3300

TTGTGTAGGA GATTGAACTG ATCGTGGCGC TGTCTCACTT TTAAAATTCG GACGGATAAA        3360

CCACATAGGG AAATCATAAG CATGTTGTCG TCTTGTAACT TTTTCCCAAC CCCAGCCGGG        3420

TTGTTCGATT CCGTCAGTCC AGCCACCGCC TAGCCAATTC TGCTCATATA CAATGATGTA        3480

ATCTAAAGTT GCTTCAATTA CCCATGCAAC GTGACCATAT CCAGCACCGT AGTTGCTACC        3540

GAATACCACC ATGTCGCCAG GTTGTGCTAA GAAGTCCGGT GTATTTGGT ATACAGTAGC        3600

TAATCCGTCG AAGTTGTTAG CGAACGGAAT ATCTTTTGCA CCTAAACCTT TTAGAAGTAA        3660

TCCAAACAAA ACTTTCCAAC CAGCATTGGC ATAATCAAAG CATTGAAATC CATACCATAA        3720

GTCCACATTG AATTGTTTTC CCTCAGAAGT TTTCAACCAC TCTATAAACT CATTTTTAGT        3780

TAATTTTGCT TGCATTGTCG CCACCTCCAT GATGATACTC ATTCACATCA AAGCCAACAT        3840

CGTTAGAGGC GTCTGTGAAA GGTTGTGATG TATCATATTC TTTTGGTGcT TTCGCGCTTA        3900

ATTCCGGCGT TAAACTACTG TCTTGTGATG ATTTCCACGT AACTTGTTGT TCTTCTTTTT        3960
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TTGGGTCAGT AATAACGCCA ATACCTGTAA GTAACGTGAG GATAGCGCCT ATAATTGCGC      4080

TAGCTTGATT TAATTGAGTA GATAAATCTA ATCCGAATAA ATCCGTGACT TGCTTGATAA      4140

ATAGCAACAA TGCTCCAACT AAACCAGTTA GTACTGCTTT GTTTTTGAAT CTCAATTTCC      4200

AGTTAATATC CATTTGTTTG CTCCTTTTAT CCAAAATAAA AAAACGACTA AAAATTAGTC      4260

GTTTAAAATT ATTCAATGGT CAATGTCGGA GATCCTGAAT AAACATCACT TATAGTGACG      4320

TACAACATCC CTGAAGGATT ACTAAAGTTG ATATTTTTAC TTGCAACTCC GCTATTGACT      4380

CCTGATATTC CTAAATCACT TGACCCTAAA TTAGTTTGCG AAATCCTCAT TATACCGCTA      4440

CGTACATTTT CTATTGTCAC CTGATAACTT TTATTGGGTT CAACTCCATT TATTGTCCAT      4500

TTTGCTGTTG ATTCTTCTAT GCTATCCGGA TATTTATTTT TAGGTAAGGG TTTTATTACA      4560

AAAGATGAAG GCTTTTTCCA TACTTGGATA TTTCCAGCAT ATACTTTTGT ATATTCTTCA      4620

CCTTCGTAAA TAAACTTCTT TACATTTTTA AAATTACCTT CCATAAAAAT CACCCTTTAA      4680

TTAAATATAA CGTATTCGGG TCTTTTTGAT ATATATAGTT ATATTCATTT TCTGTTCCTG      4740

TCCAAATTTT AACCGTCGGT TGAGATGCGC TTTTTAGTTG ATATAAATTA TCCGCTTGTT      4800

GTTTAGTAAA AGCTTGAGAT GACAAAACAT ACCGCTCGTC ATGATTATGA TTTTTTGGAG      4860

CATATAAATC ATTTAGTGTT TGTTTGAATT CCTCAAAATC TTCTGTATTA ACTTTTGAGC      4920

CAATCTGTTG CAATACACTT TCTGAAATAG AGTTGTTTTG TATTGCTTCT GCTAATTCTC      4980

TTAATGTGTT CATAGATTCA GGCGCGCTAT CAACTAGTTC AGCAATTTTT GTATCCGTAT      5040

ACGTTTTAGA GTCGTTGAGA GTTGTATCTT TGATTTTTTC AACTTCTTGC AATTTATTTT      5100

CTAACCCTTC AACATTGCG ATATTGATTT TGTCCAATAA CTCAGGTTCT GCTTTGATAT      5160

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CGTTTTTACC GGGTGCGCCT TGTTCTCCTT TTTTACCTGC TTCACCTTTT GCTCCAGGTT      5280

GTCCCGGTTC ACCTTTATCA CCTTTCGCAC CTTTAAATCT ACTTTCATTC TTTTCGATGT      5340

AAGAAATGAC ATCTTTATCT ATTTTCTCTT TAAAGTCTTT GCTCAATAAA TCTGTCGCGT      5400

TATCTTTTAA AATTCTCGTA ATAGCATCAT CTACCAATTT AACATCGATT TCTTTTGCTA      5460

CAGCAGATTC AATACCACTA TCAACGATAT TGAAAGAAAA GTTTGCGACA TGTATTTTTT      5520

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TAGGTATCTT GTAGGTAAGG AAACCTTTTA CAACATCGTC GATAATAAGG GGCTCATTTT      5640

TGAATATAGA GCCATCTTCC ATAAACAAAT GTAATCTAGG TGTTAAGCCA TGTGCTTTTA      5700

GATCGATACG ACCTTGTTTG TCATTGATAC CTATTCTTAT AGATGCTGTA TTTTCATCTT      5760
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CAACATCTTT TATTTTGTAC ATTTACACAC CTCTTTATTT ATATTTATCC CTTGTGAAGT    5880

AGATACCTTT TAAGCCGATT TGTTTATATA ACTTAGCGAT TGTACTTGCT TGATGTTGGC    5940

ACCACTCTAT AGCAGTAGCG TATTGGTGGG TAGCTGGATT CTTAGGATTC CATCTAATTC    6000

GGTACAATGT GTTTTGACCT TTATTGATGT AATCCTTTCT TACGAAGCTA GCACCGCCCA    6060

TGATTGCTTT TGCTGGAGAT GTCCAACCTT TATTCCTTGC AAACGTCATT GCGTAGTTAG    6120

GATTGTTGTC GTAAGCGCCA ATGCCGAAGT AGTTGTATAC TCCATCTTTT CCGTTAGCGA    6180

AGTTACTTGT TCCATATCCA CTTTCTAAGA AAGCATGCGC GATTAAATAA ATTTCATTAA    6240

TGTTGTGCTT TTTACAAGCT TCTGCGAACG CTTTACCTTG ATTATTCAAT GTTCCCTTAC    6300

CTTTAAGTAT CTTATTAAGT GCGCTAACTG AAACACCTTG ATACTTGCCT AAATTAAGCA    6360

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GTGCTCGTGT AGCGTTAscC AACCCCAAGC ATTAGATTTT TTCGGGTTAC CTCTTGCCAT    6480

TTGTTTATCC AGTGCTTGTT TGAATGTATA AGGACTCGTT TCTGTTATGA TCTGCGGTTG    6540

TTTAGATGCC GAACCATTGT TGGCTGTTGG TGACGAGTCT CTTACATTAG CTATATCAGC    6600

GTTTTTATTA TCTACCATAA CTTTTATTCT AGATTTTGTT ACTGTTGGCT TAGTTATAGA    6660

ATTTAATAAT TTTTCTCTGT TTTTAAATAT ATTAAGTAAT GCCTTTTCTA ATGCTTCGTA    6720

TTTATCTTTA GGAGGAACAC CGTTGTCAAT CATATTCCAA TTAACATGTT CCAACATTGA    6780

ACGCCAAATG CTGTCGTCTA CTTTTAAATT TTCAATACTT AGAGGTATCT CATATTTGGC    6840

CATCATATCT ACAGCTACAA CCATTGCGTG AATCTCATTA AAAATAAATT CATTTTTACT    6900

CGCACTATAA TCTTCACATA CGTCTATAAC TATATAATCA GGTTCATTAG GAACTTCAAA    6960

TACAGCTCTT CTAGGTGCCC AAATATTATG TCTATCAACA TAAAAGTGGG GATATTCTAC    7020

ATCCTGTTTG TATTTCTTCC TACTGTTATA TAAACTTTCT ACCGAGCTCA TCGTTTGTGC    7080

GTTTCTAATC ATTATTCCTT TAGGTTTTTC GAGTCGTCGA TTACCTTCTA CTATAAAGTG    7140

ATAAATATAT TCTGGATAAT TAACCTCTTG GCTAGAAATA GTGTACTTTA TAGTTGTTAC    7200

ATCTTTCCAA ATTGGAACTT TTTTATTATT TTTTTCGTTA TCATCACTAT CATCTTCTGG    7260

TTTAGGTGCC GGTGTAGTTT TGTCTGGATG ATATGGTGGT CTAACAAAAT ATTTAACCCC    7320

TCCACCTGGT CCATCATGAT AAGAGTGTTT AATTTTATAA GGTGGACTTC CTGTTGCGTT    7380

ATTTGTATAC CAGTTTTGAT CTACGCCATA CCAATAGTCT TTTGTGCATG GTCCCACTAC    7440

AATGTTTACA TGTCCTGCCC AACCACCAGT CCAAACACCC CAGTCGCCTG GTTGTGGTAC    7500

AAAATCTTTT GTATTTCTAA TTATCTTGAA ATCTCTACCT CTATAATTGG ATTTTTGAGC    7560
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TAAATCCCAG CATTGTGCTC CCATTCCAGA ACCAGGTACA TCAATAGCTA TTTTGTTTTT        7680

AGCGATATAT AACGCCCATT CAACCACTTC ACTAGCTGTG GGCTTTCTAT TTTTCGGATT        7740

AGGTAATCCC ATGTATGCAC CTCATTTCAA TCAAAATAAA AAGCCAGTGC CGAAGCACTG        7800

ACTCTTAACT GTTATTTACA TTTACCAAAC CAGAAGCACG CCCAGAAGCT ATATCCTAAA        7860

ATCCCTTTAA GCATGGTAAT CACCTCCTTT AAATACCAAA AACAGTTCTT AGTAAAGCTA        7920

TGACAATCGT ACTGAAGATA GTCCCTATCA AACCTAGAAT CCACATTTTT ATGTCTCTAA        7980

TATTCTTGGC ATTCTTTTCT TTATTCTTTT CATCTTCTAC CTTGTCGCGC TTTAATTCTT        8040

CAAAATTTCT ATCTAATTTG TCATAAATCT TTTCTTGCGC TCTAAGACTA TCTTCTATTC        8100

TGTCGAATTT TTCAAACATA GTCTTATCAT TTTCTTCTAA TCGCGTTAAA CGCCAATCTT        8160

GTTCATGTCG TTTGGTAAAT CCAAACATTA TGCCACCCAC TTTATTCAAA TTAAAAAGCC        8220

ACAAGCATTA CACCTGTGAC TTTTCATCTT TTGTTTCTGG ATATTTTTCT CCAGTGATTA        8280

AAGCGTATTC TTCTTTATCG ATTAAACCCT TGTCTACGTA CCACTTAATT TGCTCGTTTT        8340

TATAGTAACC CCAAACATAA AAAGTTTTAA TGTCTTTAAA AGTTGGATAA ATCATCTTCA        8400

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TTTGCATACT CGCAACCATT CCGCGAAGTT CCTCATCACT TAAATCTGAC GCACTTTGTT        8580

GGTTTGATGC ATTCGGTACG TCTTCTTTTT CGAAATTGCT ATTGTATTTA ATTTCGCCGT        8640

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GGCATTCGCT CCAGAACCTG ATGTTTTACC TAAATCAAAG TACACATCGT TATCTATTCT        8880

TAAAGTAGTG CTACTTGTTT TGGATAGTAA GCACTCATAA ATACCGCCAC CGTTGCCGTC        8940

TGAGTCAACT ACATTCGCTT TACTCAATTG AATCGCGTTA GGTAATGCGG TTAGTCCGAA        9000

TCCCTCAATA ACGCCACCTG GATAAGTTCC ACTTACCAAC AAAATAGAAT AGTTTGTGTA        9060

CGGTTCAGTT AGATTGATTG TTGTACCTAC ACCATTTGCG CCACCGTCGA ACAATACCGT        9120

TGATTTATGT TCATTAGGAA CTGTCCACTG TTGCTCAAGT CTGCCGTTTG TGATTGATCG        9180

TGTGTAAATC TTTTTAGAGT TATAAGGTGT GAAGTTAAAT AGCTTGTTTG TATCATCTTT        9240

AACGAATACC GATAAATAAC CCTCATAACT TTCAACGCTA CCTGGTAAAT CCGGCACTCT        9300

TGTTGCATAG TAATTACCAG CAGTTAAATA TCCCAAATCG CCTTGCGCAT TATTTAAGTT        9360
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GAATTTATCA TCTACATACT GCTTAGCTTG ATTTAAAGCG TTGTTAGACG TTTCTTCAAC        9480

AAATTGCTTA GTTAAGTTTC CATCATTCTT TTTATAAAAC GGGTACCATG TGCCGTAGAT        9540

TTTGTATTTT GTGTACTCAT CGTTTGAATC GTCTGGGTAC CATGTTGCAC GAGCAGTATT        9600

ATTATCAACA ACATAAACAA CTAACACACC AGATTTGCTT GATGTATAAG TTGATTCATC        9660

GAACGAAGAA CCGTCATCAA CACCATCTTG TCCAGGCTTC TCTAACGTGC CTATATCCGT        9720

CTTTTCTGGC GCATCTGTTG CATTAGTAAT ATGAATAATC CTAGATGTGT TAACTGCGCT        9780

TAAAACGCTA TCTATGGACT GCTCATACGA TTCAATTGCT TTACCGTAAT CATCTGTAAG        9840

TTTAGACTTT TGCCAATTCG TTGTTGAATT ACCTTTAACA AGGTCAGCGC CATTGATTTG        9900

TTGTTCAACT TCGTTAACAC GTTCAAAAAT CGCTTGCTCT TTTTCAACTA TTTTATCGAA        9960

TTCAGCTGTA ACAGCTTGTG TTGCACTAGT TTGCGTCGCA GTAATAGCTT GTATAGCTTC       10020

GTTTTGCTTG ATTTCGATTT GTTGAATGCC TTTTGTCGCA CTATCATTCA CTTTTGCTAT       10080

TAACGTTTGT GTATCAGCCA TATTTTGCTT TAATTGGTTA AAATCTTTAC CGACAGCTTC       10140

GATAGTATCT TGAATAGATT TGATATAAAC AAGCTTTGTT ATACCATCAA ACCCACTAAC       10200

TAAATCATTT TCAATATTGA AGCTAAATTG ACGTTCAACA ACAACATTAT TACTCCCGTT       10260

TTGTGTAAAG AATGCCTGAG CATGCACCTT GCCTGAATGT TTTAAAAATT CATTCGGTAT       10320

CACATACTGC AAACGCCCAT TAATTGCGTC TACTATCGTT AATTCGTCTG AAATATAAGC       10380

GCCTCTATCT ACGTTATAAT CATCGGTTTT TAAnACGATA GATGTTTTAA CATGTTCAGA       10440

ACTTATAGAT AAGGGTCTGT TATnCTTAGT                                        10470
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(2) INFORMATION FOR SEQ ID NO: 21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3647 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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ATCAGATCTT GAGAATCGAG TTATTAAGTC TATCGAAGAC TTAACTAAAA TCCAACCATT          60

CATGCCTACA CAAGATTTTG ATTTTAAAAC TAAAGAAATT CAATCAAACA TTTCTGAAGA         120

AAGATTTATC GAAATGATTC AGTATTCAA AGAGAAAATA ACAGAAGGGG ATATGTTCCA         180

AGTTGTGCCA TCAAGAATTT ACAAATATGC GcATCATGCT AGTCAGCATT TAAATCAACT         240

TTCGTTTCAA CTGTATCAAA ATTTAAAACG ACAAAACCCA AGTCCATATA TGTATTATCT         300
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TCAAATTGTA ACAACTAATC CTATTGCAGG TACGATTCAA CGTGGTGAGA CGACACAAAT          420

AGATAATGAG AATATGAAAC AACTACTTAA TGATCCAAAA GAATGCAGCG AACATCGTAT          480

GCTAGTTGAT TTAGGACGTA ATGATATTCA TAGAGTAAGT AAAATCGGTA CCTCAAAAAT          540

TACTAAATTA ATGGTTATTG AAAAATATGA ACATGTTATG CATATCGTAA GTGAAGTCAC          600

AGGTAAAATA AATCAAAATT TATCGCCAAT GACAGTTATT GCGAATTTAT TACCAACAGG          660

TACCGTTTCA GGTGCACCAA AATTACGTGC AATTGAAAGA ATATATGAAC AATATCCACA          720

TAAACGGGGC GTTTATAGTG GTGGTGTTGG ATACATAAAT TGTAATCATA ACTTAGATTT          780

TGCATTAGCA ATTCGAACGA TGATGATAGA TGAGCAGTAT ATCAACGTAG AAGCTGGTTG          840

TGGCGTTGTA TATGATTCTA TTCCTGAAAA AGAACTGAAT GAAACGAAAT TGAAAGCTAA          900

AAGCTTATTG GAGGTGAGCC CATGATCTTA GTTGTAGATA ATTATGATTC CTTTACATAT          960

AACCTAGTGG ATATTGTTGC TCAACATACT GACGTCATTG TTCAATACCC TGATGATGAT         1020

AATGTGCTGA ATCAATCGGT GGACGCTGTT ATTATATCTC CTGGTCCAGG GCATCCATTA         1080

GACGATCAAC AGTTAATGAA AATCATATCA ACCTATCAAC ACAAACCCAT TTTAGGTATT         1140

TGTTTAGGGG CTCAGGCACT GACTTGTTAC TACGGTGGAG AAGTCATTAA AGGCGACAAG         1200

GTTATGCACG GCAAAGTTGA TACACTAAAG GTTATATCGC ATCATCAACA TCTGTTATAT         1260

CAAGATATAC CAGAACAGTT TTCAATTATG AGATATCATT CATTAATAAG TAACCCTGAC         1320

AATTTTCCAG AAGAATTGAA AATTACTGGA CGTACCAAAG ATTGTATACA GTCATTCGAG         1380

CATAAAGAAA GACCGCATTA TGGTATTCAG TACCATCCTG AATCATTTGC TACAGACTAT         1440

GGTGTCAAAA TAATTACAAA TTTCATTAAT CTAGTGAAGG AAGGATGAAA ACCATGACAT         1500

TACTAACAAG AATAAAAACT GAAACTATAT TACTTGAAAG CGACATTAAA GAGCTAATCG         1560

ATATÁCTTAT TTCTCCTAGT ATTGGAACTG ATATTAAATA TGAATTACTT AGTTCCTATT         1620

CGGAGCGAGA AATCCAACAA CAAGAATTAA CATATATTGT ACGTAGCTTA ATTAATACAA         1680

TGTATCCACA TCAACCATGT TATGAAGGGG CTATGTGTGT GTGCGGCACA GGTGGTGACA         1740

AGTCAAATAG TTTCAACATT TCAACGACTG TTGCTTTTGT TGTAGCAAGT GCTGGcGTAA         1800

AAGTTATAAA ACATGGtAAT AAAAGTATTA CCTCaAATTC aGGTAGTACG GATTTGttTAA         1860

ATCAAATGAA CATACAAaCA ACAACTGTTG ATGATACACC TAACCAATTA AATGAnAAAG         1920

ACCTTGTATT CATTGGTGCA aCTGAATCAT ATCCAATCAT GAAGTATATG CAACCAGTTA         1980

GAAAAATGAT TGGAAAGCCT ACAATATTAA ACCTTGTGGG TCCATTAATT AATCCATATC         2040

ACTTAACGTA TCAAATGGTA GGCGTCTTTG ATCCTACAAA GTTAAAGTTA GTTGCTAAAA         2100
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AAGCAACACT ATCTGGTGAT AATTTGATAT ATGAATTGAC TGAAGATGGA GAAATCAAAA      2220

ATTACACATT AAATGCGACT GATTATGGTT TGAAACATGC GCCGAATAGT GATTTTAAAG      2280

GCGGTTCACC TGAAGAAAAT TTAGCAATCT CCCTTAATAT CTTGAATGGT AAAGATCAGT      2340

CAAGTCGACG TGATGTTGTC TTACTAAATG CGGGTTTAAG CCTTTATGTT GCAGAGAAAr      2400

TGGATACCAT CGCAGAAGGC ATAGAACTTG CAACTACATT GATTGATAAT GGTGAAGCAT      2460

TGGAAAAATA CCATCAAATG AGAGGTGAAT AATATGACGA TTTTATCAGA AATTGTTAAA      2520

TATAAACAGT CACTTTTACA AAATGGCTAT TATCAAGACA AACTTAATAC CTTGAAAAGT      2580

GTGAAGATTC AGAATAAAAA ATCTTTTATA AACGCAATTG AGAAAGAACC AAAGCTAGCA      2640

ATTATTGCAG AAAATTAAATC GAAGAGTCCT ACAGTTAATG ACTTACCTGA ACGAGATTTA      2700

TCGCAACAAA TCTCAGATTA TGACCAATAT GGTGCAAATG CCGTGTCCAT TTTAACTGAT      2760

GAAAAGTACT TTGGTGGTAG TTTTGAAAGA TTACAAGCAT TGACGACAAA AACAACATTA      2820

CCCGTATTAT GCAAAGACTT TATTATAGAC CCGCTTCAAA TTGATGTTGC TAAACAAGCT      2880

GGTGCATCTA TGATTTTATT GATCGTTAAC ATCTTATCTG ATAAACAATT GAAAGATTTA      2940

TATAACTACG CTATATCGCA AAATCTAGAA GTGTTAGTTG AAGTACATGA TCGCCATGAA      3000

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CGATTTGTTA CAAATGTGGA ACATACAAAT ACTATTTTAG AAAATAAAAA AACAAATCAT      3120

TATTATATTT CTGAAAGTGG TATTCACGAT GCATCTGATG TAAGAAAAAT CTTGCATAGT      3180

GGTATCGATG GCTTACTAAT AGGTGAGGCG CTTATGCGTT GTGACAATCT ATCTGAATTT      3240

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ACGTATTAAG CAATACGTCA ATTAACACAA TACAGTTACA CgGCACAGAA TCTATTGATT      3540

TTATACAGGA AATTAAAAAG AAATATTCAA GCATTAAAAT CACTAAAGCT TTAGCTGCaG      3600

ATGgAAAACm TwATCCCAAA caTtAAtnAA tnTTAgGGGG TCCGTGG                    3647
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(2) INFORMATION FOR SEQ ID NO: 22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5966 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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CcAcCTTGAC CACCTTTACG TGGAATCTTT TCmCCTkGAG CAACaTCGaT AATaTATATT        60

GAAAgTCAAC AAGTTCTGGA CTAAATGTTG CTGCTAAGTT ATCGCCACCA GATTCTATGA       120

AAATTAGTTC TATATCGTCA TGACGTTCTA ATAATTCGTC TATTGCTGCA AAGTTCATAG       180

ATGCATCTTC ACGAATCGCA GTATGAGGAC ATCCACCAGT TTCAACACCA ATGATACGAC       240

TTTCAGGTAG AACTCCTGAA TTTACTAATA TCTTTTCGTC TTCTTTTGTA TATATATCAT       300

TTGTAATAAC GCCGATACTC ATTTCTTTTG AAAGACGTTT TACAACTTTT TCAATTAATT       360

GTGTTTTACC TGCACCTACA GGACCACCAA TACCAATTTT AATCGGATTT GCCACAATTA       420

TAACCTCCTA TGATATGAAA tTCTAACATT GaCGTTCTCA TGCGCCATTT GATTTAGTTC       480

TAAACCAGGC GCTGTCATGC CAAAATCTGC TTCTTTTAAT TCGAAAATCT GCTTTCTTGT       540

TCCTTCTATA TAAGGAATCA TGTGAGTAAC TATCTTTTGA CCAGCAGTTT GTCCAAGTGG       600

AATAGCACGA ACAGCATTTT GAGTTAAACT TGAAACATTT TGATATAAAT AGTAATCAAT       660

AATCGTTTCA ATATCTACAC CTAAATGATG GCCTAGCATA GTAAAACAAA TAGCTGGATT       720

TnACTTTGCT TTCTTATCTT GCATTGTTG ATGATACCAA GCAATCCATG GGCTATtATA        780

AAGTTCTAAA GCCAATTTAA CCATGCGAGT CCCCATTTGT kTTGCACCAA CACGTGTTTC       840

TTTAGGTAAG TTTTGrACAr ACATCAGTTT ATCTATGTGT AATACTTTTT GTGTATCATC       900

ATTTTCCAAT GCATCATAAA CTAaACGCAT GGCTAAACCA TCAGAATAGG TAAGTTGCTC       960

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AATATATGTT TCAAGACCAA ATGAATGACT GAAAGCACCT GTTGGAAACT GTGAATCACA      1080

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CCTTATTAAC TTTACGGTCT TCTCGAACAT ATGGGATGCC TAAACTTTTT AATAAATCTT      1200

CAACTAAATA ATCATATTGT ACTAGCATTT CAGTCTCTGT AAATTGTGCT GGCAAATGAC      1260

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GCTTTTGTTT TTCTGAATTT GACAAATTGG CAATATTGCC TTGGATTTCT TCAACAATCA      1560

TTCTATGTTC CTCCTAGAAT AAGAAGTATC TTTGAGTTAA TGGTAACTCA GTTGCTGCAT      1620

TACTTGTAAT TTTTTCTCCA TCTACATATA CTTCATATGT TTGTGGATCA ACGTCTAATT      1680
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GACGCACCAT GCGTTTTAAA TTTAATGCAC GATTGATACC ATTTTCATAA GCAGTTTTAG        1800

ACACGAATGT CATTGACGTA CTTGTAAGGT TTCCGCCGTA TTGACCATAC ATTTTACGGT        1860

ACTTCATCGG TTCAGATGTA GGTATAGAAC CATTTGCATC GCCATTTACG GCAGAGTTAA        1920

TTAATCCGCC CTTTACAACT AATTCAGGTT TAACCCCAAA GAAAATTGGG TCCCATAAGA        1980

CAATGTCAGC TAGTTTGCCC GGCTCGATAG ATCCTACATA TTCAGAAATA CCATGTGTAA        2040

TTGCTGGGTT AATTGTATAT TTAGCGATAT AACGTTTGAT GCGATTATTA TCATTATGTT        2100

CAAAATCACC ATCTAAAGGA CCACGTTGTT CTTTCATGCG ATGTGCTACT TGCCATGTTC        2160

GTGTAATTAC TTCACCTACA CGGCCCATTG CTTGTGAATC GGAACTAATC ATACTGAATA        2220

CACCCATATC TTGCAGAACA TCTTCTGCTG CAATCGTTTC TTTACGAATA CGTGAATCTG        2280

CGAATGCGAT ATCTTCAGGA ATAGCCGCAT TTAAATGGTG AGTAATCATT ACCATATCTA        2340

AATGTTCATC TACAGTATTA TGTGTATAAG GCAAAGTTGG ATTTGTAGAT GAAGGTAAAA        2400

TATTTGAAAA TGCAGCGGAT TTAATTAAAT CAGGCGCATG ACCGCCACCA GCACCTTCAG        2460

TATGGTACAT ATGAAGTACA CGGTCTTTAA CAGCAGCCAT TGTGTCTTCC ATAAATCCTG        2520

CTTCATTTAA AGTATCTGCA TGTAATGCAA TTTGAACATC AAATTCATCA GCAACATCTA        2580

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AACCGACATT AATCGGTAAA CCTTCGGCAG CTTCTAACAT TCTATGAATA TGCCATGGAC        2760

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TCGTAATACC ACTTTCTAAT GCGACCTCTG CTTGTTCAGG ATTAATAAAA TGAACATGAG        2880

TATCAATACC ACCAGCAGTG ACGATTTTAC CTTCAGCGGC AATGATATCT GTTGTTGAAC        2940

CTATAATAAT GTCGACATTA TCCATTATAT CTGGGTTGCC GGCATTACCT ATGGCGAAAA        3000

TATAACCATT TTTAATGCCT ATATCAGCTT TAACCACTTT ATCGTAATCG ATAATAACGG        3060

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CCATACCGTC TCTAATAGAT TTACCACCAC CAAAAGTAGC TTCTTCACCA TAAACCGCAT        3180

AGTCTTTTTC TATTTGAGCA AATAGATTCG TATCACCTAA ACGAATGGAA TCTCCAACAG        3240

TTGGACCGTA TAAGCTCGTA TATTGATTTT GCGTCATTTT AAAGCTCATG ATCTTTTTCC        3300

TCCTTTTTTA TTCACGTTTT CAGCACCGTT ATCTCCGAAT ACACCTGCAT ATTCATCATT        3360

TTCATCAGTT GGGCGATAGA CACGTGACTC ATCGATAGGA CCATTGACCA TACCACGAAA        3420
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TTCGAAATCT AATGCTGCAT TTGCTTCATA AAAATGAAAA TGTGAGCCCA CTTGAATTGG        3600

TCGATCTCCT GTATTTTCAA CTTCGATAAC TGTTTCAGGA TGATGGTTAT TAATTTCAAC        3660

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GGTGATGTAC TGTGATTAAC TTAGTACCAT CGGGGAACGT AGCCTCGATT TCGATATCTG        3780

TAATCATGTG TTCGACACCA TCCATGACAT CTTCTTTGTT TAGAATTTGT CTACCATAAC        3840

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CGTTAACAAT CTTTTTAGAT AAGTCAGGAT TAGATATTGT TATAACAATG ATAGCAACTT        4560

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ACAATGATAG AATaCATTTC ATTCAGTCAT TATTTGAAGG ATTCAGTCAA GTATTTATCG        4800

AAGCGAGTGT AATTGGTGGC GTATGTATTT TAATCGGCAT ATTGATAGCA TCAAGAAAAG        4860

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CATTAACATT GCCATTTATT ATCGTGACAT GGATTTTATT ATTTGCTGGT ATTAAACATG        5160

ACAAAGTAGA TGCTTGATAG TTAAATCAAA CCTAATATTG TTTGAATATC ACCTTAAACT        5220

ATACAGCGAA TTGTATAGTT TAAGGTGTAT TTTTATGGAT AAAATTAAGT GCATACTTAA        5280
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GTGTTAAACT AGGAATAAAT AATTTATATT GTGTGTTGTG TGGGGTGACT AATATGAATG        5400

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CATATAAAAA TATTGAATGG TTAATTAAAG AAGGTTATGG AAAATTAACG TTACCAAAAG        5580

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AACTTGATGG TGCCACAGCA TTATCTATTG GTTGGCATGT GAGTGTCGTA GGACAAATTT        5700

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GTGCATTAGT TAATAGAGCA GTTAGTGAAG CTGAAATGGG TAGTCCAACA AGAGGGGGAA        5820

GACCAAGTAC ACATGCTGTT AAAGCTGATG ATGGGTATAT TTTAAATGGT GTGAAGACAT        5880

ATACATCAAT GAGTAAAGCA CTAACACATA TTATTGTTGC TGCTTATATA GAAGAATTAG        5940

AAAGTGTTGG TTTTTTCTTA GTAGAC                                             5966
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(2) INFORMATION FOR SEQ ID NO: 23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17310 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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CTGTGTCATC GCGAAATAGT TAGGGTCATT CATTAATCCT TTTGAACGTA TTTCATCAAA          60

ATATAACAAT TTCATTAGTA AAGGGGACTT GTTCAAACCA GCTATAATAC AAAATAGACC         120

TATAGTCACA CTGCTTATAA TATAAGAGGT AACGATCACT TTTTTGCTAT TACCTAACTT         180

AAAGATGATC ATCCCTAAAT AGAAATAAAT GACTACAAAT GCATATTTAA CTGTAGATGC         240

AAGAACTTCC TTAACCGTAA TAAATATCAA ATCATCAAAA AATaGCaAAC AArGCGTAAT         300

AATCATACGA TATGTATACA AAATAATGАm AAACTGTmAA AAATGATTTG CCTTTAATAA         360

ATGGTTAGCG AAAAACAGTA AATAAACTAA TATTAGTAAT GTGATAAAGT CAGCTATAGA         420

AACATTCACA CCGGCAATAA CCGAAGATTG CTGAATAAAA ACCGCTAAAC CGATAAGTAA         480

CAATGTTAGT AATTTACTAT TGTGTTGATT TTCCATTATA AACGTCTTCC ACTTCTTTAA         540

TCATTTTCTC CTCAGTAAAA CATTCTAAAT AACGTTTTCT AGATTGATTA CTCATTTGA         600

TGTAATCACT GTCTATTAAA TATTTTTCCA GGACTTTAGC AATAGTTTCG GGTTGGTTGT         660
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TTATTAAAAT AAACGTATCG TATTGTGATA ATAAATGACT CGCATTAATG ACATTGCCCA        840

AAAATGTGAC ATCATTTTCT AACCCAGCTT GTACAACTTG TTGCTGACAA TCATTTAATG        900

TAGGTCCATC GCCTATAAAT GTAAAATGCG CATGATTACT GTTATGTAAT TTCAATATCT        960

CTATTGCCGC GATTAGATTT TGTGGCAATT TTGGATAAGC AAATCTTGCA ATCATAACAA       1020

ATTGATGCTT TGTCGGGGCA TTAATCTGTA AATCTTGTTT ATTAGGCAAC ATTCCAACTA       1080

CTTCGCCAAT ATTGTTATGT GATTGGCTTT TTAGCGTTTG CTTAACAGCG GGAACATCTG       1140

CAATACCATT ATGTATTGTG GTTAATTTCA ATCGATTAAA TCGATATTTT AACGCTAACT       1200

GTTTATCGAA ATCTGAAACA CAAATAATGC TATCTGTAAT AAGTGACATT AATTTTTCGA       1260

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CAGTAAAAAC TATACGTGTG TCTTTCGATT TCGAAATGAa CTtCGCAATT CGTCcGACCG       1380

TtCCAGCTTT GGAAGAATGT AAATGGATAA CATCAGGTTT AATTTTCGAG AATAACTGTG       1440

CTAACACTTT GACAGCTAAA ATATCTTGTT TAAAGTCAAT TGGACCTACT AAATGTTCGA       1500

TAATAATTAC ATTAACTCTT GCATCTAGTT GTTCAATCAT TGGTCCATGA TTGCCTACAA       1560

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CACCACCATT GTCTGCTTTA GTAATACAAT ATATAATTTT CAACTGTTAC AAACCCCTTT       1680

AATGCTATAC TTTCAATTTC TTAACATGGC TATCTCATCA GATGAATAGT ATTTATAGCC       1740

ATGCAAATCA ATGATGGCAC ATATTCTTA ATGCCATTTG ATACTGTCTC AAGGGATTCC       1800

TCGTTATACT GTAACAATTG GTCACAATCT TTAAAATATA ACTTTTATTT GAACTTATTA       1860

AGTAAATTAA GACTACCTTG AGCCTTCCCC TGTAATAACA ACCATCAATG TTCTAATTGA       1920

TATATATAGT TCCATCATTA AACTACCTTT ATGTATATAT TTCATGTCAT ATTTCAGTTT       1980

TTGTTGCGGT GTTAAGTCAT ATCCACCTTG AATTTGCGCA AGTCCTGTTA ACCCTGGTGT       2040

AACAAGACAT CTTTGCTCGA AACCTATCAC TTCTGAACTA AATAATTCTA CAAATTCCGG       2100

ACGTTCCGGG CGTGGTCCAA TAAAACTCAT TTCCCCTTTA ACAACATTAA TTAGTTGTGG       2160

TAATTCATCA ATGCGTGTTT TACGAATAAA CTTCCCGACA TTTGTTATAC GATCATCATC       2220

TTTATCAGCC CATTGCGCAC CGTTTTTCTC TGCGTTTTTG CACATCGAAC GTAATTTGTA       2280

TATTTTAATT AATTTACCCA TCTTCCCAAC TCTAACCTGA CTATAAATAG GGTTTCCTGG       2340

CGAATCTATG ACGATAGCAA TGGCGAATAT AACCATAATC GGTAAAGTTA AAAATAATAA       2400

AACAATGCTT AAAATTAAGT CAATCGCACG TTTAATTGGG TAATAGCTTT TTCTCACTTC       2460

TTCTAGTTTG TCTAATTTTC TTTGATAGGC ATAACCCTTA TTATTATGGA CAGCTTCAAT       2520
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AATTAAAGTA ATCCTTTAAA CCTGTTTCTA CTGTATATTT AGGAACAAAT CCTAATGCCT        2640

TTAAGTTAGA AATATCTGCA TAAGAATGCT TAATATCTCC TTTTCGTGCT TCTTTAAATT        2700

CATGCTCGAC TGATTTTCCA TATAATTCAC CAATAATACG ATAAACCTCT AATAAATTAG        2760

TAAAAGTGCC TGTACCAATG TTATAACCGT GTCCAATTGC ATCTTTGTGT TCCATAATTA        2820

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CAAAAAATGT AAATGGCTTG TTATGCTCAA ATGAATCGAA CATCTTTGAA ATCACACCTG        2940

AATATTGTGA CTTAGGATCC TGTCTTGGCC CAAATACATT AAAAAATTTA ACAACCGCTG        3000

TTGGTATGTT ATATAACGAA CAATAATTTA ATGTCGTCCG TTCGCCGTAA TATTTATCTA        3060

TTGCATATGG TGATAATGGT AAGATTAATG ATTGATCACT TTTAGGCAAA TCAGGAAGAT        3120

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CAAAGCAATC TGACTTGTAA ATTGTTCCCA ACCCCATGCT TCAGGTTTAC CTGCTTCTTC        4020

GGCTGTTGCC ACTGCGATAC TTTCCATCAT TGGTGTTTGA CGATACCAG GTGCGAATGC         4080

ATTCACAGTA ATACCTTCAG ACGCTAAATC TTGTGCGGCT ACTTGTGTTA AACCTCGCAC        4140

TGCGAATTTT GTACTGCAAT ATAAAGACAA GCCTGGGTTA CCCTCAACGC CTGCTTGAGA        4200

TGTTGCATTG ATAATTTTAC CGCCATGATT GAATTTTTTA AATTGTTCAT GTGCGGCTTG        4260
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GCCAAATTGC GCGGCAGTTT GTCTTAcTGC GTTAAATACA TCATCACGGT TTGATACATC   4440

TGCTTTGATA GCAATAGCTT TTGTACCATC ACTTGATAAT TTAAGTGCAG CTGCTTTTGC   4500

CCCTTCTTCA TTGAAATCAA CAACTGCTAC TTTGAAACCA TCTTCCACTA AACGTTCTGC   4560

AATTTTAAAA CCAATCCCTT GTGcTCCGCC AGTTACTAAT GCTACTTTGT TGTTTGTCAT   4620

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TACAACAAAG GTAGCTCCAT TTAACAAAAT ATTCAGATAT TTAAGGTATA GTTAAACGCA   4740

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TCCCTTTACT TTTTTGAATA GTGGTAGTAT CTGCTGCAGC TACTAATTTT TTTCTACCTA   5100

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CCAGGGCCAC CAAAAATAAT ATGATTTGCT GGTTTAAAAG CAAGACCTTT TGCTATTTCA   7860

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TGTGCTTTTA ATTGTTCAAT AACAGGTTGA ACTATACGCA TTAGCCTTCA TCCCCTTTCT      8100

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CCAGATGCTT CAATTTGCTG TACAAAATGT TCATAAGTCT TATCGCCAAC TTGTTGACGT   10020

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TCATTTTTAG GAAATGTAAA TACAACCTCT CTCAATAATT GTGTATAGTC TGTTGTTGTA   10380

TCTGCCTCAT CTCCTACGAC ACGCTCAATT GGTGATGTGA TACGTATACG ATCAAAGCTA   10440

TGTGTCTTTT CAGCAGTAAA ACGATACTCT GAATCATGTC CTTCTATTGT AAAATGACCG   10500

ACACCGTCTT GATATGACGC TTTATACACA ACAATATTCT CATAAATAAG TGATGATACC   10560

AGTTGGTGCA TCACTCTAGT CTTTACACGA TTAAGAATTG TTTGATTCAC AATACGATAC   10620

CTCCTTGTTA TGACAAATTG GATTTGGTAT ATGTGTATAA ATAGGGTTTG CACCACAATC   10680

ATTCAATTTA CTCATCAAAT TCGCTTTAGC CGcAATGGTC GGCGTTTGAT ATAAATCTTC   10740

TACACAGTCA ACAAATACTG CGTTATTCGC GTATTCTTTT TTCCAAGTCA TAAGACGATG   10800

CGCTACAAGT TGCCATAACA CAACTTCATT TCTAGTCGCT TTACCAATAG TTGATACTAA   10860

ATGTCCTAAG TGATTTACTA CAACGTAATA TTTAAGACGA TGCCATGCTT CATCATGTGC   10920

ATATACAACA GGGCTTGATG CTGCCACAAC ATTTGGCACA AGCTGTTTTT CAGTAGCAAT   10980

CGTTCTAGAT AGACAAATGC CTTCAAGATC TCTGACAAAG CATACGTCGG GTATGCCATC   11040

TTTTAATTCA ATTAATGTAT TTTGTACATG TGCTTCTAGA CTAATGCCTG TGTTACTAAA   11100

CAGCTTTAAT ATCGGCAATA ATGTACGATT CAAATAACAT TCAAGCCATG CTTCTGGTGC   11160

TAAACCACTT TGCTCAATCA CTTGTGATAA CTTAGACATC GGTGAATCAG GCATCGTTTC   11220

AAATAATGAC GCCAATACAT GAATATCTTT ATCAGCATGG TAATTCGGTA TCCCTTCACG   11280

AACAATCATG GCACTATTTG TTAATAAATC CATTTCAGGT TCAACTGTTT GCCCTAATGG   11340

ATTCGGTAAC AATGCACGAT ATCCTTCTTC AAACATCAAT TTAAAATGGG GTGTTTCAAC   11400

CTCATCTTTG ACTGATGCGA TAACTTGCGC GGCATCAATT GTCCGTTCAA TCTGTTCAAG   11460
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GCCAAGGTCT TTTATTAAAC CTTGTTCACT ATATTGCATA TACTGTGGAT GCTGTCGCAA        11640

CACATTGATT TGATAAGGAT GTGTTGGTAA TAAAATAAAA TCTTTGGGTA TCTCTGATAT        11700

ATCTATGTCT GCTAATTGAT ACAACACTTT CTCAACCTGA TCTTCTTTAC CTTCTACATA        11760

GCGCGTGAGC AGAACATCTT GATGCACAGC TAAATAATGC AATTGGAATG ATGTATGACA        11820

TTCGGGTGCA TATTTCTCTA AATCTGCTTC TGAAAACCCA CTTGCACTCT TAGGAGTCGG        11880

ATGAAATGGA TGACCTAAGT ATAAAGATTG TTCTGAAACG ATATAACGAT CCTCTACGTA        11940

GTCTATTGTG TTACTTTGCA AATAACGTGC CGTGCGATGA ATGCTATTAT CGATGTCAGA        12000

CATAATTTGC GCCATATGTT GTTGCACTGC CGTTTGATTA TCTGCACTTT GAGCCATATG        12060

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AAGCCATACC TCTGGATGAT ACATATGATG CCCCATCGCA GACCAATAGC GAAATTCACC        12180

CGTTAAAGTT TCGAGCTCTG ATAATTGTAT AGACCATTGA TGATTTTGAG GTGGTACTTG        12240

ATATAAATTT TCTTCTCTAA AATATTCATT TAAAATGCGT TCGATAGCCG CATACGCTGC        12300

ATGTTGTATT AATTCTTTAT TTTGCACTTT TTTGTTTCAA CTCCCATAAT TTCATTAATG        12360

TGTGATCGTT GATTTGATTA GTGATGGTTG AACAAATTAA AAATAAACTA CTTACTGCAA        12420

ATACTACGCC CATAACGATA AACGTAGTAG CTGGTGTAGT ATAACTTGTA ATGGCAGCGC        12480

cACTaAGACT GCCAATAATT TGACCAACAA CTAACATACT GTTCGTCGTT CCAACAAATG        12540

TGCCTTTAAG TTGTTGATGA CACGCATTCA CGACAACAAA CATGACACTT TGAATCAATG        12600

CACTATATGT TAATCCTTGA AGTATTCTTG CAGCCATTAA AAACTCTATA TTCGTCGCTA        12660

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CATATGATTT ATCATTAAAG CGTCCCCATA AAGGCGCGCT TAATATCGAA GCCGTCCAAA        12780

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AAGCAAGTGG TGATAATGCA GTTAGCATGC CATACATAGC AAAGTTTGCT AAAACGCCAA        12900

CGATAATAAA TCGACATGTT TGTTGTGTGC ATAATAGACA TTGAAATGAA CGGCGAATAC        12960

CTTTATTAAT ATTTGGTGTT TGTGATTTTG GCATATGTGT CGTTTCAATC AATTTTAATG        13020

CACCGAAAAT ACAGACAATA AAAGTAATAA CGGCAATACT CATCAGTAAC GCACTAAAAC        13080

CTAATATCGA AGCTGTAACA CCGCCAATTA ATGGCCCCAC AAGAGACCCT GCGCTGACTG        13140

AACTTTGCAG TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA        13200

ACGCACTTGA TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA        13260

ACTGTAATGG TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG        13320
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CtATCATCGT CGTTACAGCT GGAGCAGCAA TCGCTATACC ACTCCACAAC TGTATTTCTA    13440
CGACTGATAG ATTTTGTAGT GATGCCATAT AAATTGGCAA TAATGGCACA AGTACTGTCA    13500
GTCCAGCAAT CGCTATAAAC TGACTGAGCC ATAAAATGCG AAAGTTACTG CGCCATATAG    13560
ACTGATTAAT CATATGTCAC CATTGGATTT GGTACGGTAG TTAAACCTGA AGGCATACTA    13620
CCTCCACCAC TATCACGTTG ATATAGCAAT GGTAATAAAA TTTGTTTGAA TGGCCACGTC    13680
TGTTTATCAA ATAAAATGTG TCTGACAGCT AGCTGATCAG TTGTAACCCA GGAAATAGTT    13740
GCCACTTCAT TTTTAAAAT TTGTTTTAAC AACGACATAA GTTCATGCTC ACTTACACCA     13800
AATAAATCTT GAATTGCATC AATAATGGCA TATAGATTTA CCGATACAGC TAATGTTTGA    13860
AAATAAGCAA AGAATGTTTC CAAATCCTCA TTAATTAGCG TATTAGGTGT ATCTTCTCTG    13920
ACGACATACT TCGGCAATGA AAGCTGATGT GCTGTTAGCC ATGGTTTATA AATTCTGACA    13980
GTATCATGAT CACGTAACAC GCATTTTTGT ACACGTCCAT CTTCAAATGA CAACAATATA    14040
TTTTGACCAT GCAACTCTGG TAATGCGCCG TATTGCATAA ATGATAGTGT TACCTTTAAA    14100
AAGACTTGCG CGATATCTTC AAATAACGTC ATGACATCAT TTTTAGAAAT ATTATCTTTT    14160
CCACAAATCA TTTGATATAA AGTGCGATCA TTTGCCGCGA GTGCTGCCAT TGACACTAGC    14220
TGTTGCGTAT CATTTTTGGC TAGCACTTCG GGATACTTTC TTAGCTGAAC AGTTAGATGA    14280
CCTAATTGAT CTTTGAAAAT ATCATTATCT TGACCCATAT ATGACCACCA AGCTGTTTCA    14340
TCACAAACCA TGACATACTT AGCTAGTGCT TCATCTTTTT CTATAAGCTG ACGTAATAAT    14400
TGTTCTGCTT GTTCTCCGTT TTTCATGTAA CGCGTAGGCG TTAGCCTTAA TGCGCCTAAT    14460
GACTGCATTG CAAATGGTAC TTTGACATGG TTATACGGTG CGCCAATATC AATTAATGAA    14520
CGCATACTTG AAGACGACAG ATAATCTCCA AATTTTAACG GTAATAGTAC AACCAACTTT    14580
TCACTAATCT CTTTCGCAAA GACGTTCGGC AGAATATGCT GATATTGCCA AGGATGTACC    14640
GGAAATAGTA CATAGTCATC TATTGATAAC CCTTGATCAT TTAACATGTC TGTCGCTTGT    14700
TCTTTTATAG GTACTGTCAA ATTTTCTAAT TCATCGATAT TTGCAGTATC GCCATGAATC    14760
ATATGTGTCT TTTTAACTGC TGCAACCATT AAAGGAAATG ATTGATTTAA TTCAGCTTGA    14820
TACACTTGAT AATCCGCTTC TCTTAATCCT CTTTTTTCTT TAGCTAATGG ATGAAATGGA    14880
CGATCTTTTA AACTTGCAAA CTGCTCTGAC ATCACAAAG GATGTGACGC TAAATCTAAT     14940
TCTGATAATT GTTTAGCAAG CTGTGTGGCA GCAGTAGTCA GTCCTTCTTC AACGCGAGCC    15000
A          CATGACTTAG ATCACAATTC ATATTAGCAA TTGTTTGCCA AAATTCAGCT    15060
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TATATCAAAA GCGTTTGTCC GTTTTCTTTA GTAATCTCAC TATTCGATAC AATTCCGGCT      15240
ATATCTTCAA ATAATAATGC ATCAACTAAA TCTCTTAATA TTATCGCTTG TGCTGTATTG      15300
ACTGCTGTAT GATTCTGCAA TGTTCAGACA CCTCGCATTC TTAATATAGG TTCAATGTTG      15360
TCCCAATATT TTGTTGTTGT GCCTGTTGAT AAATAAAATA AGCACTTGAA ATATCTTCGA      15420
TAGCCATACC CATCGGATTA AGTAATATGA TCTCATCATC GTCTTCACGT CCTGGTATGT      15480
CACCTGTCAC AAGTTGTCCT AGTTCAGCAT GAAGAGCTTC TTTGCTGAAT TTACCTTCTA      15540
ACACCAATTG GTTAATAGTT TTCTTTTCTC GATTACATTG TGACCAGTCA TCTACTACGA      15600
CTTTGTCAGC TTTAATAAAG ACTTCTTTAT GCACATCCAT GATAGAAATG TTGCTAATAA      15660
ATGCACCCTT TTGTAACCAA TCATATTCAA TGTATGGTTG ATCCGTTACG GTACATGTAA      15720
TGACTACTTC ACCATTTGAT ACTGCTTCTT TAGCATTTTC TGTCGCAATA AAATTAATTT      15780
CCGGACGCTG TTGTTGCCAT CTATCAACAA AGCGTGCACA TGCTTCAGAG AATTGATCGT      15840
AAACAAACAC GCGTTCAATA TGATCGAATT GCTCTAACAT ACTTTGTAAT TGCTTGTCTC      15900
CGATTAGCCC GCATCCAATG ATTGTTAAGT CTTTAAATCC TTTTTTAGCC AAATGCTTTG      15960
CTGCAATCAC TGAAACTGCT GCAGTACGCA TACTACTAAT TAAACTTGCT TCCATAACTG      16020
CAATTGGATA ATTCGTTTCT GGATCATTCA AAATAATGAC GCCACTTGCA CGCTCCATAT      16080
TACGTTTCGA TGGATTGTCG TGCTTACTAC CTATCCACTT AATACCTGAA ATTGCGTGTT      16140
CACCACCGAT ATGACTTGGC ATTGCAATAA TTCGATCTGC GATGTGTCCA TTTTCAGGAT      16200
CCtGTCTTAA ATACGGCTTA AGCGGTTGTA CAAAATCATT GTGCGCATGG CTGTTAATG      16260
CTTCTGTTAA TGCGTCCACA TAAACTTGTG AATGATTACC TCCCGCTTGT TCAATATCTG      16320
ATCTATTTAA ATACAACATC TCTCTatTCa TTCTGaTTTA ACTCCTTGTC TTGATTTCAT      16380
TTTTTCTAAC CATGTATCTG AATAAACTAA ATCTAAGTAA CGATCGCCTC GATCTGGTAA      16440
AATCGTGACA ATTGTTGCAC CTTCTTCAAT TGACGTTATC AACTGCTCAA TCGCTGCAAT      16500
AATCGAACCT GTTGAAcCTC CGGCAAATAT GCCTTCATAA TCAATCAGTT TTCGACAGCC      16560
CAAAGCAGAT TGATAATCAT CTACATGGAT CACTTGATTA ATTTCTGATC TATTCAATAT      16620
TTCGGGTACA CGACTAGCAC CGATACCAGG TAATTCTCTA TTAATAGGTT TGTCACCAAA      16680
AATGACTGAC CCTTTCGCAT CAACAGCAAC AATTTGTGCG TTTGGATGCA CTTCTTTTAT      16740
TTTTCTACTC ATACCCATAA TGCTACCTGT CGTGCTGACT GGCGCGACAA AATAATCTAT      16800
AGGTTGCTTA ATTGTTTCAA CAATCTCTGT GCCTGCACCA TGATAATGGG ATTGCCAATT      16860
TAACTCATTC GCATATTGAT TAATCCAATA TGCATCGTCA ATAGTGGCTA ACAGTTCTTG      16920
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TACATTGGCA CCATAACTTT TAATAATTTT CAAATTTGTT GGTGATATTT TAGGATCAAC   17040

AACACACGTG AGTTTTAATC CCTTGATTTT AGCTATCATT GCCAACGCAA TGCCTAAATT   17100

ACCAGAAGTA CTTTCAATTA AATGTGTATT CTCAGTGATT AAACCATGTT TAATACCATG   17160

TTCAATGATG TACTTGGCAG GTCGATCTTT CATGCTGCCT CCAGGATTCA TATACTCTAA   17220

CTTTGCAAAC ACTTCATGTT TCGGAAATAG TTGATGAAGT TGAACCATAG GTGTTTGCCC   17280

TACAGAATCT AACAATGAAT CGTGCACATG   17310

(2) INFORMATION FOR SEQ ID NO: 24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5423 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATACTAGTAA GCGCATCGGT TATTGACATC GAATTCAACT TTAACAGTTT TCATGTTCGG   60

TGATGTTTCa ATAGAATGTG TGTGTTGTAC TTGCGCATTT ATATTCCAC CTAAATTACT   120

TAAGTTTCCT GTAATACTAG AAATGTCAGG TGCGTTTAAT GTAGGTTGAA ATGCATCAAC   180

TACTTTATCT GCAACATTAG AAACATTACG GATAACTTTA CTTGAATGAT TATCTATACC   240

TTTAACGAAA CCTAACATTG AATACATACC AACATCCATG AATTCACGTG AAGGTGAGTG   300

AATACCTAGC GCTCTTTTGG CTGCATTTAA AGCACCTTTT GCTACACTAG CTGCTTTTTC   360

AGCTAAGTCT CTAGCCATAT TACCAATACC TCTCATCAAA CCACGGATCA TATCAGCACC   420

TGCTGATACA AAGTCATCCA CAAAGCTTTT AACTTTATTT ACTGCATTTG TCATACCTTG   480

ACTAACTTTG TTTACAACAT TAACGAATCC TTGAACAACT CTATTAACAA rGTTAATTAG   540

CGTACtTGTt ATAGTAGATA CCCaTnGCAT ACCTTTAGTG ACmATGAAGT TCCAAGCTTG   600

AGACATTTTG TCTGATATAG TTGAAACAAC TTGTGTGAAT ATGCTTACAA CTTTATTCCA   660

AATTGTCGTT AATATACCAG ATAAGAAACT CCAAATCGTA TTCCATATAT TAGAAATAAA   720

ACTCCATGCC GCTTGTAACG CAGTAGATAT AGCTGTAGTG ATAGCGTTCC AAACCTTAGT   780

TGCCACAGTA ACTATAGTGT TCCACAACGT TTGTAAGAAC GTCCAAATAG CGTTCCAAAT   840

TGTTATTGCG ATAGTCATAA TTGTGGTAAA CACTGTAGTT ATTACAGTGA CTAACAAATT   900

CCAAATCGTA GTAGCGATTG TAATTATCGT ATTCCAGATT GTACTTAAGA ACGTCCAAAT   960

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ATAAGCGACT ATTTGATTCC AAACAATCAT TATAAAATTG TAAACATTCG ATACTGCTGT          1140

AGTGATAGCT GTTAAAATAG CATTCCATAC AACCGAAGCT ACAGCTTTTA ATACATTCCA          1200

AACATTAACC ATAAACGTTT TTATCGCATT CCAAGCATTT ATAATAAAGT TTCTGAATCC          1260

TTCATTTTTA TTCCACAATA AAACGAATAT AGCTATTAAT GCAGCAATTA CACCAATTAC          1320

TATTGTTATT GGACCGCCTA AAATACCAAA CACAGTTACT AGTCCTGTGA TAGCATTTCT          1380

AATTAATCCA ATCTTACCGA ATAACAATTG GAATATAACT GATATAATTT TTAATGGTCC          1440

TTTTAATAAC ATGAACGCAC CTTTTAAAAT TGTTAATCCC GCTCTTAATA AACCGAACTT          1500

ACTTACTAAT GCAATGrTTC TACCTATTAA TCCGCCACCC ATAAAGTTAG ATACAGCAAG          1560

AATAATCGGT ATTAAAAATC TAAATGCACC AACTAAAGTT ATAATGACAC CAACTAATTG          1620

TGCTGTAGCT GGATGCGCCT CAAACAAGTT AGCTATCCAA CCAGTTATTG CAACTGCAAC          1680

GCGTAATACT GCACTAGCTA TAGGAGCCAT TGCTGTTGCG AATGCArmTA ATCCTCTTGC          1740

GATGTTTCCA ATCAATTGCA TTATTAGTGG TCCATTTGTT TGTATATAAC TGACAAAGTC          1800

TTTAAACCCT TGAGATTGTC CTACTTGTTC AGACCATTCC CTAAACTTAG CTGTCATTTG          1860

TTCAAGAGAT TGGAATATGC CAGTTGATGA TCCGCTGAAT GCATTCATCA AATTGTTAAT          1920

TCCAACGAAA ACATTTTTGA AAATATTACC AATGATAGGT AAGTTTGTTT TTGTGTATTC          1980

AATAAAACGA GTTATCGAAT TTTCTCCAGC TGCACTATTA GCCCAGTTAG AGAAAGATTG          2040

ACCTAATCTA TCCAACCAAT CAGCCGACCA TTGAAACAGT GGTGCTAATT GCGTGAATAC          2100

ATTGACTAAT CCGTCACCAA AACCACCTGC AGCACTTAAT AGCTTGTTAA ATACCGAAAC          2160

ACCCGTTGTA TTCATCATAT TAAAGAATCT TGAAGCTACA CTGCTATTTT CAGCCCATTT          2220

AAGCACGCTT TGAGACGCTT CTTCCATTCC TCTTGAAATA CCACTAAAAA ACGGTTGTAA          2280

GCTCTGCATT GCAGTTTTAA CAGTATTTAA ACCATTTGCA AGAGTTGTGA AGATAGCGGA          2340

TTGATTTTGC TTTATAATAT CAGTCCATGC TGACTTTACG CCATCTAACG CTTTTTTGTA          2400

TTCGTTTGTT GCTGAGCTAG CTTGTAAAGT GCCATCATTA AGCATCTTTA TAGCGCTGAT          2460

AGCCATTGCG CCAAACGCTA CAAATCCTGC TCCCGCTATT GCTACGGCAC CACCTAAAGC          2520

AAGTACACCA CCAGTTAACA CTTTGATAGC GTTTAATAGC GCAAATACTA CAGGTACTAC          2580

GCTCGCTATT ACAGGTATTA AGATACTAAA AGATGATGTA AGTAATCCAC CAACCATATT          2640

AGAACCTACA GTACCGAACA CACGGAACAT ATTAGCTAAA TTCCCCATCT GTCTTTGAAA          2700

ATTGTCATTT GCTTTTATTA TGTAGGCATA AGCTTCTTTT AAACCATTAG TATCGACATC          2760

TACCTTTGTT GTTTTTTTGT TCGGCAATGC GTCTAATGAT TTTTTAAACG CATAAATAGT          2820
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      AAGTTCTTCT TTAGTACGTT TGATTTTAGA GTTAGCAACA CCATTGTCCA CGTCTATAAT        2940

      AGCTTTGGCT TTAGACCTAT TTAATGCTTC GAGACTAGCT TTAGATACTT TTAACACTCG        3000

   5  ATTGAATTTA CTGTTATCTG CATTGACGTC AATATTGACA CGTTTCTTTT CTAATTCTGA        3060

      TAATTTAGCT TCTGTTTCAG CGATATCTTT AATCAACTTT TGTTTTTGCA ACTTAACTTC        3120

      TGGTGTAACT TCTTTAGAGT TTAGTTGTC TAGTTCAAAA TTCGATTCTA GTACCTTTTG         3180

  10  TTGTAAATCT TGTATACTAG CATCTAATTT AGCTTTTACA TTTTTGTTAC TAAAGGCATC        3240

      TAAAGACTTT TTAGCAACTT TGATAGTTTT TTGTAAATTT TTATCGTTAG CGTTTAATTC       3300

      AACATCTTTA GTTTGATCTG CTACTCGTTT AAATCTTTGC ACAGACTTAA CCGCACTATC        3360

  15  AATTTGCCTT TTGAATTTGG CTACACTAGC TTCAATAGTC GCTTTAATTT TATATTCCGT        3420

      CACATTAACA CCTCTCTTTC TATTGCTTAT TAAATTCTGC TATAACTTTA AAGAATTCAT        3480

      TATTTGTGG TTCGTATTCA TCACGTTCGC TACTAAATCT TATATCTTTA CCTTCGTTAA        3540

  20  GCCGTTGGAT ATTTCTTCA TAAGGCAATA CGTCGTTTGC ATTGTTAAAA ACATATTCCT        3600

      CTTTAGGTTT ATTTTCTGTC CCAACATTTT TAGTAGCTGC AGCATCACGA ATAGCAAACG        3660

  25  CAAGTTTGTA ACGTTCGAAT TCTTGGGTTA GCATTTCATA CTCTTTCGCA TACATTCGAT        3720

      AGTTATATTC TGTTAATGTC ATTTGCTCAA TAACGTTCAA ATCTGTAATA CCAAGTGTTG        3780

      ACATACAAGT TATAACGATT CTGTCGTAAG TTATTAGGcT TCCGCTGGTT TTTCTTCCGT        3840

  30  TTCCACTACT TCGACTAGGT TTCGGGTCAT AGGTCGCTTT CCCAAcTCCG TTAAAATATC        3900

      CGAACCGAAT TCTTCTAGTC CGATATTTTC TGCGATTTCA TCTAATGCTT CATCAATGTT        3960

  35  ATTAATAGTA ATTGCTTGTT TTTTTAAGTG AGATGTAGCT GCGATTAAAA cTTCGCCAAT        4020

      CACAACCGGA TTTCCACTTT CTAAACCTAC AGGCAACATT GATACACCTT GACCGATAGA        4080

      AGCTTGTTCA ACTTTTAAAC CTAATCGGTT ATCGATTTCT CTTAAAAATT TAAAACCAAA       4140

  40  ACTTAATTCT AATGACTTTC CGTTAATTTC TACATTCATA ACTTAAAATC TCCATTCATA        4200

      ATTAATTTAA ACAAAATAAA mArGCTTAAC GCCCTATTTT TATACCTCTC TTGGTGCAAC        4260

      CGGTGGTGAA TCTACTTTAG GTTGTGGAAT TGCTGTTAAA TCTTCGCCAG TTAATGCATC        4320

  45  TGCTTTTGTA GTGTCGTGGA ATCTGTATcC AGTCGCCTTA AGTTCTTTG TTACAGCCTC         4380

      AGGTAGTGTT GCAAATCCAC GTTGGAAACG ACCATTCACT CCATATTCAT ATTCATATTC       4440

  50  ATCAATACCG TTAGCTTCTG CTTTTAATTC AAATTTATTG TGGAAACCTT GGAAATATTT        4500

      CGCTTTAAAT TTAGCGGAAT CCCCATTTTT GCCTGGTATT CTACTTTCAA CTTCCCAAGC       4560
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GTCCATTGTA TCCTCTGTAT CTGTATCAGC TTCATGTGAT AAGCCGTATT CAGTTAAAAA      4740

AAGCATTTTA GTAGCATCTA CTTTTTCGCC AGCTTTTCTA AATAAAATAA TACGATCATT      4800

ACTATTTTTC ATATTTGCCA TTCAATATTC CTCCGTTTTT TAAAATGTTT TGTAAGATAT      4860

CGTTACTGAT GTGTGTAGCA ATTCTTGATT GGTAGTATCA TCAACTAACT GTGTGATGTT      4920

AGTATCTTCT TCTTCAAAGT CATAATCGTT TGTTTTAACG CTAGGTGTTA AATCATCAAT      4980

ACATCTTTTA ACAAGTCCGT CATGATGTCC TAAATCATCG CTTACACTCC AAATATCAAT      5040

AACTAAATTC GTATCGCCAG AATAACTATC AAACGTGTAC TTACTTCTAT TTGACTCCGG      5100

CATTTTTATT ACAAAAAAAG GATACGGAAT CTCTTGTTGC ATCTCTTTAC GAGAAATAAC      5160

AGGGAATCCA TATCCTTGTA GCGTTTCATA CGCTTTATTA TAAAGTTGTA AGTTCGGTGT      5220

CATGCTTTTA TCTCCTATTC AAACAACGCT TTCAATTCTT CTACAGTTGA TTTCCTAATC      5280

ACTTCGTATA CCGGCCACAT AAAAGGTTCA GCCTCCATGT ATCGAGTACC AAATTCTAAG      5340

AAACCACTAT AAGCTGCGTG CGATGTGATA GTGTATTGCA AATCGCCAGT TTTTTTATAT      5400

CTGATATTGC GTGATaAATT ACC                                              5423
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(2) INFORMATION FOR SEQ ID NO: 25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6251 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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AAACGCAGAT GTTCAATTAG AACCAGTCTA TCGTATTAAG GAAGGTATTA AACAAAAGCA        60

AATACGAGAC CAAATTAGAC AAGCGTTAAA TGATGTGACA ATTCATGAAT GGTTAACTGA       120

TGAACTAAGA GAAAAATATA AATTAGAGAC CTTGGACTTT ACTTTGAACA CATTACATCA       180

TCCTAAAAGT AAAGAGGATT TATTACGTGC TCGTAGAACC TATGCATTTA CTGAACTGTT       240

TTTATTCGAA TTACGTATGC AATGGCTAAA TAGATTAGAA AAGTCATCTG ACGAAGCAAT       300

TGAAATTGAT TATGACATAG ACCAAGTTAA ATCATTTATT GATCGTTTAC CTTTTGAACT       360

AACTGAAGCA CAGAAATCCA GTGTTAATGA AATTTTTAGA GATTTAAAAG CACCAATACG       420

TATGCATCGA TTACTTCAAG GTGATGTAGG TTCAGGAAAA ACAGTAGTTG CTGCAATTTG       480

TATGTATGCG TTAAAAACTG CTGGTTATCA ATCAGCATTG ATGGTACCAA CTGAAATTTT       540

AGCAGAGCAA CATGCTGAAA GTTTAATGGC TTTATTTGGA GATTCTATGA ACGTTGCATT       600
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     TACGATTGAT TGTTTAATTG GAACCCATGC TTTGATTCAA GATGATGTGA TTTTCCATAA        720

     TGTTGGTTTA GTAATTACAG ATGAACAACA TCGATTTGGT GTGAATCAAC GCCAGCTTTT        780

5    AAGAGAAAAA GGTGCAATGA CGAATGTGTT ATTTATGACA GCAACGCCGA TACCAAGAAC        840

     ACTAGCAATA TCAGTTTTTG GTGAGATGGA TGTGTCTTCA ATTAAACAAT TACCAAAAGG        900

10   TCGTAAACCT ATCATTACTA CTTGGGCAAA GCATGAGCAA TACGATAAAG TTTTGATGCA        960

     AATGACCTCA GAGTTGAAAA AAGGTCGTCA AGCATATGTC ATTTGCCCGC TAATAGAAAG       1020

     TTCTGAGCAT CTCGAAGATG TTCAAAATGT TGTCGCATTG TACGAGTCTT TACAACAGTA       1080

15   TTATGGTGTT TCCCGTGTAG GGTTATTGCA TGGTAAGTTA TCTGCCGATG AAAAAGATGA       1140

     GGTCATGCAA AAGTTTAGTA ATCATGAGAT AAATGTTTTA GTTTCTACTA CTGTTGTTGA       1200

     AGTAGGTGTT AATGTACCGA ATGCAACTTT TATGATGATT TATGATGCGG ATCGCTTTGG       1260

20   ATTATCAACT TTACATCAGT TACGCGGTCG TGTAGGTAGA AGTGACCAGC AAAGTTACTG       1320

     TGTTTTAATT GCATCCCCTA AAACAGAAAC AGGAATTGAA AGAATGACAA TTATGACACA       1380

     AACAACGGAT GGATTTGAAT TGAGTGAACG AGACTTAGAA ATGCGTGGTC CTGGAGATTT       1440

25   CTTTGGTGTT AAACAAAGTG GaTTGCCAGA TTTCTTAGTT GCCAATTTAG TTGAAGATTA       1500

     TCGTATGTTA GAAGTTGCTC GTGATGAAGC AGCTGAACTT ATTCAATCTG GCGTATTCTT       1560

     TGAAAATACG TATCAACATT TACGTCATTT TGTTGAAGAA AATTTATTAC ATCGTAGTTT       1620

30   TGACTAATTG CCATGCTGAT TTGTCAATTT GAGTGCAACa CTTCGTTAAT TGAGTGATAT       1680

     GACACTTGAA CTATTTAAAT GTAAAGTGGT ATTTTAACAA TTTATAAATT TTCGACTAAA       1740

35   TAATAGCTAA ATATTACAGT TATTTGTTGA GTCGGTTAAA TAGAAAGTGT TATGATATGT       1800

     GAGGAATGTT TAAGACTAGG TACTAAAAAA TGAGGGGTGA GACGTTGAAA CTAAAGAAAG       1860

     ATAAACGTAG AGAAGCAATC AGACAACAAA TTGATAGCAA TCCCTTCATC ACAGACCATG       1920

40   AACTAAGCGA CTTATTTCAA GTGAGTATAC AAACAATTCG TTtAGaTCGC ACTTATTTAA       1980

     ACATACCAGA ATTAAGGAAG CGTATTAAAT TAGTTGCTGA AAAGAATTAT GACCAAATAA       2040

45   GTTCTATTGA AGAACAAGAA TTTATTGGTG ATTTGATTCA AGTCAATCCa AATGTTAAAG       2100

     CGCAATCAAT TTTAGATATT ACATCGGATT CTGTTTTTCA TAAAACTGGA ATTGCGCGTG       2160

     GTCATGTGCT GTTTGCTCAG GCAAATTCGT TATGTGTTGC GCTAATTAAG CAACCAACAG       2220

50   TTTTAACTCA TGAGAGTAGC ATTCAATTTA TTGAAAAAGT AAAATTAAAT GATACGGTAA       2280

     GAGCAGAAGC ACGAGTTGTA AATCAAACTG CAAAACATTA TTACGTCGAA GTAAAGTCAT       2340
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TTAGAAGCCG TACAAAAGGC TGTTGAAGAC TTTAAAGATC TAGAAATTAT ACTTTTCGGT        2520

GACGAAAAAA AGTATAATCT GAACCATGAA CGAATCGAAT TTAGACATTG TTCTGAAAAG        2580

ATTGAAATGG AAGATGAGCC TGTTAGAGCG ATTAAACGTA AAAAAGATAG CTCAATGGTA        2640

AAAATGGCTG AAGCTGTGAA ATCTGGTGAA GCAGATGGAT GTGTGTCAGC AGGTAATACT        2700

GGTGCTTTAA TGTCAGCTGG TTTATTCATT GTTGGACGTA TTAAAGGTGT AGCTAGACCG        2760

GCTTTAGTAG TAACATTGCC AACGATTGAT GGAAAAGGTT TTGTCTTTTT AGACGTTGGT        2820

GCAAATGCTG ATGCTAAACC TGAACACTTA TTACAGTATG CGCAACTAGG GGATATTTAT        2880

GCTCAAAAAA TTAGAGGTAT TGATAATCCG AAAATCTCAT TATTAAATAT AGGAACCGAG        2940

CCAGCTAAAG GTAATAGTTT AACGAAAAAA TCATATGAGT TATTAAATCA TGATCATTCA        3000

TTGAATTTTG TTGGGAATAT TGAAGCGAAG ACATTAATGG ATGGCGATAC AGATGTTGTA        3060

GTTACCGATG GCTATACTGG GAACATGGTC CTTAAAAATT TAGAAGGTAC TGCAAAATCA        3120

ATCGGTAAAA TGTTAAAAGA TACGATTATG AGTAGTACTA AAAATAAATT AGCAGGTGCA        3180

ATATTGAAGA AAGATTTAGC TGAATTCGCT AAAAAGATGG ATTACTCAGA ATACGGTGGT        3240

TCCGTATTAT TAGGATTGGA AGGTACTGTA GTTAAAGCAC ACGGTAGTTC AAATGCTAAA        3300

GCTTTTTATT CTGCAATTAG ACAAGCGAAA ATCGCAGGAG AACAAAATAT TGTACAAACA        3360

ATGAAAGAGA CTGTAGGTGA AtCAAATGaG TaAAACAGCA ATTATTTTTC CGGGACAAGG        3420

TGCCCAAAAA GTTGGTATGG CGCAAGATTT GTTTAACAAC AATGATCAAG CAACTGAAAT        3480

TTTAACTTCA GCAGCGAACA CATTAGACTT TGATATTTTA GAGACAATGT TTACTGATGA        3540

AGAAGGTAAA TTGGGTGAAA CTGAAAACAC ACAACCAGCT TTaTTGaCGC aTAGTTCGGC        3600

ATTATTAGCA GCGCTAAAAA ATTTGAATCC TGATTTTACT ATGGGGCATA GTTTAGGTGA        3660

ATATFCAAGT TTAGTTGCAG CTGACGTATT ATCATTTGAA GATGCAGTTA AAATTGTTAG        3720

AAAACGTGGT CAATTAATGG CGCAAGCATT TCCTACTGGT GTAGGAAGCA TGGCTGCAGT        3780

ATTGGGATTA GATTTTGATA AAGTCGATGA AATTTGTAAG TCATTATCAT CTGATGACAA        3840

AATAATTGAA CCAGCAAACA TTAATTGCCC AGGTCAAATT GTTGTTTCAG GTCACAAAGC        3900

TTTAATTGAT GAGCTAGTAG AAAAAGGTAA ATCATTAGGT GCAAAACGTG TCATGCCTTT        3960

AGCAGTATCT GGACCATTCC ATTCATCGCT AATGAAAGTG ATTGAAGAAG ATTTTTCAAG        4020

TTACATTAAT CAATTTGAAT GGCGTGATGC TAAGTTTCCT GTAGTTCAAA ATGTAAATGC        4080

GCAAGGTGAA ACTGACAAAG AAGTAATTAA ATCTAATATG GTCAAGCAAT TATATTCACC        4140

AGTACAATTC ATTAACTCAA CAGAATGGCT AATAGACCAA GGTGTTGATC ATTTTATTGA        4200
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AACATCAATT CAAACTTTAG AAGATGTGAA AGGATGGAAT GAAAATGACT AAGAGTGCTT      4320

TAGTAACAGG TGCATCAAGA GGAATTGGAC GTAGTATTGC GTTACAATTA GCAGAAGAAG      4380

GATATAATGT AGCAGTAAAC TATGCAGGCA GCAAAGAGAA AGCTGAAGcA GTAGTCGAAG      4440

AAATCAAAGC TAAAGGTGTT GACAGTTTTG CGATTCAAGC AAATGTTGCC GATGCTGATG      4500

AAGTTAAAGC AATGATTAAA GAAGTAGTTA GCCAATTTGG TTCTTTAGAT GTTTTAGTAA      4560

ATAATGCAGG TATTACTCGC GATAATTTAT TAATGCGTAT GAAAGAACAA GAGTGGGATG      4620

ATGTTATTGA CACAAACTTA AAAGGTGTAT TTAACTGTAT CCAAAAAGCA ACACCACAAA      4680

TGTTAAGACA ACGTAGTGGT GCTATCATCA ATTTATCAAG TGTTGTTGGA GCAGTAGGTA      4740

ATCCGGGACA AGCAAACTAT GTTGCAACAA AAGCAGGTGT TATTGGTTTA ACTAAATCTG      4800

CGGCGCGTGA ATTAGCATCT CGTGGTATCA CTGTAAATGC AGTTGCACCT GGTTTTATTG      4860

TTTCTGATAT GACAGATGCT TTAAGTGATG AGCTTAAAGA ACAAATGTTG ACTCAAATTC      4920

CGTTAGCACG TTTTGGTCAA GACACAGATA TTGCTAATAC AGTAGCGTTC TTAGCATCAG      4980

ACAAAGCAAA ATATATTACA GGTCAAACAA TCCATGTAAA TGGTGGAATG TACATGTAAT      5040

ATATTTGAGC TAAAGCTCAT TGACGCAGTG GTTGACTGGT CATCCAATGG AGAATTGTCT      5100

GACCTAGTCA ACTTTGCGGG GGAAATTCTA AGCAACCTAG ATAAGGTTCC AGAATTTCTC      5160

CCTAAGAAAC ACTAATCAAT aAATTGwTAA GTGTTTCTAA AATTTCTACT TGTTTTTTAG      5220

AATTTAAAAT GGGAAAATAT AGTAGTCTAT GTATAGGCAT TTTTAAAGGA GGTGAATCGA      5280

CGTGGAAAAT TTCGATAAAG TAAAAGATAT CATCGTTGAC CgTTTAGGTG TAGACGCTGA      5340

TAAAGTAACT GAAGATGCAT CTTTCAAAGA TGATTTAGGC GCTGACTCAC TTGATATCGC      5400

TGAATTAGTA ATGGAATTAG AAGACGAGTT TGGTACTGAA ATTCCTGATG AAGAnGCTGA      5460

AAAAXTCAAC ACTGTTGGTG ATGCTGTTAA ATTTATTAAC AGTCTTGAAA AATAATAAAT      5520

CTTACATCTG GGTCGTCAGT ATTGTCGACT CAGTTTTTTT CTTTAATTAT CAATAGTTTT      5580

AACGTAAAAT TAAAGATGAT TCAAGAGCAA CACATAAAGG AGATAAAATA ATGTCTAAAC      5640

AAAAGAAAAG TGAGATAGTT AATCGTTTTA GAAAGCGCTT TGATACTAAA ATGACAGAGT      5700

TAGGCTTTAC TTATCAAAAT ATTGATTTAT ACCAACAAGC ATTTTCGCAT TCGAGTTTTA      5760

TTAATGATTT TAATATGAAT CGTTTAGACC ATAATGAGCG TTTAGAGTTT TTGGGTGATG      5820

CGGTATTAGA ATTGACGGTT TCACGATATT TATTTGATAa ACATCCCAAC TTGCCAGAAG      5880

GGAATTTAAC AAAAAATGCGT GCCaCTATTG TATGTGAGCC CtCACTkGTA ATATTTGCGA      5940
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ATCAAGGACT AGATATAGTT TGGAAATTTG CTGAGAAAGT CATTTTCCCA CATGTAGAAC   6120

AAAATGAGTT ATTAGGCGTG GTAGATTTTA AAACACAATT CCAAGAATAT GTGCACCAGC   6180

AAAATAAAGG TGATGTAACC TATAATTTAA TAAAAGAAGA GGGACCGGCA CATCATCGTC   6240

TATTCACTTC A   6251

(2) INFORMATION FOR SEQ ID NO: 26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4920 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ACCTACTGAA GTTGCTAATT TTTTGGAGCA ACTAAGCACT GAAATTGAAC GTCTTAAAGA   60

AGATAAAAAA CAACTTGAAA AAGTAATCGA AGAGAGaGAT ACTAATATTA AGTCTTATCA   120

AGACGTGGcA TCAATCTGTA AGTGaTGCTT TGATACAAGC TCAAAAAGCT GGTGAAGAAA   180

ATcAAATGGT TGGTGACGCG GTAGAAAAAG CACGCCGTTT AGCATTCCAG ACTGAAGATA   300

TGAAACGTCA ATCAAAAGTA TTTAGATCGC GTTTCCGTAT GTTAGTTGAA GCGCAATTAG   360

ACTTATTAAA AAACGAAGAT TGGGATTACT TGTTGAATTA TGATTTAGAC GCTGAACAAG   420

TGACGCTTGA AAATATTCAT CATTTGCATG AAAATGATTT AAAGCCAGAT GAAGTTGCAG   480

CAAATGCACA AAATAATGCA TCAAATACAC CAGACAATAA TCAACAATCC AATGATTCAG   540

AAACAACTAA GAAGTAAGAA TTAAATAAAG ACAGACGCGT AATATACATT TAACTTTTCA   600

CAGCGAATTA GGTAATGGTG AGAGCCTAGT AAAAGCATGT ATGTTATATC ACTGGCTTTT   660

TAATATTTAA ATAATGTAAT GAGAGAACTC TAAGTTGAGT TAATAAGGGT GGTACCGCGA   720

GCAATCGTCC CTTTTAATTT AACTTAGAGT TTTTTAAATT TTTAAGGAGT GAAAAAAATG   780

GATTACAAAG AAACGTTATT AATGCCTAAA ACAGATTTCC CAATGCGAGG TGGTTTACCA   840

AACAAGGAAC CGCAAATTCA AGAAAAATGG GATGCAGAAG ATCAATACCA TAAAGCGTTA   900

GAAAAAAATA AAGGTAACGA AACATTCATT TTACATGATG GCCCACCATA CGCGAATGGT   960

AACTTACATA TGGGACATGC CTTGAACAAA ATTTTAAAAG ACTTTATTGT ACGTTATAAA   1020

ACTATGCAAG GGTTCTATGC ACCATACGTA CCAGGTTGGG ATACACATGG TTTACCAATT   1080

GAACAAGCAT TAACGAAAAA AGGTGTTGAC CGAAAGAAAA TGTCAACAGC TGAATTCCGT   1140

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TTAGGTGTTC GTGGTGACTT TAATGATCCA TATATTACAT TAAAACCTGA ATACGAAGCT     1260

GCACAAATTC GTATTTTTGG AGAAATGGCA GATAAAGGTT TAATTTATAA AGGTAAAAAG     1320

CCAGTTTATT GGTCTCCTTC AAGTGAGTCT TCATTAGCAG AAGCAGAAAT TGAATATCAC     1380

GATAAACGTT CAGCATCAAT TTACGTTGCA TTTGACGTTA AAGATGACAA AGGTGTCGTT     1440

GATGCAGATG CTAAATTTAT TATCTGGACA ACAACGCCAT GGACAATTCC ATCAAATGTT     1500

GCGATTACCG TTCATCCTGA ATTAAAATAT GGTCAATACA ATGTAAATGG cGAAAAATAT     1560

ATTATTGCAG AAGCCTTGTC TGACGCTGTA GCAGAAGCAC TGGaTTGGGA TAAAGCATCA     1620

ATCAAATTAG AAAAAGAATA CACAGGTAAA GAATTAGAGT ATGTTGTAGC ACAACATCCA     1680

TTCTTAGACA GAGAATCGTT AGTGATTAAT GGTGATCATG TTACTACAGA TGCTGGTACA     1740

GgTTGTGTAC ATACAGCACC AGGTCACGGG GAAGATGACT ATATTGTTGG TCAAAAATAT     1800

GAATTGCCAG TAATTAGTCC AATCGATGAT AAAGGTGTAT TTACTGAAGA AGGCGGCCAA     1860

TTTGAAGGGA TGTTCTATGA TAAAGCTAAT AAAGCCGTTA CTGATTTATT AACAGAAAAA     1920

GGTGCACTAT TAAAATTAGA CTTTATTACA CATAGCTATC CACACGACTG GAGAACAAAA     1980

AAACCTGTAA TCTTCCGTGC TACACCACAA TGGTTTGCCT CAATCAGTAA AGTAAGACAA     2040

GATATTTTAG ATGCAATCGA AAATACAAAC TTCAAAGTAA ATTGGGGTAA AACACGTATT     2100

TACAATATGG TTCGTGACCG TGGCGAATGG GTTATTTCTC GTCAACGTGT GTGGGGTGTA     2160

CCGTTACCAG TATTTTATGC TGAAAATGGC GAAATTATCA TGACGAAAGA AACAGTGAAT     2220

CATGTTGCTG ATTTATTTGC AGAACACGGT TCAAATATTT GGTTTGAAAG AGAAGCGAAA     2280

GACTTACTAC CAGAAGGATT TACACATCCA GGCAGCCCTA ACGGTACATT TACTAAAGAA     2340

ACAGACATTA TGGACGTTTG GTTTGATTCT GGTTCATCAC ACCGTGGCGT GTTGGAAACA     2400

AGACCGGAAT TAAGTTTCCC AGCGGATATG TATTTAGAAG GTAGTGACCA ATATCGTGGT     2460

TGGTTCAACT CTTCTATCAC AACTTCAGTT GCTACAAGAG GAGTATCACC TTATAAATTC     2520

TTACTTTCTC ATGGTTTTGT TATGGACGGT GAAGGTAAGA AAATGAGTAA ATCTTTAGGT     2580

AATGTGATTG TACCTGACCA AGTGGTTAAA CAAAAAGGTG CTGATATTGC GAGACTTTGG     2640

GTAAGTAGTA CGGACTATTT AGCTGATGTT AGAATTTCTG ATGAAATTTT AAAACAAACA     2700

TCTGATGTTT ATCGTAAAAT CAGAAATACA TTAAGATTTA TGTTAGGTAA CATTAACGAT     2760

TTCAATCCTG ACACAGATAG CATTCCTGAA TCAGAGTTAT TAGAAGTGGA TCGTTACTTG     2820

CTAAATCGTT TACGTGAATT TACTGCAAGT ACGATTAACA ACTATGAAAA CTTTGACTAC     2880
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CAAACAGTGT TATATCAAAT TTTAGTTGAT ATGACGAAGT TGTTAGCACC AATCTTAGTG   3060

CATACAGCTG AAGAAGTTTG GTCTCATACA CCACATGTTA AAGAAGAAAG TGTTCACTTA   3120

GCAGACATGC CTAAAGTTGT AGAAGTAGAT CAAGCTTTAT TGGATAAATG GCGTACATTT   3180

ATGAATTTAC GTGATGATGT GAACCGTGCA TTAGAAACTG CTCGTAATGA AAAAGTTATT   3240

GGTAAATCAT TAGAAGCTAA AGTTACGATT GCTAGTAACG ATAAATTTAA TGCATCTGAA   3300

TTCTTAACTT CATTTGATGC ATTACATCAA TTATTTATCG TGTCACAAGT TAAAGTTGTA   3360

GATAAGTTAG ACGATCAGGC AACAGCTTAT GAACATGGTG ATATTGTCAT CGAACATGCA   3420

GATGGTGAAA AATGTGAAAG ATGTTGGAAC TATTCAGAGG ATCTTGGTGC TGTTGATGAA   3480

TTGACGCATC TATGTCCACG ATGCCAACAA GTTGTAAAAT CACTTGTATA ATTGAAATTG   3540

TATAAAGTAC TCATACAGAT GATATAAATT AAAGCTCTCT TCATAATCAT GTTGTAGTTT   3600

TTGTTGACAT GATGAAGAGA GTTTTTTTGT GAATAAAAAA ATGACCAAGT TACCGGTCAT   3660

ATATGTAAAA AATGTGCGAT TTACTAAAAT AAAAATTATT CAGGAATGGT ACAAATTCTC   3720

TGAGGCATAT AAATGCGTTA TAGTTGCTAT TCTCAATTAT GTTCGCGATA ATTTTAAGTA   3780

AAAGTAAGCA CAGATATTGA ATTTGATAGG AGTTAATTGA ATGTATCATA ACAGTAACGC   3840

AAACTTTGTC AATGGTATCA CTTTAAATGT GAGAGATAAG AATGAATTAA AGCCATTTTA   3900

TGAGGACATA TTAGGATTAA ATATTATAAA TGAGACATTA ACATCGATAC AATATGAAGT   3960

AGGTCAAAAT AATCATGTCA TTACACTTGT TGAATTACAA AATGGACGTG AACCTTTAAT   4020

GTCCGAAGCG GGACTGTTTC ATATCGCAAT TAAACTACCT CAAATTAGTG ATTTAGCTAA   4080

TTTACTAATT CATTTAAGCG AATATGATAT TCCAGTTAAC GGAGGTATAC AGCCTGCTTC   4140

GTTATCATTA TTTTTTGAAG ACCCGGAAGG AAACGGTTTT AAATTTTATG TTGATAAAGA   4200

CGAAGCGCAA TGGACGAGGC AAAATAATTT AGTAAAAATT GATATTAGAC CATTAAATGT   4260

ACCGAGATTA GTGAGTCATG CAACAAAATT GTTATGGTTA GGTATTCCAG ATGACGCTAT   4320

TATAGGTGCA TTGCATATTA AGACAATTCA TTTATCAGAG GTAAAAGAGT ACTACCTCGA   4380

TTATTTTGGA TTAGAGCAAT CGGCATATAT GGATGATTAT TCAATATTTT TAGCATCGAA   4440

TGGCTATTAT CAACATTTGG CCATGAATGA TTGGGTATCA GCAACGAAAC GTGTAGAAAA   4500

TTTTGATACG TATGGATTAG CAATTGTTGA CTTTCATTAT CCTGAAACAA CACATTTAAA   4560

TTTACAAGGT CCGGATGGTA TCTATTATCG CTTTAATCAT ATCGAAGTTG AAGATTAGTA   4620

TATACTTTGA ATGGACGAAC CATATAATGA ATCGTTTTTA ATGATCTTTT TATACAAGTT   4680

ATGAAGGAGG CTGGGACATT AAGTTCTTAG GCAATGTAAA AAGCTGATTT CTATTAATTA   4740

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TTTTCCTTAT ATTAATTGCC ATTAATACAA AACCTAGCTC TCGTTTAACT TTATTTATTC       4860

CTCGAACTGA CATTCGnGTG AACTCAAAAT nGCCTACTTn CTTAAATTAC CAATATCTAT       4920
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(2) INFORMATION FOR SEQ ID NO: 27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 626 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

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TGGATTGCCA TTACATGGAC AAGATTTAAC TGAATCAATT ACACCATATG AAGGTGGTAT        60

CGCTTTTGCA AGTAAACCAT TAATTGATGC TGATTTTATT GGTAAATCTG TATTAAAAGA       120

TCAAAAGAA AATGGTGCAC CAAGAAGAAC AGTGGGATTA GAATTACTTG AAAAAGGAAT        180

TGCAAGAACT GGTTATGAAG TTATGGATTT AGATGGAAAT ATTATTGGAG AAGTAACTTC       240

AGGAACACAG TCTCCATCAT CAGGAAAATC AATTGCACTT GCAATGATAA AAAGAGATGA       300

GTTTGAAATG GGTAGAGAGT TGCTTGTTCA AGTTCGTAAG CGTCAATTAA AAGCGAAAAT       360

TGTTAAGAAA AATCAAATTG ATAAATAATT AAAAAGGGGT GTGCATTGTG AGTCATCGTT       420

ATATACCTTT AACTGAAAAA GACAAGCAAG AAATGTTACA AACAATTGGT GCAAAATCTA       480

TAGGAGAATT ATTCGGTGAT GTACCAAGTG ACATTTTATT AAATAGAGAT TTAAATATTG       540

CTGAAGGCGA ACGGAGAACA ACGTTACTTA GAAGATTnAA TCGCATTGCA AGCAAGAGTA       600

TCACTAGAGG AACGCGTACA TCGTTT                                           626
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(2) INFORMATION FOR SEQ ID NO: 28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1126 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

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nGGAAGTGGT GTATATATTT GTAATGAGTG TATTGAATTA TGCTCAGAAA TCGTCGAAGA        60

AGAATTAGCT CAAAACACTT CTGAAGCGAT GACAGAATTA CCTACTCCTA AAGAAATTAT       120

GGATCATTTA AACGAATATG TTATTGGTCA AGAAAAAGCT AAAAAATCTT TAGCTGTAGC       180
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AACCTTAGCC AAGACGTTGA ATGTACCATT TGCAATTGCA GATGCGACAA GTTTAACTGA        360

AGCTGGTTAT GTAGGCGATG ATGTTGAAAA TATCTTGTTG AGATTAATTC AAGCAGCTGA        420

CTTTGACATT GATAAAGCCG AAAAAGGTAT TATTTATGTA GATGAAATTG ATAAAATTGC        480

ACGTAAATCT GAAAACACAT CTATAACACG TGACGTTTCA GGTGAAGGTG TTCAACAAGC        540

ATTGCTTAAA ATCTTAGAAG GTACGACTGC AAGTGTTCCG CCACAAGGTG GACGCAAACA        600

TCCAAACCAA GAAATGATTC AAATTGATAC AACAAATATC TTATTTATTC TTGGTGGTGC        660

CTTTGATGGT ATTGAAGAAG TGATTAAGCG CCGTCTTGGT GAAAAGTTA TTGGTTTCTC         720

AAGCAATGAA GCTGATAAAT ATGACGAACA AGCATTATTA GCACAAATTC GCCCAGAAGA        780

TTTGCAAGCC TATGGTTTGA TTCCTGAATT TATCGGACGT GTGCCAATTG TAGCTAATTT        840

AGAAACATTA GATGTAACTG CGTTGAAAAA CATCTTAACG CAACCTAAAA ATGCACTTGT        900

GAAACAATAT ACTAAAATGC TGGAATTAGA TGATGTGGAT TTAGAGTTCA CTGAAGAAGC        960

TTTATCAGCA ATTAGTGAAA AAGCAATTGA AAGAAAAACA GGTGCGCGTG GTTTACGTTC       1020

AATCATAGAA GAATCGTTAA TCGATATTAT GTTTGATGTG CCTTCTAACG AAAATGTAAC       1080

GAaGGTAGTT ATTACAGCAC AAACmATTAA TGrAGaACTG AACCAG                      1126
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(2) INFORMATION FOR SEQ ID NO: 29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4392 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

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ATTGACTTCT TAGCAATnAA TaTGAGTGAA GAACGTACTG TTGAAGTACC AGTTCAATTA         60

GTTGGTGAAG CAGTAGGCGC TAAAGAAGGC GGCGTAGTTG AACAACCATT ATTCAACTTA        120

GAAGTAACTG CTACTCCAGA CAATATTCCA GAAGCAATCG AAGTAGACAT TACTGAATTA        180

AACATTAACG ACAGCTTAAC TGTTGCTGAT GTTAAAGTAA CTGGCGACTT CAAAAATCGAA       240

AACGATTCAG CTGAATCAGT AGTAACAGTA GTTGCTCCAA CTGAAGAACC AACTGAAGAA        300

GAAATCGAAG CTATGGAAGG CGAACAACAA ACTGAAGAAC CAGAAGTTGT TGGCGAAAGC        360

AAAGAAGACG AAGAAAAAAC TGAAGAGTAA TTTTAATCTG TTACATTAAA GTTTTTATAC        420

TTTGTTTAAC AAGCACTGTG CTTATTTTAA TATAAGCATG GTGCTTTTTG TGTTATTATA        480

AAGCTTAATT AAACTTTATT ACTTTGTACT AAAGTTTAAT TAATTTTAGT GAGTAAAAGA        540
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CTTACTAAGC TAAAGAATAA TGATAATTGA TGGCAATGGC GGAAAATGGA TGTTGTCATT          660

ATAATAATAA ATGAAACAAT TATGTTGGAG GTAAACACGC ATGAAATGTA TTGTAGGTCT          720

AGGTAATATA GGTAAACGTT TTGAACTTAC AAGACATAAT ATCGGCTTTG AAGTCGTTGA          780

TTATATTTTA GAGAAAAATA ATTTTTCATT AGATAAACAA AAGTTTAAAG GTGCATATAC          840

AATTGAACGA ATGAACGGCG ATAAAGTGTT ATTTATCGAA CCAATGACAA TGATGAATTT          900

GTCAGGTGAA GCaGTTGCAC CGATTATGGA TTATTACAAT GTTAATCCAG AAGATTTAAT          960

TGTCTTATAT GATGATTTAG ATTTAGAACA AGGACAAGTT CGCTTAAGAC AAAAAGGAAG         1020

TGCGGGCGGT CACAATGGTA TGAAATCAAT TATTAAAATG CTTGGTACAG ACCAATTTAA         1080

ACGTATTCGT ATTGGTGTGG GAAGACCAAC GAATGGTATG ACGGTACCTG ATTATGTTTT         1140

ACAACGCTTT TCAAATGATG AAATGGTAAC GATGGAAAAA GTTATCGAAC ACGCAGCACG         1200

CGCAATTGAA AAGTTTCTTG AAACATCACG ATTTGACCAT GTTATGAATG AATTTAATGG         1260

TGAAGTGAAA TAATGACAAT ATTGACAACG CTTATAAAAG AAGATAATCA TTTTCAAGAC         1320

CTTAATCAGG TATTTGGACA AGCAAACACA CTAGTAACTG GTCTTTCCCC GTCAGCTAAA         1380

GTGACGATGA TTGCTGAAAA ATATGCACAA AGTAATCAAC AGTTATTATT AATTACCAAT         1440

AATTTATACC AAGCAGATAA ATTAGAAACA GATTTACTTC AATTTATAGA TGCTGAAGAA         1500

TTGTATAAGT ATCCTGTGCA AGATATTATG ACCGAAGAGT TTTCAACACA AAGCCCTCAA         1560

CTGATGAGTG AACGTATTAG AACTTTAACT GCGTTAGCTC AAGGTAAGAA AGGGTTATTT         1620

ATCGTTCCTT TAAATGGTTT GAAAAAGTGG TTAACTCCTG TTGAAATGTG GCAAAATCAC         1680

CAAATGACAT TGCGTGTTGG TGAGGATATC GATGTGGACC AATTTCTTAA CAAATTAGTT         1740

AATATGGGGT ACAAACGGGA ATCCGTGGTA TCGCATATTG GTGAATTCTC ATTGCGAGGA         1800

GGTATTATCG ATATCTTTCC GCTAATTGGG GAACcAATCA GAATTGAGCT ATTTGATACC         1860

GAAATTGATT CTATTCGGGA TTTTGATGTT GAAACGCAGC GTTCCAAAGA TAATGTTGAA         1920

GAAGTCGATA TCACAACTGC AAGTGATTAT ATCATTACTG AAGAAGTGAT CAGCCATCTT         1980

AAAGAAGAGT TAAAAACTGC ATATGAAAAT ACAAGACCCA AAATAGATAA ATCAGTGCGC         2040

AATGATTTGA AAGAAACGTA TGAAAGCTTT AAATTATTCG AAAGTACATA CTTTGATCAT         2100

CAAATACTAC GTCGCTTAGT AGCGTTTATG TATGAAACAC CTTCGACAAT TATTGAGTAT         2160

TTCCAAAAAG ATGCAATCAT TGCAGTTGAT GAATTTAATC GTATTAAAGA AACTGAAGAA         2220

AGTTTAACAC TAGAGTCTGA TTCGTTTATT AGCAATATTA TTGAAAGTGG TAATGGATTT         2280
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TCATGTAAAC CTGTCCAACA ATTTTATGGG CAATATGACA TTATGCGTTC TGAATTTCAA          2460

CGATATGTTA ATCAAAACTA TCATATCGTG GTTTTGGTCG AAACCGAAAC TAAAGTTGAA          2520

CGTATGCAAG CGATGTTAAG TGAAtGCAT ATTCCATCAA TAACAAAATT GCATCGCTCA           2580

ATGTCATCGG GGCAAGCAGT GATTATTGAA GGCAGTTTAT CTGAAGGATT TGAACTACCT          2640

GATATGGGAT TAGTTGTCAT TACTGAGCGT GAgcTTTTTA AATCAAAACA GAAAAAGCAA          2700

CGAAAACGTA CGAAAGCTAT CTCAAATGCT GAAAAAATTA AGTCTTACCA AGATTTAAAT          2760

GTGGGAGATT ATATTGTTCA TGTGCATCAT GGTGTTGGTA GATATTTAGG TGTTGAGACG          2820

CTCGAAGTGG GGCAAACGCA TCGTGATTAT ATTAAATTGC AATATAAAGG TACGGATCAA          2880

CTATTTGTTC CAGTAGATCA AATGGATCAA GTTCAAAAAT ATGTAGCTTC GGAAGATAAG          2940

ACGCCAAAAT TAAATAAACT CGGTGGCAGT GAATGGAAAA AAACAAAAGC TAAAGTTCAA          3000

CAAAGTGTTG AAGATATTGC TGAAGAGTTG ATTGATTTAT ATAAAGAAAG AGAAATGGCA          3060

GAAGGTTATC AATATGGGGA AGACACAGCT GAGCAAACAA CATTTGAATT AGATTTTCCA          3120

TATGAACTTA CGCCTGACCA AGCTAAATCT ATCGATGAAA TTAAAGATGA CATGCAAAAA          3180

TCGCGTCCAA TGGATCGCTT GCTATGTGGT GATGTTGGTT ATGGTAAAAC TGAAGTTGCA          3240

GTGAGAGCAG CATTCAAAGC TGTAATGGAA GGAAAGCAGG TTGCATTTTT AGTTCCTACA          3300

ACTATTTTAG CTCAGCAACA TTATGAGACG TTAATTGAGC GTATGCAAGA TTTTCCTGTT          3360

GAAATTCAAT TAATGAGTCG TTTTAGAACG CCTAAAGAGA TAAAACAAAC TAAGGAAGGA          3420

CTTAAAACTG GATTTGTTGA CATAGTTGTT GGTACACACA AATTACTTAG TAAAGATATA          3480

CAGTATAAAG ATTTAGGGCT GTTGATTGTA GATGAAGAAC AACGATTTGG TGTACGCCAT          3540

AAAGAGCGTA TTAAAACATT AAAACATAAT GTAGATGTAC TAACATTGAC TGCAACCCCA          3600

ATAGCTAGAA CATTGCATAT GAGTATGCTA GGTGTGCGGG ATTTGTCAGT GATTGAAACG          3660

CCGCCAGAAA ATCGTTTCCC AGTTCAAACA TATGTATTAG AACAGAACAT GAGTTTTATC          3720

AAAGAAGCTT TAGAAAGAGA ACTATCCCGT GATGGCCAAG TGTTTTATCT TTATAATAAA          3780

GTGCAATCCA TTTATGaAAA ACGAGAACAA CTCCAGATGT TAATGCCAGA TGCTAACATT          3840

GCAGTTGCTC ATGGACAAAT GACAGAGCGC GATTTAGAAG AAACGATGTT AAGTTTTATC          3900

AATAATgAAT ATGATATTTT AGTAACGACG ACGATTATTG AAACAGGTGT CGATGTCCCA          3960

AATGCAAATA CTTTGATCAT TGAAGATGCA GATCGCTTTG GATTGAGTCA GTTGTATCAA          4020

TTAAGAGGTC GTGTTGGTCG TTCAAGTCGT ATTGGTTATG CATACTTCTT ACATCCAGCA          4080

AATAAGGTAC TAACTGAGAC TGCAGAAGAT CGATTACAAG CGATTAAAGA ATTTACGGAG          4140
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TTAGGTAAAC AACAGCACGG CTTTATTGAT ACAGTTGGAT TTGATTTGTA CAGTCAAATG   4260

TTAGAAGAAG CTGTAAATGA AAAACGTGGT ATTAAGGAAC CAGAATCTGA GGTGCCAGAA   4320

GTCGAAGTTG ATTTAAACTT GGATGCATAT TTGCCAACAG AATATATTGC AAATGAACAA   4380

GCTAAAATTG AA   4392

(2) INFORMATION FOR SEQ ID NO: 30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 729 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTTCTTTTGA ATCTATATCG AGGTGGTTGG TAGGTTCATC TAAAATAAGT ACATTGTCAC   60

GTTGCAACAT AAGTAGTGCT AGTTGTAAAC GTGCTTTTTC ACCACCAGAT AAATCATTAA   120

TTATCTTTTT AACATCGTCT TGTACAAATA AGAAACGTCC AAGAACTGCT CGAATATCTT   180

TTTCATTCAT TAACGGATAT TGATCCCACA CATAATCTAA AATCGTTTTA CTAGATTTAA   240

ATTCTGCTTG CTTTTGATCA TAATAACCAA TTTGTAAATT TGCGCCGAAA GTAATATCGC   300

CATTAAGCGC TTTTTGTTGA TTAGCAATAG TTTTAATTAA GGTCGATTTT CCAATACCAT   360

TTGGCCCAAT GATTGCTATA TGATCGCCTT TAGAGACCTC TATACTCATA GGTTTGGTAA   420

TTGCAGTTTG ATAACCGATT TCTAAATTTT TTACATGCAT GACGTCATTA CCTGTATTCC   480

GGTCAAAGCC AAATTGAATA TTTGCACTTT TGGCATCTAA CATTGGTTTA TCAATGCGTT   540

CCATTTTTTC TAAAATCTTA CGTCTACTTT TTGCCATTCC ACTTGTTGAA GCACGGGTAA   600

TATTTTTCTC AACAAAAGTT TCTAATCGTT TTATTTCTGC TTGTTGACTT TCATATTCTT   660

GCATTCGTTT TTGATAATAT AAATCCCGTT GCTGTATAAA TTCCTCGTAA TTACCAACAT   720

AGCGTTTGA   729

(2) INFORMATION FOR SEQ ID NO: 31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13856 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

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TGATGTTTCG ATACATTTGT TGCACCTTGT GGATATACTT TAAAGGTTGT GTCGTATGTT      120

TCCTTACTAT CTTTAGCTTC AGATTCCTGT GATTCAACCG TTTTATATTT TTCAAGTGCA      180

TGTCCTTCAA TATCAACTCG TGGAATAATG CGATTCAACC ATGCTGGTAA ATACCACGAA      240

CCTTTtCCAA ACAATTTCGt TAATGCAGGA ATTAACATCA TtCTGACTAC GAAGGCATCA      300

AAGAGTACAC CAAACGCTAA TGCCATACCC ATTGATTTAA TCATGACATC TTCTTGGAAT      360

ACAAACGCAA AGAAGACACT AAACATAATT AATGCAGCTG CTACAATAAC AGGACCGCTT      420

TCTTTCAATC CTACTTTGAT AGAATAATCA TTATCCCCTG TTTTACTATm yyCTTCATGr      480

ATTCGCGACA TAAGGAAGAC TTCATAATCC ATCGCTAATC CAAATAAGAT ACCTATAGTA      540

ATAACCGGTA AAAATGCTAG CATTGGTCCT GTCGTTCAA TACCAAACAG ACCTTTCATA       600

AAACCATCTT GCATTACTAA TGTTGTAAAT CCTAATGTTG CCATTAATGA CAAGACGAAT      660

CCTAAAACTG CTTTTAATGG TATTAGAATT GAACGGAAGA CAATCATTAA TAAGAAAAAT      720

GCTAATACAA CAATGACTGA GGCAAATAAA GGTATCGCCT CATTTAACTT TTTAGACATA      780

TCAATATTAA TGACACTTTG TCCCGAAATC TCCGTTTTGA ACCCATATTT ATCTTGTGCA      840

TCTTTATGAT AATCTCGTAA ATCATGCACT AAATCATTTG TACTCTCTGC ATTAGGCCCT      900

TGCTTAGGTA TCACGACCAT CAAAGCGTAA TCATTATCTT TACTCATTTG TGGTGGCGTA      960

ACGATATCTA CATTTTTCTT ATCTTTAATA TCTTTATATA CAGACTGTAA ATCTTGTTGT     1020

AATCCTTGTG GATCATCCTT TTTATCTTTC ACATTTATCA ACATCGGTAT TTGGCCATTA     1080

AATCCTTCAC CAAATTTATC CGAGATAATA TCGTAAGCTT TTTTCTGTGT AGAATCTGCT     1140

GGTTTAACAC CGTCATCTGG AATACCAAGT CGCATATGAC TAACTGGTAT TGCAGCTGCT     1200

ACTAATATGA TTAAACCTAG TAATACTGCC GCAAGTGCAT TTCCTGTAAT AAATTTAGAC     1260

CATGGCGTAT CAATATCTTT TTTGAATTTA GACTGTAATT TATTCACTTT AATGCGTTtA     1320

TGGAAAATGC TTATTAATGC AGGTAATAAA GTTAAAGCGC TAAGTACTGC AAAAACAACA     1380

CTAATTGCCG AAGCAAATCC CATTACCGCT AAGAAGTCAA TGCCTACTAA TGATAAACCA     1440

CATACTGCAA TTACAACTGT TACACCAGCA AAAACAACTG CACTACCTGC TGTTCCTATT     1500

GCAAGACCAA TGCCTTTAAT GTAATCTGTT TCAGTTTTCA TAACTTGTCG ATATCTGAAT     1560

AAAATAAATA ATGCATAATC GATACCAACT GCTAGTCCAA TCATTACGGC TAATGTCAGT     1620

GTGACATTTG GTATATCGAA TGCATAAGTT AACAAACTGA TAATACCTAC ACCAGAGGCT     1680

AGACCAATCA ATGCACTTAT AATTGGTAAT CCTGCAGCAA TGACTGAACC GAATGTGATT     1740

AACAGTACAA CAAATGCAAC AATAATACCA ACTAGTTCAG AATTACCGCC TACTTCTGTA     1800
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AAATGACTTT TAACATTATC TCTAGAGCCA TCTTTTAAAG ATGTTTGACT AACGTCATAT        1920

GTGATATCTG CAAATGCAGT TGTTTTATCT TTACTAATTT GCTTATTTTC ATAAGGATCT        1980

GATATTTTAT CAATGTGCTT GTCATCTTTT TTAATATCAT CTAACGTTTT CTTAATATCT        2040

TTAGTAATGT TCGGTTGCAC AATACCATCA TCTTTAGTCG TCTTAAAGAC AACACGTATT        2100

TGTGCCTTTT CACTATCTTG ATTAAAATGT TTTTCAATCT TTTTATTCGT ATCTAACGAC        2160

TCTAATCCTG TCATTTTAAT ATCATTGTCA AATTTCGGTG CATTTGTAGC AAGTGGTATC        2220

AATATTGCAG CTACAATCAC TATCCATGCA ATGACCGCGG ACCATTTATG TTTTGCGATG        2280

AATGTCCCCA TCTTATATAA AAATTTTGCC AAAGTATATT GCCTCCTTTT AAAATCAACG        2340

TTATAGTTTA AATATACAGT GTAGATTATT GTTCGATTAT AGTATCTATC CCCGACCTCT        2400

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AAGAGACTGA TTTACGAGTT ATAAAGACAA AAAAAGCATT GTCGAGTAGC TTGCTACAAT        2520

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TTGATTGGCC TGGCGAAGAT ATTGATAACA TTTTCCATAG ATTAATCAAT ATTAAGATTA        3000

AATAGTAGAT GAGAAACTCA TGAGCGTTAC CAACATTCAT AATAAAAACG ATAGTGkACA        3060

CGTTÄATGAA TTCGTGTACT ACTATCGTTT TTTATTTTTA TCGTGCTTAT CGCTATTAAA        3120

ACAACTGATA CACAACACAT AAACTATGAA GAAAAAAATA AATCCGCTAT CTAAATGACT        3180

TTGACTCAGT TGTTTAAATG ACCAAATTGC TAATACAATT CCCATTATTA TTGAAATAAC        3240

GTATCTCACA TTCTTATACC TATAATCCTT TTCTAAAAAT ATGGTTGCTA TTACTTAATT        3300

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TTAGAACATT TCTGAAACAA CCTTTTGTTC TAAGAAGTGT AATAAGTAGT CTGGACTACC        3420

TGTTTTAGCG TCCGTACCTG ACATTTTGAA ACCACCAAAT GGATGGTATC CAACAACTGC        3480

TGAAGTACAG CCTCTGTTAA GGTATAAATT GCCTACATCA AATTCGTTTA CCGCTTTAAT        3540
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GTAACCTTTT GAATCATCAG TGCCGCCACC TTGTTCTAAT TTACCTTCTT CTTTACCAAT      3780

CTCAATATAA TTTTTAATCT TATCAAATTG TTTTTTATTA ATAACTGGGC CCATATACGT      3840

ATTGTCTACA GTATTGCCCA ACGTTAATTC TTTTGTTAAT TTGATTGATT CTCTAATAC       3900

TTCGTCATAA ACGTCTTTAT GCACAATTGC ACGTGAACAT GCTGAACATT TTTGACCAGA      3960

AAAACCAAAT GCTGACGTTA CAATAGCTTC TGCTGCCATA TCTGTATCAA TATTTTCATC      4020

AACTACAATG GCATCTTTAC CACCCATTTC AGCGATAACA CGTTTCAAGA AGTTTTGACC      4080

TTCTTGAACA ACGGCACTAC GTTCATAAAT TCTAGTACCT GTCGCACGTG ATCCTGTAAA      4140

TGTAACGAAA TGCGTATCTT TATGATCAAC TAAGTAATCA CCAATTTCTT TCGGATCACC      4200

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TGGTGCTAAA GTTGTACCAG CCATAATCGC AAACGGGAAG TTCCACGGCG GAATTGTAAC      4380

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CTTACCTTGA GCCAAGTCCA TCATTGAACG TGCATAGTAT TCAATAAAAT CAATACCTTC      4500

AGCTGCATCA CCAACTGCTT CATCCCATGG CTTACCTGCT TCATAAACCA TAATTGCTGC      4560

AATTTCCGCT TTTCGACGAC GAATAATTGC CGAAACACGT AACATAAGCT CTGCACGATC      4620

ATTTGCTGAC CATGTTTTCC AAGATTATA AGCTTCGTTT GCTGCTTTAA ACGCATCTTC       4680

AACATCTTGT TTTGTTGCCT TTGATGCATT TGCAATCACT TGTGATGTGT CTGCAGGATT      4740

GATTGATTTA ATTTTGTCAT CTTTGAAAAT CTTCTCTCCA TTAATCACTA ATGGTATGTC      4800

TTGACCTAAT TCTTTTTCCA CGTCTTTCAA TGCTTTCTTA AACATATCCA CATTTTCTTG      4860

GACTGAAAAA TCGTAACCAG GTTCATTTTT AAATTCTACT ACCATGTACA CTTACCCCCT      4920

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CAAGTATTTT GAAATTGATT GGTTACTTTT TAAAATTTAT ATGGGTCGCA ACTGCTACTT      5100

TATCGTTTCG TCATTTAATG TTTCGGATGG TAGGTCATTA TCAATTTTAC GAACGACTTT      5160

ACAAGGGTTT CCAACCGCTA AGCTGTGTGG CGGAATATCT TTAGTGACAA CACTACCAGC      5220

ACCAATCACA CTGCCTTCTC CAATCGTCAC CCCTGGTAAC ACGGCTACAT GACCGCCAAA      5280

CCAAGTATTA CTGCCAATAT GAATGGGTCC GGCTTTTTCA AAACCTTCAT TTCTATGATG      5340

GAAATTAAGT GGATGTGTCG CTGTGTAGAA TCCACAATTA GGTCCTATAA AAACATTATC      5400
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TCCTAGTTTA ACGTTCCAAC CATAATCTGT ATCAAAAGGA ATCGAAATAC TTACATTGTC      5520

TGTTGTTGTT TGAAATAATT GATCAATTAA TTCCTTTCTT TTATTTGTAG CACTCGGTCT      5580

TGTATGATTT AATTCAAAGC AAATATCTTT CGCTCGTGCA CGTTCATTGA TTAAGTATTG      5640

ATCAAAGTTT GCATCGTACC ATTTTTCTGC TAACATTTTT TCTTTTTCAG TCATTACACC      5700

TTTCAACTCC TAATAACTTA TTTACTTGTT TAAAAGTTAA TCAAATAAAC CTTCGCCTAT      5760

GCAACTAATA CGCTATAACA TTATGAAATC ATGACCTTAT CACCCTTATC TATACAATTC      5820

TCGCATCAAA TACTGCTAAA GTAGTAGATA AATTCAATAC TACAGACGCA TTCATTTTTT      5880

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CATCCATCTT AATAATTTTA AAAATTTACA TGCGAAAGAA TTTAACCCAT CTGATTTCTT      6120

TTAAGTCACC TAAGAATTGC AAATCCAGAA GTCATTTAAG TTTTACCTTT CATTCATACA      6180

TCCTTTAATA TTAATTACGA CTTCTTTTAT ATAGATGCTA AGTAGAGAGA TTGTTGTGCA      6240

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ATTTATGAAA TGGTTCGTTG GCTAAATGGC TCAACAACGC AACCGCATTT ATACTTTGAA      7140
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TTAAAAGATG GTAATGAAGT GATGATTCCT CTAAATGAAG TACATGTTGG AGATACACTT        7320
ATCGTTAAAC CAGGTGAAAA GATACCTGTT GATGGCAAAA TTATTAAAGG TATGACTGCC        7380
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GTAATTGGTT CAACGATGAA CAAAAACGGT ACTATTACTA TGACAGCAAC AAAAGTTGGC        7500
GGGGACACTG CGTTGGCAAA TATTATTAAA GTTGTCGAAG AAGCTCAAAG TTCTAAAGCG        7560
CCGATTCAAC GATTGGCAGA TATTATTTCT GGTTATTTCG TTCCTATCGT TGTTGGTATC        7620
GCACTATTAA CATTTATCGT GTGGATTACT TTAGTTACAC CAGGTACATT TGAACCTGCA        7680
CTTGTTGCGA GTATTTCCGT TCTCGTCATT GCTTGTCCAT GCGCATTGGG ACTTGCTACA        7740
CCAACTTCTA TTATGGTAGG TACTGGTCGC GCTGCTGaAA ATGGTATTTT ATTTAAAGGT        7800
GGCGAGTTTG TTGAACGCAC ACATCAAATT GATACCATCG TTTTAGATAA GACGGGTACC        7860
ATTACAAATG GTCGTCCAGT CGTGACAGAT TATCATGGTG ACAATCAAAC GCTACAACTA        7920
CTTGCTACTG CTGAAAAAGA TTCTGAACAC CCATTGGCAG AAGCCATTGT CAATTATGCA        7980
AAAGAAAAGC AATTAATATT AACTGAGACA ACAACATTTA AAGCAGTACC TGGCCATGGT        8040
ATTGAAGCAA CGATTGATCA TCACCATATA TTGGTTGGTA ACCGTAAATT AATGGCTGAC        8100
AATGATATTA GCTTGCCTAA GCATATTTCT GATGATTTAA CACATTATGA ACGAGATGGT        8160
AAAACTGCTA TGCTCATTGC TGTTAATTAT TCATTAACTG GTATCATCGC AGTGGCAGAT        8220
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ACCATTCGTA ATATTCGTCA AAATCTATTT TGGGCATTCG GCTATAATAT TGCCGGTATC        8640
CCTATAGCTG CATTGGGCTT ACTTGCGCCA TGGGTTGCTG GTGCTGCAAT GGCACTAAGT        8700
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ATTGGCTCTA TAATGTCGCG GTTTAyaGTt GGATCTTCGC TCCAACTGCA TATATAGTnA        8880
CACTTTTCGC TTGGCGAATT AGTGTATCTT ACCTAATAGc TCCGCCTATT AGGTTCCATC        8940
ATTATTATAA ATAATAAGTA CACTACGGtT TACAGTTGGA TCTTCGCTCC AACTGCATAA        9000
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GAAATTTTAA ATGTTGAAGG TATGAGCTGT GGTCACTGCA AAAGTGCTGT TGAATCTGCA      9120

TTAAATAATA TTGACGGTGT CACTTCAGCT GACGTTAACC TTGAAAATGG TCAAGTAAGT      9180

GTTCAATATG ATGACAGTAA AGTTGCTGTA TCTCAAATGA AAGACGCAAT TGAAGATCAA      9240

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CCCTTTTTAA AATGTTTAAA TAATTCAGCA TTAAATAGAT AATGATTATA TTTCGTTGCA      9720

GGTACATGTA ATGTCACGAT ATCAGCACCT TCAACCGCTT CCTCAATCGT ATCTTTGTAA      9780

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AACCATACAT ATATGCCACC TTTAGCATGA ACAAATGGCA AATCAGCTTT TGCAAGCATG     10620

GCTTCGAATC GGTCACGACG TGTTTTAAAT ACATTGCTTT GTTCTTCTAA AAAATCATCA     10680

TAATGATTCA AAGCATATAT TGCGGCATCT TGTAATGCAC CAAACATCCC AGCATTTGTG     10740
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CCATTTTCCG AAGCAAGTAT ACTAGGATTT TTAGCGTCGA AACCGAAAGC ACCATAAGCA      10920

AAATCATGCA CGATTTTAGT GTCTGTACCT TTAAATTTAG cTATCGCTTC ATCAAAAACT      10980

TCTTTCGTAG CTGTCGATCC AGTTGGATTA TTTGGATACG TTAAATAAAT GAGTTTTGTT      11040

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GCAAGTGATT TATCAGCGAC CGCTGGTACA TACACATAAA TAGAAGGATC ATATGATAAA      12420

CGTCCCTCAA ATATTTCTTC AATATTGCCT CTAAAGTCAT CTGAAAAAAT AACATTATGA      12480

AGTCTCACTT GATCTGTCAC ATCAATATCT ATACCGATAT ACATTAAAAA TGCTGAACAA      12540

GAGTAATCTA AGTCTGCAAT TTTATGTGGT GGATACTTTT TAATAGGTGC AAAATCTGGC      12600
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ATGTCACCAT TCACTTTTAT CGCATCGGCC CGTTTGAATT TAGGATCAAT AATAATTTGC      12720

TCAATTTCAG CATTTAGTTC AATATTAACG CCTAAGTCTT TATTTAATTG CGCTAGcCCT      12780

TGAGCCATGC CATACATACC GCCTTTAATA AAATGCACAC CAAACATCAT TTCAATCATA      12840

GGAATAATTG AATATAGTGA CGGGCCTCGT TTTGGATCAA TTCCTATGTA TAACGTTTGA      12900

AACGCTAAAA GCTTTTGTAT CTTTTCGTTA TCAATATAAT GTTCAATTAG CTGATCTGCA      12960

TGATTTAACG TTTTTAACTT AGCACCTTGC ACAAGTGACG TCATATTATA AAAGTCACTC      13020

GGTTTGCGAT ACGTTCTTTC TAAGAAATAG CGACGTGCAA TTTCATATTT TTTATAAACA      13080

TCCGTTAAAA AGGACATAAA ACCATGCGTT GAACCAGGTT CTATACTTTC TAGCATTTGC      13140

TGTAATTCAG CTAAATCTGT AGGCACCGTT ATACGATCAT CGTGGTCAAA ATACACATCG      13200

TAAATATAAC GTAATTGTCT CAATTCAATA TAATCTTCAT AATTTTTACC ACACGCTGTA      13260

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CCGTCTTTCT TTAATTGATT CATACGCCCG CCTACATTAT TATTTTTTTC AAATATCGTC      13380

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ATTACTGCAA TCTTCATTAT TCAACCACCT ATATTCTATG ATATTACTA TTTATTTCAT       13500

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CCTGTCTCAC TTCGTCCAGT ATTTCAATAT ATATACGTGC TGCTAATTCT ATGATTGGTT      13620

GTGCTTCAAT ACTAAATACT TTGATTTGAT CCATAACATC TTGAAAATCT TTTTCTGCGA      13680

TAGCTGCATA ATATTCCCAT AAGTCAATAT AATGATTATT AACACCATTT TGGTACACTT      13740

CAGCAATATC AACTTCATAT TGCTTTAATC GTTGCTTACT AAAATATATC CGTTCATTGT      13800

CAAAATCTTC ACCGACATCT CTTAATATAT TAAnGGGATC CTCTAGAGTC GACCTG          13856
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(2) INFORMATION FOR SEQ ID NO: 32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10088 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

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ATATATAAAT ATAGATTAAG TATATAGATT AATCAACTTT TTTGGAAGAG CAAATCACGC          60

AATCAACAAA TAATATAAGA AGTTTTTGCG ATAGTTTTAA AATAGCTGTA ATAGAATACT         120
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ATAATTGGTT AATATATGAG TAATTAGAAA ATAGACAAAG GATGACGATT TATGTATATC      300

AATATGAAAG ATTATGGGTT AACAGGCATA AACAAAACTA AAGATACTCG AGCAATACAA      360

CGTGCGTTAA ATCGTGGAAG ATGTAAACCA ACGACAGTTT ATATACCGAA AGGGACGTAT      420

GATATTTGCA AACCATTAAC GATATATGGC AATACAACAC TTTTGTTAGA TAATGAAACT      480

ATTTTACGCC GATGTCATTC TGGTCCTTTA TTAAAAAATG GTCGTCGCTT TGGTTTTTaT      540

CGTGGTTATA ATGGACACAG TCATATTCAT ATTAAAGGCG GCAAGTTTGA TATGAATGGT      600

GTATCGTATC CTTATAACAA TACAGCTATG TGCATTGGGC ATGCTGAAGA TATTCAATTA      660

ATAGGTGTGA CCATTAAGAA TGTAGTGAGT GGTCATGCAA TTGATGCTTG TGGGATTAAC      720

GGACTCTATA TTAAAAGCTG TTCATTTGAA GGATTCATAG ACTATAGTGG CGAACcTTTT      780

ATTCTGAAGC AATACAATTA GACATTCAAG TACCTGGTGC TTTTCCAAAA TTCGGAACgA      840

CAGATGGTAC GATAACGAAA AATGTCATTA TCGAAGATTG TTATTTTGGA CCTTCAGAAT      900

TGCCCGAAAT GGGAAGTTGG AATCGTGCTA TTGGCTCACA TGCAAGTAGA CATAATCGAT      960

ACTATGAGAA TATTCATATT AGAAATAATA TATTTGAAGA TATACAAGGT TATGCATTAA     1020

CTCCCTTGaA GTATAAAGAT GCTTTCATTA TTAATAATAA GTTTATTAAC TGTGaGGGTG     1080

GCATTAGATA TTTAGGAGTT AGAGATGGTA AAAATGCAGC AGATGTGaTG ACAGGaAAAG     1140

ACTTAGGTTC CCAAGCAGGC ATAAATATGA ATATAATTGG AAATGAATTT AAAGGATCAA     1200

TGTCTAAAGA TGCGATACAT GTACGTAATT ATAATAATGT TAAACATAAA GATGTATTAA     1260

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TGTTTTTAAG TCCTGTTGAA GCGGGTATTC AAGTTACTAC AATCAATGTA GATGAAATAA     1380

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TGACGGTAAT GATAATACAA GATAGACAAC TTTCTATACT CTAATATAGT GAGTTGAAGT     1560

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CGACTTGGTG GATTACTGAA GCAATTCCTA TTGCAGCAAC GAGCTTATTA CCAATTGTGT     1860

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TTATCTTTTT GTTTTTAGGT GGATTTATTT TGGCAATTGC AATGGAAAGA TGGAATTTAC     1980
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TTGGATTCAT GGTGGCAACA GGATTCTTAT CTATGTTTGT ATCGAACACT GCAGCTGTAA      2100

TGATTATGAT TCCGATTGGT TTAGCAATTA TTAAGGAAGC ACATGATTTA CAAGAAGCCA      2160

ATACGAATCA AACAAGTATT CAAAAGTTTG AAAAATCTCT AGTTTTAGCA ATTGGCTATG      2220

CAGGTACGAT TGGTGGCTTG GGTACATTAA TCGGAACCCC GCCATTAATT ATTTTAAAAG      2280

GACAATACAT GCAACATTTT GGACATGAAA TTAGTTTTGC TAAATGGATG ATTGTAGGGA      2340

TTCCAACGGT CATTGTTTTG TTAGGTATTA CTTGGCTCTA TTTAAGATAT GTTGCGTTTA      2400

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AACATCGCCG TATCATTGAC TGGGAAGTTG CAAAAGAGCT CCCTTGGGGT GTATTAATTT      2700

TATTTGGTGG CGGTTTAGCA TTAGCGAAAG GTATTTCTGA AAGTGGTTTA GCAAAATGGT      2760

TAGGCGAACA GTTGAAATCA TTAAATGGTG TTAGTCCGAT TCTTATTGTA ATTGTCATAA      2820

CAATCTTTGT CTTATTTTTA ACTGAAGTGA CATCTAATAC TGCAACTGCA ACGATGATTT      2880

TACCGATTTT AGCAACGTTG TCTGTTGCTG TTGGAGTGCA TCCATTACTA CTTATGGCAC      2940

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CGAGACTCAA TCCAGGATAA ATTAATATTA AACAAAGCAA ATGTATTAAG CACACTTGCT      3540

AACAACCCAG GTTTATCATG CATTGGTGTA ATTAAAAACA TCAATGATGT CGCATTTTGA      3600

TCAAATTGCT GCTGATTTTT TATAACTAAA AAACGTGTCA CGTTATGTGG ATAGTCTTCA      3660

ATATGTGTAT CAATAGGTGT AAAACCATAA GctTCGCCAC TACCTAAAGG TGCAATTGCT      3720
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TTTTTAATAT CAGAAATGGA ATCTGTTCCA TTACCATATA ATGCAAAGTT AATATCTAAA        3900

CGTATTTCAC CGTGTGCAAA GACATCTTGC TGTGCAAGTG CATCTGCCAC AATGTTGATT        3960

GTTCCTTCTA TAGAATTTTC AATAGGGACA ACACCAATCG ATGTGTCATC ATCTGCAACT        4020

GCCTTGATGA CTTCAAATAA ATTTGACTTT GGTTGAAAAG TTGCTTCATT TTCAGAAAAA        4080

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TGCTACACCT CTACTAACTT AATGATGGAA AGGGCACTGG TTAGCATTTG ATTCTTTCTT        4200

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TTGTGCTTCG TTACGTTCGA ATAGTTCGAA TTGCTTTGCA GCGGTCAAAT GATCGACAAT        4380

TGATACGCCT TCTTTTTTAA AGGAATGATA CACAGCATAG TTCAATTCAA CAAGTGCTCG        4440

ATCTTTATTA AATGAATTAT TTTTAAGTGT ATCAAATTCA AACGCATCTG CAACTTTTTC        4500

TAGTAAATTG TAACGGTAAT CATCAATAAA GTTACGTACG CCAATTTCAG TTACCATATA        4560

CCAACCGTTA AAGGGTGCAG TTGGATATAC AATGCCACCG ATTTTTAAGT CCATATTGGA        4620

AATGATAGGG ACTGCATACC ATTTTAAGTT CAATTTTCTT AATTTTGGAT AATGATTATG        4680

TTCAATAGGT ACTTCTTTAA TTAATGAAGT AGGATATTCG TAAAATTTAA CTGACTCATT        4740

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GAACGATGCT TCGTCAGTAA CATCTCTTGC ATCAATGACA TTTAACGAAT CCCAAAATAA        5040

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CTCTTTAAAT AACATTAACA ACACCTCGCT TTATATTATA GTCTACATTA TTAAAATACT        5280

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TAAGGGGCTC TTATGTATAT AAAAAAAATGA ATTATGATAA AATGTAAGAA AATATTTAGG      5400

TCGATTGGAG AGATACAAGT GTACCAATTA GAAGACGACA GTTTAATGTT ACATAATGAC        5460

TTATATCAAA TAAATATGGC TGAAAGTTAT TGGAATGATA ATATTCATGA AAAAATGGCT        5520

GTATTTGATT TGTATTTTAG AAAAATGCCA TTTAATAGTG CTATGCTGT TTTTAATGGT        5580
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TTAAAGTCTA TTGGCTACAA GGATGATTTC TTATCATATT TAAAAGATTT AAAATTCACA      5700

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GTAGAAGCAC CATTGATTCA AGCGCAATTA ATAGAAACAA TTTTATTAAA CATTGTAAAT      5820

TTCCATACAT TAATTACAAC AAAGGCTAGC AGAATTCGTC AAATTGCATC AAATGATAAA      5880

TTAATGGAGT TTGGTACACG TCGTGCGCAA GAAATTGATG CAGCATTGTG GGGCGCTAGA      5940

GCTGCTTACA TCGGGGGCTT TGATTCTACA AGTAATGTTA GGGCGGGGAA ATTATTTGGT      6000

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CGTATGCTTG ATGAAGCAGG ATTTACTGAA ACTAAAATTA TCGCGTCTAA TGATTTGGAT      6300

GAAGAAACGA TTACGAGTTT GAAAGCACAA GGTGCAAAAG TAGATTCTTG GGGCGTTGGT      6360

ACAAAGCTGA TTACAGGATA CGATCAACCA GCATTAGGTG CAGTATATAA ACTTGTAGCT      6420

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CATCATAATA TTTATGAAAA TGGTAAATTA GTATATCAAA TGCCAACAGA AGATGAATCA      6720

CGTGAATATT TAGCACTAGG ATTACAATCT ATTTGGGATG AAAATAAGCG TTTCCTGAAT      6780

CCACAAGAAT ATCCAGTCGA TTTAAGCAAG GCATGTTGGG ATAATAAACA TAAACGTATT      6840

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TCTTACAGAT TTCCAAAAAG GAAATGAAAA AGCGCGTGAA CGTATGAAAG TACAATTTTC      7320
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TGTAACTTAT GAGGCGATTG ATAATTATTT AGAAGGTAAG CCAGTTACGC CAGAAGAACA    7620

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ACGTAAATTG ATGGATACGA TAAAAAATTT AGATCCGAAA GCATTTATCA TTGCGTATGA    8460

ACCTCGAAAC ATACATGGTG GATTCTGGAC TAAAGGCATT CGTCGTAGAA AGCTTAAAGA    8520

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AAmCAATtGC TGATTGTTTG TCACGAATGA AAtGCAAGGG TATATGCCGG TAAAACGTAT    8640

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CGTTTTTGTA GGTAAGAAAA TCCAATAACA TAATCCAATT TAAATAAAGA CTATTTGAAG    8760

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CAAGATGCTC GATCCATATT GTATGAGAAA CCCCCAGCAA GCTATATAAA GCATATGCTG    8880

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CCAAAGCTTC TGTGTTCATA ATTGTTAGTA GTATTTTATT ATCATTTGGT ATAAATATTT    9120

CAATAACAAT TGAGCTATTA TTTTTATTAT ATAATGTGAG TTGTTTGTGT TCTGTATTTA    9180
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AATTACATTT GAATTTATCA ATACTAAATA ATTCAATTTG TTCCATAATA TTATTTACCT      9360

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TGTTACCTTG AGTTTCTCTT ATCTTGAAAT TCTCAAGTTT ATTTATATAT TGsTCGTTGT      9900

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GTTGCGTTAC ATTATTGCCA GTAGGTATAC TCTCAGTCTT TnTnAACTnT nTATCTTCTA     10020

GACGTGGTGT TTTTAGTACT AGTTTAGCTT TATGATTTTG AGTACCACAT AGTAACCTTT     10080

TGAGTTGT                                                             10088
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(2) INFORMATION FOR SEQ ID NO: 33:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 7563 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

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CGGAAACGnA CCCnATGCGT ATGCTTGACG TGCCAAAATT AAATACGAAG TTCATAGCTT        60

TGAGGTACCA GAAGAACATT TATCTGGTCA AGAAGTCGCA GnACTCATAC AAGCAAATGT       120

TAAAACAGTA TTTAAAACGC TTGTTCTAGA AAATACAAAA CATGAACATT TTGTATTTGT       180

TATCCCAGTA AGTGAAACTT TAGATATGAA AAAGGCAGCT GCTTTGGTTG GAGAGAAGAA       240

ATTGCAGCTT ATGCCTTTAG ATAATTTGAA AAATGTAACG GGATACATTC GTGGTGGGTG       300

TTCGCCTGTT GGTATGAAAA CATTGTTTCC AACAGTCGTT GACAAATCGT GTGAAAATTA       360

TAGTCATATC AGTGTGAGTG GTGGGCTTCG AACAATGCAA ATCACAATAG CTGTTGAGGA       420
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TGCCACACTC CTTTTTGATT GAATTAGCAT TTTACGATCA TAAACAGTCA TTATAATTGA    600

GTATTTGAAC ATAAAAATGT AATTTTATCG TAACAATTTG AGTGTTTGTG ATTGTTTTTG    660

GTAATTTATG ATTGAAAAGT GAAAGCGTAC TCATTATAAT ACAAAGTGAG ATGGGGTGAT    720

GATGATAATT ACTGaAAAAA GACACGAGTT AATATTAGAA GAACTTTCGC ACAAAGATTT    780

TTTGACTTTA CAAGAATTAA TAGATCGAAC TGGTTGCAGT GCTTCAACAA TACGArGAGA    840

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AGAAAATCGT ATGGTTGAGG CGAATTTAAC TGAAAAATTA GCAACGAATC TTGATGAAAA    960

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TGCTGGTTCA TCTACATTGG AGCTAATTAA ATATATTCAA GCGAAAGATA TCATTGTGGT   1080

AACCAATGGT TTAACACATG TAGAAGCTTT ACTTAAAAAA GGTATTAAAA CAATTATGCT   1140

AGGTGGTCAA GTTAAAGAAA ATACACTTGC TACGATTGGT TCTAGTGCTA TGGAGATATT   1200

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AGAATACCAA CAAAAGTATC ACTTTATAGG AGGGACTTTA TGATTTATAC AGTGACTTTC   1500

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AAAGAAATCA GTATTAAAGC AGTTAATCCA CAAGGGAAAG TGGTTAATAC AGTTGGCTCT   2220

GGTGATAGTA CAGTTGCAGG CATGGTGGCT GGAATTGCTT CAGGTTTAAC GATTGAAAAA   2280
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CGGGACGCTA TAGAAAAAAT AAAATCACAA GTTACGATTA GCGTACTTGA TGGGGAGTGA          2400

AAATAATGAG AGTAACAGAG TTATTAACAA AAGATACAAT AGCAATGGAT TTAATGGCAA          2460

ATGACAAAAA TGGTGTTATT GATGAGTTAG TAAATCAATT AGACAAAGCA GGTAAATTAA          2520

GTGATGTCGC GTCATTTAAG GAAGCGATTC ACAATCGAGA ATCACAAAGT ACAACTGGTA          2580

TCGGCGAAGG TATTGCCATT CCACATGCCA AAGTGGCCGC AGTTAAGTCA CCAGCTATTG          2640

CGTTTGGTAA ATCTAAAGCA GGCGTAGATT ATCAAAGTTT GGATATGCAA CCAGCACACT          2700

TATTCTTTAT GATTGcAGcG CCAGAAGGTG GCGCCCAAAC ACATCTAGAT GCTTTAGCTA          2760

AGTTGTCTGG TATTTTAATG GATGAAAATG TACGTGAGAA ATTATTACAT GCTTCATCAC          2820

CTGAAGAAGT ACTAGCGATC ATAGATGAGG CTGATGATGA AGTGACAAAA GAAGAAGAGG          2880

CAGAAGCTGA AGCACAACAA GTTGCAACTG CAGAACAATC ATCTAAACAA TCTAATGAGC          2940

CATATGTGTT AGCAGTAACT GCTTGTCCAA CAGGTATTGC ACACACATAT ATGGCACGTG          3000

ATGCATTGAA AAAGCAAGCG GATAAAATGG GTATTAAAAT TAAAGTAGAA ACGAATGGTT          3060

CAAGCGGCAT TAAAAACCAT TTAACTGAAC AAGATATTGA AAATGCAACA GGTATCATTG          3120

TTGCTGCTGA TGTTCATGTT GAGACGGATC GCTTCGATGG TAAAAATGTC GTAGAAGTAC          3180

CAGTAGCAGA TGGTATTAAA CGCCCAGAAG AATTAATTAA TAAAGCATTA GATACAAGTC          3240

GTAAACCTTT TGTTGCCCGT GATGGTCAAA GAAAAGGTAA CTCAAATGAC AGTCAAGAAA          3300

AATTAAGCCC AGGTAAAGCA TTCTATAAAC ACTTAATGAA CGGTGTTTCT AACATGTTGC          3360

CACTTGTAAT ATCTGGTGGT ATTTTAATGG CAATTGTATT TTTATTTGGA GCAAATTCAT          3420

TTAATCCAAA AAGCTCAGAG TACAATGCGT TTGCAGAGCA GCTTTGGAAC ATTGGTAGTA          3480

AAAGTGCATT CGCGTTAATC ATTCCAATTT TATCTGGATT CATTGCACGT AGTATTGCGG          3540

ATAAACCTGG TTTCGCTTCA GGTCTTGTAG GTGGTATGTT AGCAATTTCA GGTGGTTCAG          3600

GATTTATTGG TGGTATTATT GCAGGTTTCT TAGCAGGTTA CTTAACACAA GGTGTTAAAG          3660

CCATGACACG TAAGTTACCA CAAGCATTAG AGGGATTAAA GCCAACATTA ATTTATCCAC          3720

TATTAACAGT GACGGCTACA GGCTTATTGA TGATTTATGC CTTTAATCCA CCAGCATCTT          3780

GGTTAAATCA TTTGTTATTA GATGGATTAA ACAATTTATC AGGTTCTAAT ATTGTATTAT          3840

TAGGTTTAGT TATTGGCGCT ATGATGGCGA TTGATATGGG CGGTCCATTC AACAAAGCGG          3900

CATATGTTTT TGCAACAGGT GCGTTGATTG AAGGTAATGC AGCACCAATT ACAGCTGCAA          3960

TGATTGGTGG TATGATTCCA CCGTTAGCAA TTGCGACAGC GATGTTAATT TTTAGACGTA          4020
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TGATTGGTTC AGGTATAGGT GGCGCAATTG CTTTAGGCTT AGGTTCACGA ATTACTGCGC    4200

CACATGGTGG TATTATTGTA ATTGTTGGTA CTGATGGTGC ACACTTACTT CAAACTCTTA    4260

TTGCACTTCT AGTTGGCACA TTAGTTTCAG CATTAATTTA CGGTTTAATC AAACCAAAGT    4320

TAACTGAAAC AGAAATCGAA GCTTCAAAAT CAATGGACGA GTAGTTTTAA TGATGTAAAA    4380

TGATTGTTAG CAAAGAGCTT CATATTAAGT TGTATGTTCA ATGAATATAT GTTAGTTTTA    4440

TATATCGTGT TAACGGTAGC TTATACAAAG CTGTAAAAAC ACTTTCTATT AATTCAGTTT    4500

TTATGAATTG ATATGAAAGT GTTTTTATTT TTAGATAAAT GAATGAAGAA ATAGACACCA    4560

CAAATGTATA GACTTTTTTA ATATTTTGCA AAAAGTTATG CCAAACGAAG CAGATATAGT    4620

AAAATATGAG TGTCTTAAAG TGAAAATTTA TAAATAAAGA AGGGTTTATA CGTGTCAGAA    4680

TTAATTATAT ATAACGGCAA AGTTTATACT GAAGATGGCA AAATCGATAA TGGTTACATT    4740

CATGTGAAAG ATGGACAGAT TGTTGCAATT GGAGAAGTGG ATGATAAAGC AGCAATTGAT    4800

AATGATACGA CAAATAAAAT TCAAGTGATT GATGCTAAAG GTCATCATGT ATTACCAGGT    4860

TTTATTGATA TACATATTCA TGGTGGTTAT GGTCAAGATG CAATGGATGG GTCATACGAT    4920

GGCTTAAAAT ATCTATCCGA AAATTTGTTG TCTGAAGGGA CGACATCATA CTTGGCCACT    4980

ACAATGACGC AATCGACTGA TAAAATAGAT AATGCACTTA CAAATATTGC TAAATATGAA    5040

GCGGAgCAAG ATGTTCACAA TGCAGCGGAA ATTGTAGGTA TACATTTAGA AGGACCATTT    5100

ATATCTGAAA ATAAAGTTGG TGCTCAACAT CCGCAATACG TTGTACGCCC ATTTATCGAT    5160

AAAATTAAAC ATTTTCAAGA GACTGCTAAC GGATTAATAA AGATTATGAC GTTTGCACCT    5220

GAAATTGAAG GTGCAAAAGA AGCGCTTGAA ACGTATAAAG ATGACATTAT TTTTTCAATT    5280

GGTCATACAG TAGCAACATA CGAAGAAGCA GTTGAAGCTG TTGAGCGAGG AGCTAAACAT    5340

GTCACGCATT TATATAATGC AGCGACGCCA TTCCAACATA GAGAACCAGG TGTTTTTGGA    5400

GCAGCATGGT TGAATGATGC TCTACATACC GAAATGATTG TTGATGGCAC TCATTCTCAT    5460

CCGGCATCGG TTGCAATTGC TTACCGTATG AAAGGTAATG AACGTTTTTA TTTAATTACC    5520

GATGCAATGC GTGCAAAAGG TATGCCTGAA GGAGAATATG ATTTGGGTGG ACAAAAAGTA    5580

ACTGTTCAAT CGCAACAAGC ACGTCTTGCA AATGGTGCGC TTGCTGGTAG TATTTTAAAA    5640

ATGAATCATG GGTTACGTAA CTTAATATCA TTTACAGGTG ATACATTAGA TCATTTATGG    5700

CGAGTAACAA GTTTAAATCA AGCCATTGCA TTAGGTATCG ATGATAGAAA AGGTAGTATT    5760

AAAGTAAATA AGGATGCAGA TCTTGTTATT CTAGATGATG ATATGAATGT AAAATCTACA    5820

ATAAAACAAG GCAAGGTTCA CACATTTAGC TAATAAATAA TCATAATTAA ATGTATGCAA    5880
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TTTTCTGGGG GTGTCTAAAT GGGAAGGCGA TAACATGTAG TTGTAATTTA AGTCATAGTG   6000

ATAAATTTGA ATGCGTGTTA CCCATGAGTG ACACATATAA CATGGAGGTG AATCCCTAGA   6060

AATAGGGAAT TAATTGGAAA CTTCGACCAT AATTAGTTTG ATTATATTTA TTCTATTAAT   6120

TGCATTAACC ACTGTATTTG TTGGTTCAGA ATTTGCATTA GTAAAAATTA GAGCAACAAG   6180

AATTGAACAG CTAGCAGATG AAGGAAATAA ACCTGCTAAA ATAGTAAAAA AGATGATTGC   6240

TAATCTAGAT TATTATCTTT CTGCTTGTCA GTTAGGTATA ACAGTAACAT CTTTAGGGTT   6300

AGGTTGGCTT GGTGAACCAA CGTTTGAAAA GCTATTACAC CCAATATTTG AAGCAATCAA   6360

TTTACCAACT GCATTAACGA CGACGATTTC GTTTGCAGTG TCATTTATAA TCGTTACGTA   6420

TTTGCATGTA GTACTTGGTG AATTAGCGCC TAAATCTATA GCTATTCAAC ATACTGAAAA   6480

GCTTGCTTTA GTATATGCAA GACCATTGTT CTATTTCGGT AACATTATGA AACCATTGAT   6540

TTGGCTGATG AATGGTTCTG CACGTGTTAT TATTAGAATG TTTGGTGTAA ATCCTGATGC   6600

CCAAACTGAT GCAATGTCAG AAGAAGAAAT CAAAATTATT ATTAACAATA GTTATAATGG   6660

TGGAGAAATC AACCAAACTG AATTGGCATA TATGCAAAAT ATCTTTTCAT TCGATGAAAG   6720

ACATGCAAAA GATATAATGG TACCTAGAAC TCAAATGATT ACACTAAATG AACCTTTTAA   6780

TGTAGACGAA TTACTAGAAA CAATAAAAGA ACATCAATTT ACGCGTTATC CAATTACTGA   6840

TGATGGTGAT AAAGACCACA TTAAAGGATT TATTAACGTC AAAGAATTTT TAACTGAATA   6900

CGCTTCTGGA AAAACGATTA AAATAGCAAA CTATATAcAT GAGTTGCCAA TGATTTCAGA   6960

GACAACACGT ATCAGTGATG CATTAATTAG AATGCAACGT GAACATGTAC ATATGAGTCT   7020

TATTATAGAT GAATATGGTG GAACGGCAGG TATTTTAACG ATGGAAGATA TTTTAGAAGA   7080

AATCGTTGGA GAAATTCGTG ATGAATTTGA TGATGATGAA GTGAATGATA TCGTTAAAAT   7140

TGATAATAAG ACATTCCAAG TAAATGGCAG AGTACTATTG GATGATTTAA CTGAAGAGTT   7200

CGGTATAGAA TTTGATGACT CTGAGGATAT TGATACGATA GGTGGATGGT TACAATCTCG   7260

TAATACCAAT TTACAAAAAG ATGATTACGT GGATACAACT TATGATCGCT GGGTTGTTTC   7320

AGAAATCGAT AACCACCAAA TTATTTGGGT GATATTAAAC TATGAATTTA ATGAAGCGAG   7380

ACCTACTATC GGACAGTCTG ATGAAGATGA AAAATCAGAA TAGATATTAA TATATAAACC   7440

AACTAAGAAT GATTTAATTC ATTTTTGGTT GGTTATTTTT TTGACTAAAA TTAAnGAAAA   7500

GTGAAAATAG TATTGGAACT CAATATCTTT AATGATTTAA TGAATAAnTT TTATTGAAAG   7560

CGA   7563

(A) LENGTH: 3492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

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TTATATCAAC TTCATGGCGG AACCATTGAT GACCCATTAG ACGAAACAAT AAGCGCATTT        60

sATGAATTGA AACAAGAAGG AATTATACGT GCTTACGGTA TTTCTTCTAT TCGCCCAAAT       120

GTAATTGATT ATTATTTAAA ACATAGTCAA ATCGAAACGA TAATGTCTCA ATTCAATTTG       180

ATTGATAATC GTCCAGAATC ATTATTAGAT GCAATTCACA ACAATGATGT TAAAGTATTG       240

GCAAGAGGAC CTGTGTCTAA AGGATTATTA ACTTCAAACA GTGTTAATGT GCTCGACAAT       300

AAATTTAAAG ATGGTATTTT TGATTATTCT CATGATGAAT GGGTGAAAC AATAGCCTCT       360

ATTAAAGAAA TTGAAAGTAA TTTATCTGCA TTGACATTTA GTTATTTAAC ATCACATGAC       420

GTGCTTGGTT CCATCATTGT AGGTGCAAGT AGCGTCGACC AATTAAAAGA AAATATTGAA       480

AACTATCATA CTAAAGTTAG TTTAGATCAG ATTAAAACAG CAAGAGCTCG TGTAAAGGAT       540

TTGGAATATA CCAATCATTT AGTGTAGAAG TCATTTTCAG TAATAAAAAC AGCAGCATGA       600

GGCGTTTCAT TATAAAAATG CCTTACTGCT GTTGTTTATG TACAATTCGC TATAATTTAT       660

GATTATGATT ACTCACTTAT GATAGAAATT AAAGCGTTGT CCTCACGCAT CAGTATTTAG       720

TAATTTCGCC TTGCGGCATT GCCTTAAGCA AACTTCTGCC ACTTCATCTC TTAATAATTT       780

TATTAAAACA TCTTTCTATA TTTCACTTCG CATGTTGATT CATCATTATT AGTTATTATT       840

TGTACACCCA GCACATTTCC TTGCAACACA AGTAGTTTGA ATTTTTCACA AGTATAATAT       900

AATGTACCGT CTGAAATTTG GTCTACAGAA ATATCGCCTA AAATATCCAG CACTGTAAAT       960

TCTTCAAATA CTGATAGTTG TTCCGCATAT CGTACACAAA GTCTTACCAC ACTCTCCGAT      1020

TGACAGTTCA TTGCCATCCC ACCTATTTAT GCTTTATTTT TAAATAATTT AGGGAAACAT      1080

CGTTCAAAAA ATCTAGGCGC AATTTGATAC ATTTTCAACG CATGaTGCAT CCATTTAGGC      1140

CGATTAATTT CCAATTGTTT TGTTTTAATG CCATAAATGA TATCTTCTGC AAGCTGATTA      1200

GCATCAAGCA TAATTTCCCC CATCTTTTTA gCATACTTCA TTGATGGGTC GGCTTTTTGA      1260

TGAAAAGGTG TATCAATCGG GCCAACATTA ACTGTCATGA TATGTAAGTT TGGTGACTCT      1320

AGTCTTAAAG CATTCATTAA TGCATAAAAC CCTGCTTTCG ATGCCCCATA ATGTGCAGCA      1380

TTTGCTTGTG TGGAAAATGC AGCTTGACTT GAAATACCTA CAATATGTGC GTTAGATGTT      1440

AAATATGGTC TCAACACAGT ATATAAAACA TTAAAACTAA TTAAATTAAG CTGATACGTT      1500
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      TAAATGAATC CATCGAATGA TGTATTGTCT TCAAATTGCA GTGCCTGTAT CGACTTCAAA       1620

      TCATTTAAGT CACAAGGAAT AACATTTATA GTTTTCCCCA ATTCCTGTTC AAAGATTCTA       1680

  5   GTTGCTTTAT CAACATCACG CACCAACAAC GTTACATGCA CTTTATTTTC TAGTAACTTT       1740

      CGGACAATCG ATAAACCTAA ACCACTCGTA CCACCAGTCA CTATAAAATG TTGTCCTTTC       1800

      ATCAATTAAC CTTCCTTTTC AATTATATAG AATGCAATTT ATCAACTTTA CATAATTGAG       1860

 10   ACAAGTTGAT TATCTTTCCT AATATATATA CAATAATAAG AAAATATAAC ATACAAATCA       1920

      AAAACTAAAG GGATGTGaCG TTAATGrAAC TCGTATTTTA TGGAGCTGGT AATATGGCAC       1980

      AAGCTATATT TACAGGrATT ATTAACTCmA GCAACTTAGA TGCCAATGAT ATATATTTAA       2040

 15   CAAATAAATC TAATGAACAA GCTTTAAAAG CATTCGCTGA AAAACTAGGT GTTAACTATA       2100

      GTTATGAtGA TGCGACATTA TTAAAAGATG CAGAyTATGT ATTTTTAGGT ACCAAACCAC       2160

      ATGACTTTGA TGCTCTAGCA ACACGCATCA AACCACATAT TACAAAAGwC AATTGCTTCA       2220

 20   TTTCAATTAT GGCAGGTATT CCGATTGATT ATATTAAACA ACAATTAGAA TGCCAAAATC       2280

      CaGTTGCTAG AATTATGCCA AACACAAATG CGCAAGTTGG ACACTCTGTT ACTGGCATTA       2340

      GTTTTTCAAA CAACTTTGAC CCTAAATCTA AAGATGAAAT TAACGATTTA GTTAAAGCAT       2400

 25   TTGGTTCTGT AATTGAAGTA TCAGAAGATC ATTTACATCA AGTAACAGCT ATCACCGGAA       2460

      GCGGCCCAGC ATTTTTATAT CATGTATTCG AGCAATATGT TAAAGCTGGT aCsAAACTTG       2520

      GTCTAGAAAA AGAACAAGTT GAAGAATCTA TACGCAACCT TATTATAGGT ACAAGTAAGA       2580

 30   TGATTGAACG TTCAGAtTTG AGCATGGCTC AATTAAGAAA AAATATTACC TCTAAAGGTG       2640

      GTACGACACA AGCTGGCCTT GATACATTGT CACAATATGA TTTAGTATCT ATTTTCGAAG       2700

      ATTGTCTAAA CGCTGCCGTC GACCGTAGTA TTGAACTTTC TAATATAGAA GACCAATAAA       2760

 35   AACAZACCCG CCAACACATG TATGCATCAT CGCAAGCACT GTGTTTGACG GGTTATTTTT       2820

      ATAATTTATT GTTATTTGGC AAGCATTGTT TATTACTTTG TCATTAGATT TTAAAACTAT       2880

      CAAAATCTTT TACAAAATTA AAATTAGGTG TATCTTCATT TTGTATCAAT GTTTGATAAA       2940

 40   TTTCATTTAT ATCTTCTGTA TTATAGCGAT TGCTCAAATG TGTAATCAAC GTACGTTTAA       3000

      CATTGGCTTC TTTTATCAAT GCAAATACGT CTTCAATATG GCTATGATGA TAATTGTTGG       3060

 45   CTAAATGCTT TTCACCATCT ATATAGGTCG CTTCATGTAC CATCACATCA GCATCTCTAG       3120

      AAATCACACG TTCATTAGAA CATGGTTTTG TATCACCAAA AATTGCTACA ACTGGACCCT       3180

 50   GTTTGGACTC ACCTCTAAAA TCTTTTGATT GATAAACTTG ACCATTATGT TCAAATGTAT       3240
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CATGATTAAG TAAATGCGCC TCTACAGTAA AACCATCCAT GATGATATGT CAGATGATCA    3420

TCGATTTCAA TATATGtAAT TGGATAGTTT AAATGTGACT CTGATAAATT CATAGACATT    3480

TCCACATATG CT                                                       3492
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(2) INFORMATION FOR SEQ ID NO: 35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1973 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

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ATCTAGCGGT ACAAGCGTCT TGGAGGCTAG TATGTTGAAC ATTGTAAACC CTGAAGATCA      60

CTTCGTTGTC ATTGTTTCAG GTGCCTTTGG TAACCGATTT AAACAAATTG CACAAACTTA     120

TTACAAAAAT GTGCATATTT ATGACGTAAC ATGGGGAGAA GCTGTAGATG TCAAAGATTT     180

CATCAATTTC CTTTCAACTT TAAATGTTGA AGTTAAAGCA GTATTTAGTC AATATTGCGA     240

AACATCTACG ACAGTGCTAC ACCCTATTCA CGAGTTAGGA AATGCCATTA ATCAATTTAA     300

TAGTAATATT TATTTTGTAG TTGACGGCGT AAGTtGCATT GGTGCTGTTG ATGTTGACAT     360

TAACAAAGAT AAAATTGATG TACTTGTTTC TGGTAGTCAA AAAGCAATTA TGTTACCTCC     420

AGGATTAGCT TTTGTAGCTT ATAGCCACCG TGCAAAAGAA CATTTCAAAG AAGTAACTAC     480

GCCAAAATTT TATCTAGACT TAAATAAATA CATTTCGTCA CAAGCTGACA ATTCTACACC     540

GTTCACACCA AATGTGTCTT TATTTAGAGG TGTAAATGCA TACGTTGAAA CCGTAAAAGC     600

AGAAGGTTTC AATCACGTAA TAGCACGACA CTATGCAATT AGAAATGCAT TAAGAAGCGC     660

CTTAAAAGCA TTAGATTTAA CTTTATTAGT CAATGATAAA GATGCATCTC CAACGGTTAC     720

AGCATTCAAA CCTAATACAA ATGATGAAGT GAAAATAATC mAAGATGAAC TTAAAAATnG     780

CTTTAAAATA ACAATTGCnG GTGGTCAAGG CCATCTTAAA GGTCAAATTT TnAGAATTGG     840

TCATATGGGG AAAATTAGTC CTTTCGATAT TTTATCGGTA GTATCTGCTT TAGAAATTAT     900

TTTAACTGAA CACCGTAAAG TTAACTATAT CGGTAAAGGT ATATCAAAAT ATATGGAGGT     960

TATTCATGAA GCAATTTAAT GTACTCGTTG CAGATCCCAT ATCAAAGAT GGTATCAAAG    1020

CATTATTAGA TCACGAACAA TTCAATGTAG ATATTCAAAC TGGCTTGTCC GAAGAAGCAT    1080

TAATCAAAAT TATACCTTCA TACCATGCTT TAATCGTTCG TAGTCAAACT ACGGTTACTG    1140

AAAATATCAT AAATGCTGCT GATTCTTTAA AAGTAATCGC ACGCGCCGGT GTTGGTGTAG    1200
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GTAATACGAT TTCAGCTACT GAACATACAC TGGCAATGTT ATTATCAATG GCACGAAATA   1320

TTCCGCAAGC ACACCAATCA CTTACAAATA AAGAATGGAA TCGAAATGCA TTTAAAGGTA   1380

CTGAGCTTTA TCATAAAACA TTAGGTGTCA TTGGTGCTGG TAGAATTGGT TTAGGTGTTG   1440

CTAAACGTGC GCAAAGTTTC GGAATGAAAA TACTAGCTTT TGACCCTTAC TTAACGGATG   1500

AAAAAGCAAA ATCTTTAAGC ATTACGAAGG CAACAGTTGA TGAGATTGCC CAACATTCTG   1560

ATTTCGTTAC ATTACATACA CCACTAACAC CTAAAACAAA AGGCTTAATT AATGCTGTCT   1620

TTTTTGCCAA AGCAAAACCT AGTTTGCAAA TAATCAATGT GGCACGTGGT GGTATTATTG   1680

ATGAAAAGGC GCTAATAAAA GCATTAGACG AAGGACAAAT TAGTCGGGCA GCTATCGATG   1740

TGTTTGAACA TGAACCTGCA ACTGACTCGC CTCTTGTTGC ACATGATAAA ATTATTGTTA   1800

CACCTCATTT GGGTGCTTCA ACAGTCGAAG CTCAAGAAAA AGTGGCAATT TCTGTTTCAA   1860

ATGAAATCAT CGAAATTTTA ATTGATGGTA CTGTAACGCA TGCAgTGAAT GCACCTAAAA   1920

TGGACTTAAG CAATATAGAT GATACTGTAA AATCATTCAT CAATTTAAGC CAA   1973

(2) INFORMATION FOR SEQ ID NO: 36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7620 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGTGTTTCAG ATGTCACTGG TTGATTTTTA ATTGTAGACG GGTATTTTGG GCTTTCGCCA   60

TATTTATTTG CCGGCTTACT GTCAAAGCAT AGGAATACTA TCATAACAAT TGTTAGGCCT   120

AAATÀAACAA AATAAAGAAG TACTAACAAA ATATTAAGAC CCATCGGCAT TAATGTAAAA   180

TCACTGTCAT AATAACTATC GATAATCTGT AATACTATAT AAAATATAAT ACTGAATACT   240

GTCATAATCA TTGGAAATAA CATTGTTCTT GATATATCGT GAAATCTTCG AACGCACAAC   300

GCTAAATTTG GAATAAACGT TGCCAAACTA TAGACAAAAG TATACACAGA TGTAAGGATA   360

ATCATCAATA TACTCATAAC TATTAATGTT TCGTTATCCG CCGCTATAGA AATAAAGAAT   420

AGAAATAGGT TTATTATTAG CACACACACA GCTGGAACCA TAAGTATCAA ATGCCATAGT   480

GCCATATACC AATATTCACT ACGTCTTGAT CTCCCCTTAA AATTTACATA ATTTTTCCAA   540

AATAAAACGA ATGATTTCAT AAAACCTACT TGAGGTAATT GTTCCATTGT AATCTCCCTT   600

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GTAAAATGAA AACCCGCTAC AAGTACACAT CTATATGGAG ACTCATTTGA AAGTCAACGC      780

TTCGTTAACT ATACTAAAAA TATGTCATAC TGCAATGTTC ACGTTTAAAA GAGTCTCAAT      840

CTATGCAAAT AAAATATTCC ATAACAAAGT ATATACTTTA CATTTTTATA ATTCTTAACA      900

ATACTATTTT ATCAAACATT TACCACAATA AAAATATCTT TTTCATTTTT ATTTAAATTA      960

ATCATATAAT TGCGAGGAGA ATATTATGGA TTTCGTTAAT AATGATACAA GACAAATTGC     1020

TAAAAACTTA TTAGGTGTCA AAGTGATTTA TCAGGATACC ACTCAAACGT ATACAGGCTA     1080

CATCGTGGAA ACGGAAGCTT ACTTAGGTTT GAATGATCGT GCGGCTCATG GCTATGGCGG     1140

TAAAATAACA CCTAAAGTCA CGTCATTATA TAAACGTGGT GGTACAATTT ATGCACATGT     1200

CATGCATACG CATTTACTCA TTAATTTTGT AACAAAATCT GAAGGTATAC CTGAAGGCGT     1260

ACTTATCCGC GCAATTGAAC CAGAAGAAGG TTTATCCGCT ATGTTCCGTA ACAGAGGTAA     1320

GAAAGGCTAC GAGGTAACGA ATGGCCCAGG AAAAATGGACT AAGGCATTTA ACATTCCACG     1380

GGCTATCGAT GGCGCTACGT TAAATGACTG TAGATTGTCT ATTGATACTA AGAATCGTAA     1440

ATATCCTAAA GATATTATTG CTAGTCCACG AATCGGTATT CCAAATAAAG GTGATTGGAC     1500

ACATAAATCT TTACGTTACA CAGTGAAAGG TAATCCATTT GTGTCTCGCA TGCGTAAATC     1560

AGATTGTATG TTTCCCGAAG ATACTTGGAA ATAAATGCCA TCTTTCATTG ATTACTATCA     1620

TGAAAATGAA ATCTATCTCC TTATAAGTCA ATCAATCGTG CCGTCAACAT GCGGATGGGT     1680

TGATTGTTTT TCTTTGTATC CATCATATTT TTTGATTCAT CTCCTCTTAT TGAACTTGTT     1740

CTTAATTATA AAATATAACA ATAGAATTAT TTATAATTAT TAAATTTAGA TGCATTAATA     1800

TTATTGATAT TATTTTCAAA AACTAGAAAT ATTGATTTGT TGCATGTATA ATGTTAAAAG     1860

CGCCCTTTTA TAACGCTTAC ATATAAAAGC TTATTTAGGG AGAGGGATAT TCAACAAGGG     1920

GGATTTGAAA ATGATAGAAC TTAATGCAAT TACAACATTA TGTTTAGCTT GTATCCTTTA     1980

TTTACTTGGT AAGGCTATCG TTAATCACGT TAATTTTTTA AAACGTATTT GTATACCAGC     2040

ACCAGTGATT GGCGGCTTAA TCTTTGCTAT TTTAGTTGCG GCTTTGGATT CATTTGGCAT     2100

GGTTAAGATT AAATTAGATG CTTCATTCAT TCAAGATTTC TTCATGTTAG CATTCTTTAC     2160

GACAATCGGT CTTGGTGCAT CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT     2220

ATACTTTATG TTTTGTGCTA TCATTTCAGT CATTCAAAAC ATAGTTGGTG TATCACTAGC     2280

AAAAGTATTA AATATTAAAC CTTTGTTAGG ATTAACAGCA GGTTCCATGT CTATGGAAGG     2340

CGGTCATGGT AATGCTGCTG CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC     2400

ACTGACAGCG GCTCTTGCAG CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TTATCGGTGG     2460
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ATTTAAAGAT TATAGCCAAG TAGCATATAA CGAACATTTA CATAGTAAAT TTAATGCCAC      2580

TGAAGTATTC TTCATTCAAT TTACAATCGT TGTATTCTGT ATGGCAGTTG GAAGTTATTT      2640

CAGTCATTTG TTTACAGCTC AAACAGGGAT TAATGTTCCA ATTTACGTTG GCTCATTATT      2700

TGTAGCTGTT ATTGTCCGAA ATATCTCTGA AAGTTTTAAT TTTAATATTG TAGATTTAAA      2760

AATTACTAAT CAAATTGGCG ATGTCGCATT AGGTATTTTC TTATCTCTTG CGCTAATGAG      2820

CATTCAATTA ATCGAAATTT ATAAACTTGC TATACCTCTT ATTATTATCG TTTTAGTTCA      2880

AGTTGTCGTT ATGATTTTAT TTGCTGTTTT AATTTTATTT AGAGGTTTAG GAAAAGATTA      2940

TGATGCTGCA GTAATGGTAG GTGGTTTTAT CGGTCATGGG CTTGGTGCAc GCCAAATGCC      3000

ATGGCAAATT TAGATGTTAT TACTAAAAAA TATGGAAACT CACCTAAAGC ATATTTAGTT      3060

GTACCTATTG TTGGTGCATT CTTAATCGAT TTAATTGGTG TTATAGTCAT TATGGGATTC      3120

ATACAATGGT TTAGTTAAAC ACCAAACTCA TAAATAAAAG AGGAGGCCTT CGCCTCcTcT      3180

TTTATTTATC CTCGATGTAT ATTCAAGTTA CGTTGTTCTA TCCATGACAA TATTTCCGGA      3240

CTAAATACGA TTTGTTTTTG TGTTAAGTCG TCAATATTTT TAGCATCTAA CATCGTCATT      3300

ATTGATTTCA TGTGTTCAAT AAATGATTCT ACATAAGCTA CTGTATGTGC AATGCCATTA      3360

TTTTCAACTT GATTTAAAAA CGGACGTGAC ATACCAGTTG CCTTTGCACC AAGTGCTAAA      3420

CTTTTAATTG CATCGAGTGG TGTACGTAAA CCACCACTCG CGAAAACTGA AATTTCGCTT      3480

TGATAAGCCG TTGTTTCAAG TAATGACTCA ACTGTAGACT GTCCCCATGA TGATAAGTAA      3540

TCCATATCTT TATTTGCACG ACGTTCATTT TCAATATCTA CAAAGTTAGT ACCACCTTTG      3600

CCACTAACAT CGACATACTT GACGCCTATT TGTTGTAAGT CATGCATTAA TTCTTTGCTC      3660

ATACCAAATC CAACTTCTTT TATAATGACT GGAACAGACA CTCGTGATAC AATCGACGCT      3720

ATATTATCTA ACCAAGTCAC AAATTCACGA TTCCCTTCAG GCATAACTAA TTCTTGAGGA      3780

GAATTAACAT GGATTTGTAA CGCTTGTGCC TCAAGTAATT CAACTGCTTC CAAAGCCTTT      3840

TCTACTGGTA CGTCCGCACC AACATTGCTA AAAATCATGC CTTCAGGATT CATTTTTCGC      3900

GCAATCGTAA ACGTCTCAGC CATGCGTGGA TTTCTCAATG CCGCATGTGT TGATCCAACT      3960

GCCATCGCTA AGCCAGTTTC TCTTGCAACT ACAGCTAGCT TTTCATTGAT GTTTTTCGTC      4020

CACTCGCTAC CACCCGTCAT TGCATTAATA TAAACCGGAT ATGCCATCGT TAAGTCAGGC      4080

GTCTGTGATG TCAAATCGAT ATCATTTACA TTAATTGATG GGATAGAATG ATGCACAAAA      4140

CGCATCTTAT CAAAATCTGA ATGCATTGCG TCAGATTGGG CCATTGCTAT TTCAACATGT      4200
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ATTACAGCTA AGCAAATATA ATATCCATAA TGTAAATGTA ATGCCGGCAT ATTTACAAAG      4380

TTCATACCAT AAATCCCAGC TATGAATGTT AACGGTGAAA ATATAACTGA TACTAATGTC      4440

AGTACTTGCA TAATACTATT CATTCTAAAT GACGTGTATG ACTCAAAATT TTCTCGTATT      4500

TCGTTTGTCA TTTCTTGAGC AGTACGAATG ATATTACGTT GCTTAATCAA GTGGTCATCG      4560

ATATGTTGAA TGTATAGCGA ATGTTTATTA TCTATAATCA AATCACCATT TTGTTTCATT      4620

GTATCAATTA GCTCTTGCAT AGGAAACAGT ACACGTTTTA CTTTAATCAA ATCCGAACGT      4680

AACTTAAAGA CACTATCCAT GACCATTTTA TTAAAGCGAT CATCTACATG GCGGTCTTCA      4740

AAATGATAAA CACTATCTTC AAGTGCATAT ACAAAGTTGA AATATTTATC AACCATCATA      4800

TCTAAAATTA ATATGACGAC ATCTGCACAA TCTAATTCTG CATCTAATGT ATTCATATAC      4860

TTATAGACTA CTTTATTTAA TGATTCCAAC GTTTGATGAT GATATGTTAC TAATACATTG      4920

TCTTGTATAA AAATATTTAG TGCTATTGGT GAATAGTTTG ACCCCATAAT ACTATGGAAT      4980

ACTAAGTATT GATAATCTTT ATAAGATTTA TATTTAGCTC GTGGCATACC GTTAATTGCA      5040

TCATCCACTT CTAAATCATT AAAATTAAAA TGTGCTTTAA ACCATTCATT TTCTTGTTCA      5100

TTCGGTTCAT CAAAATCATA CCAAACAATA GTCGCATCTT TTGGTATCTC TTTGATATCA      5160

TCAACTACTT TAAACGGTTC ATATGTAGTT TGATACCGTA TCTTTAAAGC CATCGATACT      5220

CCCCCTAAAT AACGAATTCT CTATTATTTT ATCATGAATT AAATAACGTG TATGTCTTAA      5280

TTTATTTTAG TATGATAGTC ACTAAGGAGA TGGTTATTAT CAAACAACTT TTTACACATA      5340

CTCAAACCGT AACATCTGAA TTCATTGACC ATAACAATCA TATGCATGAT GCAAATTATA      5400

ATATCATTTT TAGTGACGTC GTGAATCGTT TTAATTACAG CCACGGTCTT TCTTTAAAAG      5460

AACGCGAAAA TTTAGCATAT ACGCTATTTA CACTAGAAGA ACATACGACA TACCTCTCAG      5520

AATTGTCTCT TGGCGATGTA TTTACTGTTA CTTTATATAT TTATGATTAC GATTATAAGC      5580

GGTTGCATTT ATTTTTAACA TTAACTAAAG AAGATGGTAC ACTAGCATCA ACAAATGAAG      5640

TAATGATGAT GGGAATTAAT CAGCACACAC GTCGTTCTGA TGCTTTTCCT GAATCATTTT      5700

CAACACAAAT AGCACACTAT TATAAAAATC AATCAACTAT CACTTGGCCT GAACAATTAG      5760

GACATAAAAT AGCAATTCCA CACAAAGGAG CATTAAAATG ACAGATGCAT TACAACAAAA      5820

GATTCATATC GAATTACTAG ATTTATTAGA TGATGTTAAG TTTGAATTAA CAGAATTAAA      5880

TGCACAAAAA GGGTTATACA TTAACGGACC AGCAAATCAG CTACTTAAGC GTGGCGTGCA      5940

TATGGCTTAT GTTCAAGGAC AAAAGCAAGC CATCGATAAT ATTATGACTA TTGTGGAACA      6000

ACAGCTTGAA AGATCAACAT TTCCTAGAAC ATTATGATAA ATTTCAAAAT GAGGTTGCTC      6060
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ATAATTTTTT AGATCAATTT TATCAAATTA AAGGGCAATA CTTTATCATC ACACATATCA   6180

ATACACTTAT TGGTGATTTT CACTCAGAAG CTCATTAACA ATTAGTCTAT ATAACCCTTG   6240

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TCGTAACTGG GTCATTTATA TGTTATTAGT TATTTTGTGT TACATCCTCA TCTATCGATT   6360

TGGCAATTTG TTTAATAGCT TTATGTGATT GTCTAATTGG ATAAATTGGA AAATCATGTA   6420

CCATCTTAGG ATAATCATAA AACTCAATGT ATTGATGATG TTGCAACATC ATTTGTTCAA   6480

ATAGCTTCAT ATCAGGATGT GTCATTTCAC GTCCACCACC AAACATATAA ACTGGTGGCA   6540

ATCCTTCTAT TGTGCCATTA ATTGGCGATA TGCGCTTATC TGTTAATGGT AGGCCATTCG   6600

CCCATTTTTT CATAATCTCA TTGACACCAA ACTGACTTAG aACCGCATCT TGTTCGATTA   6660

AGGCGTCCGA AATATCTTTA TTAGATAGTG TTGCATCTAA AATTGGTGAG ATTAAATACA   6720

ATTTATTCGG TAATGGCTGT TGATTAkCTA AAAGAGATTG TACAAAGGAT AATGCCAGTG   6780

CACCACCTGA ACCATCACCC ATGACTACGA CATTTTGATG TCCTACTTCA GATACTAATT   6840

GaTCATAAAC ACGTTGTATC GCTTGGnAAA GTATCGTCaA TATGnAAACT CTGGTGTCTT   6900

TGGATAGATA GGCAGTACAA CCTCATATAA TGtACTTAAA GTGATTTTAT CCCAACAATC   6960

TCCAATGGAA CGGTGATGGT TGTAGTGCAT TGAATCCACC GTGAATATAT AAAATTTTCT   7020

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CTAAATTTGC TTTAACATTT AATGTTGAAG GCTGCTTATG TTTTTTTCTA TTTTCAATTT   7140

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GAAGCAAATA TTTATTGACA ACGCTATTCA TAACACGGTT TCTAATCAAT GTCTTAACCT   7260

ACCTTTATAT ATTTTATGTA TCCAATGATk GTCTATCCCC TACATTCTTT GCCAAAAAAA   7320

GTATATAATG TAGAAGATAT TTTCTTTTTC ACTTTCAAAT TTAAGACTAC AATTGAACAG   7380

TGATTTTTCA TCATTATAAC AGACAACTAG ACATATTGAT AAGTAAAGAA AAGAACTTTA   7440

TACGGAGGTA CCTTGCATGA CAAATCCAAA TCAACGATTA GAACCATTTG ATGAGACATT   7500

TCAACAACCG AATATTCATC GTGGTAAGCG ATATGGTAAG AAAAAACGTT CATTGGTAAG   7560

CATGATTATT CAAATCATTG TTGTwATATT AACCACCATC GCTGGAATAC AGCATGGTGG   7620

(2) INFORMATION FOR SEQ ID NO: 37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9834 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

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GTCATtACCG amTTTCtTAG AaTCATTTAA AGATGATAAA TATACAAACG TTGGTAATTT      60

AAAAGAAGTG AATTTTGATA AAATTGCTGC GACGAAACCC GAAGTAATCT TTATCTCTGG     120

ACGTACAGCT AATCAAAAGA ATTTAGATGA ATTCAAAAAA GCTGCACCTA AAGCGAAAAT     180

TGTTTATGTT GGTGCAGATG AAAAGAACTT AATTGGTTCA ATGAAACAAA ACACTGAAAA     240

TATCGGAAAA ATTTACGATA AAGAAGATAA AGCTAAAGAA TTAAATAAAG ATTTAGATAA     300

CAAAATTGCT TCAATGAAAG ATAAAACGAA AAACTTCAAT AAAACTGTTA TGTATTTACT     360

AGTTAACGAA GGTGAATTAT CAACATTTGG ACCTAAAGGT CGTTTTGGTG GATTAGTTTA     420

CGATACATTA GGATTCAATG CAGTTGATAA AAAAGTAAGT AATAGCAATC ATGGACAAAA     480

TGTTTCTAAC GAATATGTTA ATAAAGAAAA TCCAGATGTT ATTTTAGCGA TGGATAGAGG     540

TCAAGCGATA AGTGGTAAAT CAACTGCGAA ACAAGCATTA AATAATCCTG TATTAAAAAA     600

TGTTAAAGCA ATTAAAGAAG ACAAAGTATA TAATTTAGAT CCTAAATTAT GGTACTTTGC     660

AGCTGGATCA ACTACAACTA CAATTAAACA AATTGAGGAA CTTGATAAAG TTGTAAAATA     720

ATTTTAAAAG AGGGGAACAA TGGTTAAAGG TCTTAATCAT TGCTCCCCTC TTTTCTTTAA     780

AAAAGGAAAT CTGGGACGTC AATCAATGTC CTAGACTCTA AAATGTTCTG TTGTCAGTCG     840

TTGGTTGAAT GAACATGTAC TTGTAACAAG TTCATTTCAA TACTAGTGGG CTCCAAACAT     900

AGAGAAATTT GATTTTCAAT TTCTACTGAC AATGCAAGTT GGCGGGGCCC AAACATAGAG     960

AATTTCAAAA AGGAATTCTA CAGAAGTGGT GCTTTATCAT GTCTGACCCA CTCCCTATAA    1020

TGTTTTGACT ATGTTGTTTA AATTTCAAAA TAAATATGAT AGTGATATTT ACAGCGATTG    1080

TTAAACCGAG ATTGGCAATT TGGACAACGC TCTACCATCA TATATTCATT GATTGTTAAT    1140

TCGTGTTTGC ATACACCGCA TAAGATTGCT TTTTCGTTAA ATGAAGGCTC AGACCAACGC    1200

TTAATGGCGT GCTTTTCAAA CTCATTATGG CACTTATAGC ATGGATAGTA TTTATTACAA    1260

CATTTAAATT TAATAGCAAT AATATCTTCT TCGGTAAAAT AATGGCGACA scgTGTTTCA    1320

GTATCGATTA ATGAACCATA AACTTTAGGC ATAGACAAAG CTCCTTAACT TACGATTCCT    1380

TTGGATGTTC ACCAATAATG CGAACTTCAC GATTTAATTC AATGCCAAAT TTTTCTTTGA    1440

CGGTCTTTTG TACATAATGA ATAAGGTTTT CATAATCTGT AGCAGTTCCA TTGTCTACAT    1500

TTACCATAAA ACCAGCGTGT TTGGTTGAAA CTTCAACGCC GCCAATACGG TGACCTTGCA    1560

AATTAGAATC TTGTATCAAT TTACCTGCAA AATGACCAGG CGGTCTTTGG AATACACTAC    1620

CACATGAAGG ATACTCTAAA GGTTGTTTAG ATTCTCTACG TTCTGTTAAA TCATCCATTT    1680
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AGTGTTCTTT TTGAATAATG CTATTACGAT AATCTAACTC TAATTCTTTT GTTGTAAGTT    1800

TAATTAACGA GCCTTGTTCG TTTACGCAAA GCGCATAGTC TATACAATCT TTAACTTCGC    1860

CACCATAAGC GCCAGCATTC ATATACACTG CACCACCAAT TGAACCTGGA ATACCACATG    1920

CAAATTCAAG GCCAGTAAGT GCGTAATCAC GAGCAACACG TGAGACATCA ATAATTGCAG    1980

CGCCGCTACC GGCTATTATC GCATCATCAG ATACTTCGAT ATGATCTAGT GATAATAAAC    2040

TAATTACAAT ACCGCGAATA CCACCTTCAC GGATAATAAT ATTTGAGCCA TTTCCTAAAT    2100

ATGTAACAGG AATCTCATTT TGaTAGGCAT ATTTAACAAC TGCTTGTACT TCTTCATTTT    2160

TAGTAGGGGT AATGTAAAAG TCGGCATTAC CACCTGTTTT AGTATAAGTG TATCGTTTTA    2220

AAGGTTCATC AACTTTAATT TTTTCATTTG GGATAAGTTG TTGTAAAGCT TGATAGATGT    2280

CTTTATTTAT CACTTCTCAG TACATCCTTT CTCATGTCTT TAATATCATA TAGTATTATA    2340

CCAATTTTAA AATTCATTTG CGAAAATTGA AAAGAAAGTA TTAGAATTAG TATAATTATA    2400

AAATACGGCA TTATTGTCGT TATAAGTATT TTTTACATAG TTTTTCAAAG TATTGTTGCT    2460

TTTGCATCTC ATATTGTCTA ATTGTTAAGC TATGTTGCAA TATTTGGTGT TTTTTTGTAT    2520

TGAATTGCAA AGCAATATCA TCATTAGTTG ATAAGAGGTA ATCAAGTGCA AGATAAGATT    2580

CAAATGTTTG GGTATTCATT TGAATGATAT GTAGACGCAC CTGTTGTTTT AGTTCATGAA    2640

AATTGTTAAA CTTCGCCATC ATAACTTTCT TAGTATATTT ATGATGCAAA CGATAAAACC    2700

CTACATAATT TAAGCGTTTT TCATCTAAGG ATGTAATATC ATGCAAATTT TCTACACCTA    2760

CTAAAATATC TAAAATTGGC TCTGTTGAAT ATTTAAAATG aTGctACCGC CAATATGTTT    2820

TGTATATTTT ACTGGGCTGT CTAAGAGGTT GAATAATAAT GATTCAATTT CAGTGTATTG    2880

TGATTGAAAA CAATTAGTTA AATCACTATT AATGAATGGT TGAACATTTG AATACATGAT    2940

AAAGTcCTTT GATATTGAAA ATTAATTTAA TCACGATAAA GTCTGGAATA CTATAACATA    3000

ATTCATTTTC ATAATAAACA TGTTTTTGTA TAATGAATCT GTTAAGGAGT GCAATCATGA    3060

AAAAAATTGT TATTATCGCT GTTTTAGCGA TTTTATTTGT AGTAATAAGT GCTTGTGGTA    3120

ATAAAGAAAA AGAGGCACAA CATCAATTTA CTAAGCAATT TAAAGATGTT GAGCAAAAAC    3180

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AAACTGATAC AACTGATAAA AATAGTAAAG AATTTAAGGC ACTACAAGAA GATGTTAAAA    3300

ACCATCTCAT ACCTAAATTT GAAGCATATT ATAAGTCAGC AAAAAATTTG CCTGATGATA    3360

CAATGAAAGT TAAGAAATTA AAAAAAGAAT ATATGACGCT TGCAAATGAG AAGAAGGATG    3420

AATTATATCA ATTAAAAAAA TTCATAGGTT TATGTAATCA ATCTATCAAG TATAACGAAG    3480
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AATTAGCTGA TAATAAAAGT GAAGCAACTA ATCTTACGAC AAAATTAGAA CATAATAATA   3600

AAGCGTTAAG AGATACTGCG AAGAAGAACC TAGATGATAG TAAAGAAAAT GAAGTAAAAG   3660

GCGCGATTAA AAATCACATT ATGCCAATGA TTGAAAAGCA AATTACCGAT ATTAACCAAA   3720

CTAATATTAG TGATAAGCAT GTTAATAATG CAAGGAAAAA CGCAATAGAA ATGTATTACA   3780

GTCTGCAGAA CTATTATAAT ACACGTATTG AAACAATAAA GGTTAGTGAG AAGTTATCAm   3840

AAGTCGATGT AGATAAGTTG CCGAAAAAGG GTATAGATAT AACTCACGGC GATAAAGCCT   3900

TTGAAAAAAA GCTTGAAAAA TTAGAAGAAA AATAACTATA ATCATTTTTC AAAGTTAAAA   3960

ATTTTGAATT TATGGTTAAC ATGTCAACTT ACTATGTGTA TAATGGTAAA CATTGATATT   4020

AACTATATGT ATAAAAATGT CACGCAGATG CTATTTAAAT GTGATAAATA TTTTTAGAGG   4080

TGAATAGAGT GGCTATAAAG CTAAGTTCAA TTGACCAATT TGAACAGGTT ATTGAGGAAA   4140

ATAAATATGT TTTTGTATTA AAACATAGTG AAACTTGTCC AATATCGGCA AATGCGTACG   4200

ATCAATTTAA TAAATTTTTA TATGAACGCG ATATGGACGG TTATTATTTG ATTGTCCAAC   4260

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AAGCATTTTA TTTTGTAAAT GGTGAAATGG TTTGGAATCG AGACCACGGT GATATCAATG   4380

TGTCGTCATT AGCACAAGCA GAAGAATAAT GAAACTATAG GGTTGGAACA TTTTGCCTTA   4440

CACTACTAGA CGTGAATAGC ACAACTTAAA TTCGTGTGAA TCAGAGTAGT TTGGCTATAA   4500

TGATGTTCTG ACCTTTTATT TTATGTCACC TTTAGAAGCA GTTAAGTTAG TACTTTTTTA   4560

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CCAATAAGAA AATTTAAACA TGATTTGTAA GTTAGTTTAA TAGGAAATAT ATGCTAAACC   4680

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CAAATTGAAA CTGCAGATGT AGTTCAAGTA CCATTGTTTA ATGGAAGACA TGAATTATTA   4980

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AATTTATTTT TAAAAGGTAA AAAACCAATT GTTGAACGAA CAAGTTATGG TTTAGGAGAA   5160

ATGATTAAAC ATGCATTAGA TAACGACGCA AAACATGTTG TAATTTCACT AGGTGGGATT   5220

GATAGTTTTG ATGCTGGTGC AGGTATGTTA CAAGCATTAG GTGCTCAATT CTATGATGAC   5280

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GATATGTCGA ACTTACACCC TAAAATGGAA ACAGCAAGAA TTCAAGTAAT GTCGGATTTT    5400

TCAAGTCGAT TATATGGTAA GCAAAGTGAA ATCATGCAAA CTTATGATGC GCATCAGTTG    5460

AATCATAATC AAGCAGCAGA AATCGATAAT TTAATTTGGT ATTTTAGTGA GTTATTTAAA    5520

AGTGAATTGA AAATTGCAAT TGGTCCAGTT GAACGTGGTG GTGCTGGTGG TGGAATTGCA    5580

GCAGTCTTGA ATGGACTGTA TCAAGCTGAA ATATTAACCA GTCATGCATT AGTAGACCAA    5640

CTAACACATT TAGAAAATTT AGTTGAACAA GCGGATTTAA TTATTTTTGG AGAAGGATTA    5700

AATGAAAATG ATCAGTTGCT AGAAACGACA ACATTGCGTA TTGCAGAACT TTGTCATAAA    5760

CATCAAAAGG TTGCCATTGC AATTTGTGCA ACTGCTGAAA AGTTTGATTT ATTTGAATCA    5820

CAAGGGGTTA CAGCAATGTT TAATACATTT ATCGATATGC CAGAAACTTA TACTGACTTT    5880

AAAATGGGtT ACAAATTAGG CATTATACGG TTCAGTCTTT AAAACTGTTG AAAACACATT    5940

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CATTTATGAT GGTTAGCAAA ACGAATTAGA AGATCGAAAG TATACGTAAA AAATATGAAA    6060

AATCACGCTA TCATTGCACT GAATGTTAGC GTGATTTTTA TATATTAATT AAGCCTGAGT    6120

TGAACTAGTA TATAATCGTT GGTTTTTAGT GATTTTCAGC GATATCTTCT ACAATTCCAA    6180

TGATTACTTG TACTGCTTTT TCCaTAACAT CAATGGATGC aTATTCATAT GGGCCGTGGA    6240

AGTTACCGCA ACCTGTAAAG ATGTTTGGAG TTGGTAACCC CATAAATGAC AATTGTGAAC    6300

CATCTGTACC ACCGCGAATA GGTTCAGTGT TTGCTGGAAT ATCTAATTTG GCAAAGACAC    6360

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GATCCGATAT ATCAACTTTA ACTGGATAAT TTTCAAAATG GGCATTGATA TCGTCACGTA    6480

TTTCTAAAAT ACGTTTCTTA CGCAATTCGA ATTGTTTTTT ATCATGATCA CGAATAATGT    6540

ATTGC̄AAAGT TGCTTTTTCA ACAGTTCCTT CAAAGTTCAT TAAGTGATAA AAGCCTTCGT    6600

ATCCTTCTGT TCGCTCCGGA ACTTCACTAT CAGGTAGCAA ACTATCGAAT TGTTCACCTA    6660

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GACCGATTTC TTCGTCTGGT GTAAATCCAA TGCGAATGGT ACCATGTTTA ATTTCTGGAT    6900

GTTCTTGTAA ATAACAAATA GCTTCCATAA TTTCCACAAT ACCCGCTTTA TCGTCTGCAC    6960

CTAGTAACGA TGTACCATCA GTTACCATTA ATGTATGACC AACTAAACTG TTAAGTTCTG    7020

GAAATACTTT AGGATCTAAG ACACGTTTAG TATTGCCTAG TTTGTATGGC TTACCATCAT    7080
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GCGCCAAAAA TCCAACTGTT GGGACGTCGA CATCGATGTT ACTTTCTAAT GTAGCAAATA      7200

AGTAGCCATT TTCATCTAAA TCAGTTGGCA ATCCTAATTG TTGTAATTCT TTTTCTAATA      7260

AATGTAACAA ATCCCATTGC TTTTCAGTTG AAGGTGTTGT TGTAGATTTT GGATCAGATT      7320

GCGTATCAAT TGTCGTATAT CTTGTTAATC TATCTATCAA TTGGTTCTTC ATTATATTCG      7380

ACCCCTTAAA CTCTATTATT CATGTTGTAA GATTTTTTAT ATGTCTTACC TTTGATTTTA      7440

CCATACAGTT GTTTGATACG TGTGTATAGG TAATATAGAA TTTCAGAAAC TAATATACCG      7500

AAAGCAATCG CACCTGAAAT CAGTGTAcTT CTAAAAATGT ATTTACAGCA CTTGTATAAT      7560

CATTTGATAC TAAAAAACGA GTCGCTTGAT AAGCTGCACC ACCAGGTACT AATGGTATAA      7620

TGCCTGGCAC TATGAATATA ATTACCGGTC GTTTATATCT GCGACTCATA GTATGACTCA      7680

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TCGATCGTTT AATGAAAAAA TAATTGCAGT TGAACTGACA AAACTATATG TATTATGAAG      8520

ACCATAACTA TGTGCGATAC GGTTCATTGT ATCTTCAACT CGATATGTTT CAGCACCTGA      8580

TTCaAGTAAA ATTCTACCTG CAATTAATAC AACATCAATC ACTTTGTTTT CATCTATAAT      8640

TGTGATTGAA TCTGGCATAT CAATTCACCT CCAATGATAT GTGTTATTTA TTTGAACAAT      8700

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CTTGTATGGT TCAAATTTAA ATAAGAAAAA CTGTTAATCT TTGCTATTAT ACTATGATTT      8820

AATAATAGCA AAGGATTAAC AGTTTTGTCG TTGTTATAAA TTGATAATAG GGTTAAACAT      8880
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TTTACGCTGT GATTTTGGAT CGTCATCTGT TAAATAACCA ACACCGATAG ACACTGACAA          9000

TTTAATAACT TCTTTGTTTG GTAAATGGAA TGATGATTTT TCAACACCCG AACGAATATT          9060

TTCAGCTAAT TTAACACTTT GATCAAGTGA ATAATTGTGA ATGACAACTG AGAACTCTTC          9120

GCCACCATTT CTAAAAATTT TAAATTGATT CGGCACATAG TTTTTAAGTA ATTGAGACAT          9180

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GTAAATAGGA CTCACTAACG CGACACCAAA TAAAATGATT ATTGTAACAA CATTAAGTAT          9540

TAATAATGAT AGCACATCAT TTTGTTTTAA AAATGGTCCA ATAGCACTTG TTACTGCAGC          9600

AATAACAATC AACGTAACAC CGTACATAAT CGAGTTGTTA AATACTACAA TTTCAACAAT          9660

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TAAAGGAACG AATGTTAAGT GAATTAAATA ATCTTCACGA TAAGGGATAG GGTAGACAGA          9780

TAATAATAAT GATACGATTG TCATTAAAAC AGTGACATAA GCCTTAGAAA AAAC              9834
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(2) INFORMATION FOR SEQ ID NO: 38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23439 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

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TCTCAATCAG ATGAAAAATT GCATATCGTA GGTTTTACAG AAAGTGCAAA ATATAATGCG           60

TCATCAGTCA TTTTCACGAA TGACGCTACC ATTGCCAAGA TCAATCCTAG ATTGACTGGA          120

GATAAAATTA ATGCAGTTGT TGTACGTGAT ACAAATTGGA AAGACAAAAA ATTAAACCAA          180

GAGCTTGAAG CGGTAAGTAT TAATGACTTT ATTGAAAATT TACCAGGTTA TAAACCACAG          240

AACTTAACAT TAAACTTTAT GATTTCATTC TTATTTGTCA TTTCAGCTAC AGTTATAGGC          300

ATTTTCCTAT ATGTCATGAC ATTACAAAAG ACGAGTTTAT TTGGCATATT AAAAGCTCAA          360

GGATTTACGA ATGGCTATTT GGCGAATGTG GTAATTTCGC AGACGGTCAT ATTAGCACTA          420

TTTGGTACGG CATTTGGCTT ACTGTTAACA GGCGTTACAG GTGCATTTTT ACCTGATGCA          480
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TCTGTATTAG GAAGTTTATT CTCCATTTTA ACAATTAGAA AAATAGATCC GTTAAAGGCG   600

ATTGGGTAGG AGGTGTAGCA AATGTTGAAA TTTGAAAATG TAACAAAGTC ATTTAAAGAT   660

GGGAATCGTA ACATTGAAGC GGTTAAAGAT ACAAATTTTG AGATAAATAA AGGTGATATT   720

ATAGCATTGG TTGGACCTTC TGGCTCTGGT AAAAGTACAT TTCTAACTAT GGCAGGTGCT   780

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CAAAAAGCAT TGGCAAAAGT TAGAATGTCT GAAATAGGTT TTATTTTACA AGCTACAAAC   900

CTTGTACCAT TTTTAACGGT AAAGCAACAA TTTACATTAT TGAAAAGAA AAATAAGAAT   960

GTTATGTCTA ATGAAGACTA TCAGCAACTT ATGTCACAAT TAGGTCTAAC TTCATTGCTT   1020

AATAAGTTAC CTTCAGAAAT TTCAGGTGGT CAGAAACAAC GTGTGGCGAT AgCaAAGCGT   1080

TATATACGAA TCCGTCGATT ATTTTAGCGG ATGAACCTAC CGCGGCGTTA GATACTGAAA   1140

ATGCGATTGA AGTCATTAAA ATTCTACGTG ATCAAGCCAA ACAAAGAAAG AAAGCATGTA   1200

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GTGCCGGTAT TTTTATGTTT ATGTATTATT TGAATAAACT TTCACATTCA ATTAATAATA   1380

ATTATTATCG AAAATCAGAA ATATTCCGTG AAATATAATA TTTTTTGTAG TAAAATGGCC   1440

TCTAAGTATT CAATATTTAA ATATGGGGAT TGAATATAAA ATTATCGTAA TGGGGGTCAA   1500

TGGTTATGGA TTTATTGATA GGTACTTTAT TTTTATTTTT GGTCTTAGTG ATTTTTACAT   1560

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CATTAGCTCG TCTTATTGCA GTATTATTAA CGCCAGTAGT GAATAGTACA TTGATTCGAA   1980

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TAGGTTTAAC GGGTGTACCT ATGGCTATTG GTGCCATGGC AGCATTTAGT TCGGCATTTA   2160

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GTATTGAACC TTTATCACAA GCAGATATTG TATCAGCCAA TCCAATTCCA ATCTATATTA   2280

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CGTATCTGTT TATGAGCTTA ATAAATTGTA TGAATAATAT GGTTGATCGA ATAACTGTTT   15720

ATCATGATGA TAAATTGAGT TTTTTAAAAT AATGATATAT TACATCATTG TTATAGCGTT   15780

TAAGAAATCA ACAACTTTAC GATAAATAGT GATTGCTTCG TCATTAGGTC TACGATCAAA   15840

ATCATGCTCG TTTTTATTCA CGCGTTCAAA TGTTGAATGT GGAACATGAT TCATGATATG   15900

TTCGCTTTCC TCAACGGGAA CATCATAATC GCCATTACAA TGCGCAATGA AAACAGGTGG   15960

AAGTGTTTTA AGTTCATCTG GTGCAATATT ATATTTGAA TTAGTATAAT CAGCAATGTT   16020

AATCATATTT ATCCATTTAC CTGTGCCACG TGCATAAACG TAGATTAAAA AACGTTGTGC   16080

GATTTGATCT TGAACAACCG GTGTTGGTGA AGTGAGTTGT GCAATCATTG TTTCGTTTAC   16140

GCTTTGAGCT ATTTTTGCGT AATAACTATT AGTTGTTTTA AAAGGTTCAG TGTTGATGCG   16200

ACTATAACCA TAAAAATCAA TAACACCATC AATATCTCTG TCTCGTGCAA TTAATAGACT   16260

TAAATATGCA CCTGATGATC TGCCAAAGGT AAAAATAGGG CAATTAGAAT ATTGTGATTG   16320

AATCGCATCG AATGAtGCgn AGnACATCCT CAATAATGCA ATCGAGACTT ACTTCTGGTA   16380

ATAAACGATA ACTTAGTTGA ATTAAATCGT AATGTTCCGT AAgATATCGA TATACTGTGG   16440

GGATAAATCG TTAGCTTTAC CGAACATTAA TCCACCACCG TGGATGTAGA CAATAGCGCC   16500

TTTTGTTGGT TGATTTTTTG CTTTAATAAT TGTGTAAGGT AATGCAAATG CATCTTTAGT   16560

AATTACTTTA TCTTTAATTT CAGTCACGAT TTAATAGGCT CCTTATTTTT GATATTGATG   16620

TCATTATAAC ACTGTCTTAA ATTTCCATGA AAAATAGTCT TAAGACGATG AGTCATGATA   16680

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CATCATTTTA ACAATATCTT TAAAAGCAGC ATGTGGAATG GCTAAATCTT CTAAATCTGC      16800

CATAGAAAAT TCAAGATTGA TATCATGTGG TCGCTGTTCA GCAAGTTTAT GCACAAAGTC      16860

AGGTTCTGTG ACAAAAGGCG AAGACATGCC GACCATATCT GCATGTTGTA AAGCATCTAA      16920

AGCAGACTCT GGAGAATTAA TCCCGCCACT TGCAATTAAA GGGATACGAC CTGCTAAATG      16980

TTCATAGACA ATTTGGTTAA CTGGTCGACC GAAATGATCA CCTGGTGTAC GAGACGTATT      17040

TTGATAAATA TGTCGACCCC AGCTAGCGAT TGCTAAGTAT TGGATGTTTG AAACGTCCAT      17100

GACCCAATTG ATTAATTGGT TGAACTCGTC AATGGTATAT CCTAAATCAC TGCCTCTGGT      17160

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ACCGTAATGG TCTGTACGTT TATTCGAAAA AGTTGAGAAA AATGTTTGAA TCAGCAAACG      17340

TTGTGCAATC GAAATTTCCA CACCATCAAA ACCTGCTTTA ATCGCGCGTA ATGTAGCATC      17400

GCGATACTGC TGAATGATGC TATTGATTTT CTCATGAGAC ATGGCGATAA CATCGTGTTC      17460

AATCGGTGAA TGCAATGTCA TAGGGCTTGG TCCATACACC TTTCCAAAAT TTAAAATGGC      17520

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CATCGTAGAT GCCATGTTAG TTAATCCAGG GATACAAGCA TCATGATCAA TATTAAAGCC      17640

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TGATGTGTTT ACGGTCATTG GTGATAATAC AAAGCGATTC GAAATTTTGA TGCCATTAGG      17820

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AATATTGTTT TCAAAGTACC ATGGAAAGAA TGAATAATCA ATGATGAACA GTCTTGATAG      17940

AATAGAATTG GTACATGGAA AGTATTTTTA AAATTAAACT AATGAATGGC ATTTGTAGGT      18000

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AACGTTATCA TATACGTGGG TATATGAAGA GGGAATGGTA TTAAGAACGC TAAAATGTTA      18120

TGTCGGTTTG ACATGACAGG ATAAGTTTGG AGATGACGGA TTGGTTAAAT TAAGCGTATT      18180

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ACTTGCAAAA TTAGCAGATC GACTTGGCTT TAAGCGAATT TGGTTTACGG AACATCATAA      18300

TGTACCAGCG TTTGCGTGTA GTAGTCCAGA ACTTTTGATG ATGCATACAT TGGCGCAGAC      18360

AAATCACATA CGAGTTGGCT CTGGTGGTGT GATGCTGCCG CACTATCGAC CTTATAAAAT      18420

TGCTGAGCAT TTTAGAATGA TGGCAGCGTT ATATCCAAAT CGTATTGATT TAGGTATTGG      18480
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TAGTTACGAT GAATCGATTT CGTTATTACG TGATTATCTT ACAATAAAGG ATAAACCAAG    18600

TGCGCATACG TTAGGTGTCC AACCACACAT TGATCATTTT CCAGAAATGT GGTTATTAAG    18660

TAGTAGCGCA ACATCTGCCA AAATAGCTGC CGAACTAGGT ATAGGGCTTT CTGTTGGAAC    18720

ATTTTTGCTA CCAGATATAA ATGCGATACA TACAGCGAAG GATAACATTG ATATTTACAA    18780

AAAACATTTC CAAGCATCAA CGATTAAAAT GGACGCAAAG GTGATGGCAT CTGTATTTGT    18840

CATTGTAGCT GATAACGAAG CGGAAGTAGC AGCATTACAA CATGCCTTAG ATGTTTGGTT    18900

ATTAGGTAAA TTACAATTTG CAGAATTTGA AGATTTTCCT TCAGTAGACA CAGCACAAAA    18960

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AAAGTTAGCC AATTATTTAT GGGTAGAAAA AGTAGGAGAT TTGTATGTGT TTAGTATGAC    19260

ACCTGAATTG CAAGATGATA TTGGGACAGT AGGTTATGTT GAATTCGTAA GTCCAGATGA    19320

AGTTAAAGTG GATGATGAAA TTGTGAGTAT CGAAGCATCG AAAACGGTCA TTGATGTGCA    19380

AACGCCATTG TCAGGAACGA TTATTGAGCG AAATACAAAA GCGGAAGAAG AACCGACAAT    19440

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AGCATTCCTA GCATTACCGG AGGCTTAAAT GGAAACGTTA AAATCAAATA AAGCGAGACT    19560

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ACATGTTACG GATTTGAAGG ATTTGAAGCC GATAAAAGGT GACAATATCT TTGTTTGGCA    19800

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TCAAGTTCGA CTTGATTGTG CAGAGATCAT TCGACAACAA GGGCGCAATG AAGGTGTAGG    19980

TAAAGCCAAA ATAACACGTG GATATAATTT GCCAGCAAAG TATATAATTC ATACGGTTGG    20040

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TCTTAGCTGT CTTAAATTGG CTGATCAACA TAGTTTAAAT CATGTCGCTT TTTGCTGTAT    20160

ATCTACAGGT GTATTTGCTT TTCCTCAAGA TGAAGCAGCA GAAATTGCTG TTCGAACAGT    20220

AGAAAGCTAT CTCAAAGAAA CAAATTCAAC ATTGAAAGTC GTGTTCAATG TATTTACAGA    20280
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CAATGTCTCT GTTAATGGAT GACAAGACAA AGCAGGCTGA AGTATTGCGT ACTGCGATTG        20400

ATGAAGCAGA TGCGATAGTG ATTGGAATTG GTGCAGGCAT GTCTGCATCT GACGGATTTA        20460

CATATGTAGG AGAGCGTTTT ACGGAAAATT TCCCAGATTT TATTGAAAAA TATCGCTTCT        20520

TTGATATGTT GCAAGCGAGT TTACATCCTT ATGGCAGTTG GCAAGAGTAT TGGGCATTTG        20580

AGAGTCGTTT TATTACATTA AACTATTTAG ATCAACCTGT AGGTCAGTCT TACCTCGCTT        20640

TAAAATCCTT GGTGGAAGGT AAACAGTACC ACATTATAAC TACGAATGCA GATAATGCTT        20700

TCGATGTAGC TGATTATGAT ATGACTCATG TATTTCATAT ACAAGGGGAG TATATACTGC        20760

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TGTGATGCCC CAATGGAAGT GAATAAACGT AAAGCGGAAG TTGGGATGGT TGAAGATGCT        20940

GAATTTCATG CGCAACTACA TCGTTATAAT GCTTTTCTAG AGCAACATCA AGATGATAAA        21000

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CGCTATGCAA GTTTATGTTA ACCAGCATAT CTTTTTAGAT GAAGATATTT TATTCCCTTA        21360

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GTATGTTGAT AAAGGTGCCG TTAATATGTG TTGTATTTTA GAACAAGACA CTTCAATTTA        21540

TGGTGATTTT CAACGATTTT ATCAACCAGC TATAAAGGCG TTGCATACAT TAGGTGCAAC        21600

AGATGTGGTA CAAAGCGGTA GAAATGATTT AACATTGAAT GGTAAAAAAG TGTCAGGCGC        21660

CGCAATGACA TTAATGAATA ATCGTATTTA TGGCGGTTAT TCGCTATTAC TTGATGTTAA        21720

TTATGAAGCA ATGGATAAAG TGTTAAAGCC TAATCGCAAA AAGATTGCAT CGAAAGGGAT        21780

TAAATCTGTG CGCGCACGTG TTGGTCATCT TAGAGAAGCA CTGGATGAAA AGTATCGTGA        21840

TATAACCATT GAAGAATTTA AAAATTTAAT GGTGACGCAG ATTTTGGGAA TCGATGACAT        21900

TAAAGAGGCG AAACGATATG AATTAACGGA TGCAGATTGG GAAGCGATTG ATGAATTAGC        21960

TGATAAAAAG TATAAAAATT GGGATTGGAA TTATGGCAAG TCACCCAAAT ATGAATACAA        22020

TCGAAGTGAA AGATTATCTT CAGGTACGGT AGACATAACA ATTTCTGTTG AACAAAATCG        22080
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AGAAGCATTA CAAGGAACAA AAATGACAAG AGAAGATTTA ACGCATCAGT TAAAGCAATT    22200

AGACATCGTT TATTATTTTG GCAATGTTAC GGTAGAAGCA TTAGTGGATA TGATTTTAAG    22260

TTAATATTGT TATTTTATGT ATGCTGAATC ATTGGAAGTG TTTGCTTGCT CTTGAAAAGG    22320

TGACAATAGT GTTTGGTGAA GGTTGAACAT ATGAGTGGAA ATTATTGCCT TTAACTATTC    22380

AAAGTATGAT ATATATATGG TTTTTGTTTC TAAATGATTG GGTATTTGAA AATAGATGAG    22440

TTTAATATTT TAAGGAATAT AATGATGTTT ACTTTTATAA TTCATATAGA ATATTAAGCA    22500

ATATAAGTCT GTTGATATAT ACAAAATATA ATGACTGCTA TAATGAGTAA TCAATAGACA    22560

CAAAGAGGAG ATTATGTGAT GAATAATAAA GTATTAGTAA CCGGTGGTAC AGGGTTTGTT    22620

GGCATGCGAA TTATTTCACG ATTATTAGAA CAAGGTTATG ACGTACAAAC GACGATACGT    22680

GATTTAAGTA AAGCTGATAA AGTAATTAAA ACAATGCAAG ACAATGGCAT TTCCACAGAG    22740

CGATTAATGT TTGTCGAAGC GGATTTATCA CAAGATGAAC ATTGGGATGA AGCAATGAAA    22800

GATTGCAAGT ATGTCTTGAG TGTAGCATCT CCGGTGTTTT TCGGTAAAAC AGACGATGCA    22860

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GGGTGTTAAA CGTGTGGTAA TGACTGCAAA CTTTGGTGCA GTTGGTTTTA GTAATAAAGA    22980

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ATATGAAAAA TCAAAATTGT TAGCTGAAAA GGCAGCGTGG GATTTTGTTG AGAATGAAAA    23100

TACAACAGTA GAATTTGCCA CAATCAATCC AGTTGCAATT TTTGGGCCAT CATTAGATGC    23160

ACACGTTTCA GGAAGCTTTC ATTTATTAGA AAATTTATTG AATGGTTCAA TGAAACGTGT    23220

ACCGCAAATT CCGTTAAATG TTGTTGATGT GAGAGACGTA GCTGAACTGC ACATTTTGGC    23280

AATGACAAAT GAACAAGCTA ATGGCAAGCG ATTTATTGCG ACGGCTGATG GACmAATTwA    23340

tTTGTTGGGA ATTGcCAAAt TAATTAAAGA AAAGGGCCTG GAAATAGCTC CAAAAGTTCC    23400

TACTAAAAAA TTACCCAGCT TTATTTTGAG CnAnGnGCC                          23439
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(2) INFORMATION FOR SEQ ID NO: 39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4522 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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CCCTTTGAGA GTATATCATC TAGTCAAATT ATGCCTGTCA TTAGAGCGAC TAGCTTTGAT    60
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TATTATGCAG TCGATTTAGG GAAATCATAT CGTCTAATTG ACGAAAGCAT GTTAGAGGAT        180

TTGAAGTTAA CTGAACAACA AATAAGAGAA ATGTCTCTGT TTAATGTTAG AAAATTGTCA        240

AATTCATATA CGACTGATGA AGTAAAAGGT AATATTTTTT ATTTTATTAA CTCAAATGAC        300

GGGTATGATG CAAGTAGGAT ACTAAATACT GCATTTTTAA ATGAAATTGA GGCACAATGT        360

CAAGGCGAAA TGCTCGTAGC AGTGCCACAC CAAGATGTGT TAATTATTGC AGATATACGC        420

AATAAAACAG GATATGATGT GATGGCACAT TTAACAATGG AATTTTTCAC TAAAGGTCTA        480

GTTCCAATTA CATCATTATC CTTTGGATAT AAACAGGGTC ATCTTGAACC GATATTTATT        540

TTAGGTAAAA ATAATAAACA AAAAAGAGAT CCAAACGTGA TTCAGCGTTT AGAAGCAAAT        600

CGTCGTAAAT TTAATAAAGA TAAATAGAAA TAATTGGATA AGGAGTTTTG TCATAATGAA        660

TTTATTTTAC AATCCTAAAT ATGTAGGAGA TGTCGCATTT TTACAAATTG AACCAGTTGA        720

AGGTGAATTA AACTACAATA AAAAAGGTAA TGTTGTTGAA ATTACtAATG AAGGTAATGT        780

TGTAGGTTAT AATATTTTTG AAATTTCAAA AGATATAACA ATTGAAGAAA AAGGTCATAT        840

TAAATTAACT GATGAACTTG TAAATGTATT CCAAAAGCGT ATTTCAGAAG CTGGTTTTGA        900

TTATAAATTA AATGCTGATC TATCACCGAA ATTTGTAGTT GGCTACGTTG AAACTAAAGA        960

CAAACATCCT GATGCAGATA AATTAAGTGT ACTAAATGTA AACGTTGGAA ATGACACATT       1020

ACAAATTGTA TGTGGCGCGC CTAACGTTGA AGCTGGACAG AAAGTTGTTG TTGCTAAAGT       1080

AGGTGCAGTG ATGCCTAGCG GTATGGTAAT TAAAGATGCT GAATTACGTG GTGTTGCCTC       1140

AAGCGGTATG ATTTGTTCAA TGAAAGAATT GAATTTACCT AATGCACCTG AAGAAAAAGG       1200

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CCTATGAGCG TAGCTTATGA AAATGAAAAT GTTGAACAAT CTGCAGATAC TATTTCAGAT       1500

GAAAAAGAAC AATACCATCG AGACTATCGC AAACAAAGCC ACGATTCTCG TTCACAAAAA       1560

CGACATCGCC GTAGAAGAAA TCAAACAACT GAAGAACAAA ATTATAGTGA ACAACGTGGG       1620

AATTCTAAAA TATCACAGCA AAGTATAAAA TATAAAGATC ATTCACATTA CCATACGAAT       1680

AAGCCAGGTA CATATGTTTC TGCAATTAAT GGTATTGAGA AGGAAACGCA CAAGCCAAAA       1740

ACACATAATA TGTATTCTAA TAATACAAAT CATCGTGCTA AAGATTCAAC TCCAGATTAT       1800

CACAAAGAAA GTTTCAAGAC TTCAGAGGTA CCGTCAGCTA TTTTTGGCAC AATGAAACCT       1860
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AAACAAAAAT ATGATAAATA TGTAGCTAAG ACGCAAACGT CTCAAAATAA ACAATTAGAA        1980

CAAGAAAAAC AAAATGATAG TGTTGTCAAA CAAGGAACTG CATCTAAATC ATCTGATGAA        2040

AATGTATCAT CAACAACAAA ATCAATGCCT AATTATTCAA AAGTTGATAA TACTATCAAA        2100

ATTGAAAATA TTTATGCTTC ACAAATTGTT GAAGAAATTA GACGTGAACG AGAACGTAAA        2160

GTGCTTCAAA AGCGTCGATT TAAAAAAGCG TTGCAACAAA AGCGTGAAGA ACATAAAAAC        2220

GAAGAGCAAG ATGCAATACA ACGTGCAATT GATGAAATGT ATGCTAAACA AGcGGAACgC        2280

TATGTTGGTG ATAGTTCATT AAATGATGAT AGTGACTTAA CAGATAATAG TACAGATGCT        2340

AGTCAGCTTC ATACAAATGG CATAGAGAAT GAAACTGTAT CAAATGATGA AAATAAACAA        2400

GCGTCAATAC AAAATGAAGA CACTAATGAC ACTCATGTAG ATGAAAGTCC ATACAATTAT        2460

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GTTTCGAATG TAACGTCTCA ACATCAATCA GCACTACAAC ATAACGTTGA AGTAAATGAT        2580

AAAGATGAAC TAAAAAATCA ATCCAGATTA ATTGCTGATT CAGAAGAAGA TGGAGCAACG        2640

aATAAAGAAG AATATTCAGk AAGTCAAATC GATGATGCAG AATTTTATGA ATTAAATGAT        2700

ACAGAAGTAG ATGAGGATAC TACTTCAAAT ATCGAAGATA ATACCAATAG AAACGCGTCT        2760

GAAATGCATG TAGACGCTCC TAAAACGCAA GAGTACGCAG TAACTGAATC TCAAGTAAAT        2820

AATATCGATA AAACGGTTGA TAATGAAATT GAATTAGCAC CGCGTCATAA AAAAGATGAC        2880

CAAACAAACT TAAGTGTCAA CTCATTGAAA ACGAATGATG TGAATGATAA TCATGTTGTG        2940

GAAGATTCAA GCATGAATGA AATAGAAAAG AATAACGCAG AAATTACAGA AAATGTGCAA        3000

AACGAAGCAG CTGAAAGTGA ACAAAATGTC GAAGAGAAAA CTATTGAAAA CGTAAATCCA        3060

AAGAAACAGA CTGAAAAGGT TTCAACTTTA AGTAAAAGAC CATTTAATGT TGTCATGACG        3120

CCATCTGATA AAAAGCGTAT GATGGATCGT AAAAAGCATT CAAAAGTCAA TGTGCCTGAA        3180

TTAAAGCCTG TACAAAGTAA GCAAGCTGTG AGTGAAAGAA TGCCTGCGAG TCAAGCCACA        3240

CCATCATCAA GATCTGATTC ACAAGAGTCA AATACAAATG CATATAAAAC AAATAATATG        3300

ACATCAAACA ATGTTGaGAA CAATCAACTT ATTGGTCATG CAGAAACAGA AAATGATTAT        3360

CAAAATGCAC AACAATATTC AGAGCAGAAA CCTTCTGTTG aTTCAACTCA AACGGAAATA        3420

TTTGAAGAAA GTCAAGATGA TAATCAATTG GAAAATGAGC AAGTTGATCA ATCAACTTCG        3480

TCTTCAGTTT CAGAAGTAAG CGACATAACT GAAGAAAGCG AAGAACAAC ACATCCAAAC        3540

AATACTAGTG GACAACAAGA TAATGATGAT CAACAAAAAG ATTTACAGTC ATCATTTTCA        3600

AATAAAAATG AAGATACAGC TAATGAAAAT AGACCTCGGA CGAACCAACA AGATGTTGCA        3660
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CCAAGTGTTT CATTACTAGA AGAACCACAA GTTATTGAGT CGGACGAGGA CTGGATTACA       3780

GATAAAAAGA AAGAACTGAA TGACGCATTA TTTTACTTTA ATGTACCTGC AGAAGTACAA       3840

GATGTAACTG AAGGTCCAAG TGTTACAAGA TTTGAATTAT CAGTTGAAAA AGGTGTTAAA       3900

GTTTCAAGAA TTACGGCATT ACAAGATGAC ATTAAAATGG CATTGGCAGC GAAAGATATT       3960

CGTATAGAAG CGCCTATTCC AGGAACTAGT CGTGTTGGTA TTGAAGTTCC GAACCAAAAT       4020

CCAACGACAG TCAACTTACG TTCTATTATT GAATCTCCaA GTTTTAAAAA TGCTGAATCT       4080

AAATTAACAG TTGCGATGGG GTATAGAATT AATAATGAAC CATTACTTAT GGATATTGCT       4140

AAAACGCCAC ACGCACTAAT TGCAGGTGCA ACTGGATCAG GAAATCAGT TTGTATCAAT        4200

AGTATTTTGA TGTCTTTACT ATATAAAAAT CATCCTGAGG AATTAAGATT ATTACTTATC       4260

GATCCAAAAA TGGTTGAATT AGCTCCTTAT AATGGTTTGC CACATTTAGT TGCACCGGTA       4320

ATTACAGATG TCAAAGCAGC TACACAGAGT TTAAAATGGG CCGTAGAAGA AATGGAACGA       4380

CGTTATAAGT TATTTGCACA TTACCCATGT ACGTAnTATA ACAGCATTTA ACnAAAAAGC       4440

CCCATATGAT GAAAGAATGn CAAAAATTGT CATTGTAaTT GATGAGTTGG CTGATTTAAT       4500

GATGATGGTC CGCAAGAAGT TG                                               4522
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(2) INFORMATION FOR SEQ ID NO: 40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 751 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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TCAAGTTTAC GGATACGTAT ATATTTTGCA TGACATTTAG TGCAATAATA TTCATAATTT         60

GCCCGTTGTT GATAGCTTTC AATGCTGTTA CAAAATCTAG GCGCTCCAAC CTGTTGGCTC        120

AATCGTTTAA AATCTTGATC TTTATGTTGA TAACCTTTAC CAGCAATATG CAAGTGATAA        180

TGACACAATT CGTGCAGTAT AATTTTTACA ACAGCATCTT CTCCATAATG CTCATATTGT        240

TTTGGATTAA TTTCAATATC ATGGGACTTT AAAAGATAAC GTCCGCCTGT TGTACGTAAC        300

CTTTTATTAA AATATGCACA ATGTCGAAAC GTACGTCCAA ATTTTTCTTC CGAAAGATTC        360

TCAACCATTC GCTGAAGTTT GTCATTATTC ATGTGGATCA ATCATCGTTA ATGATACTTT        420

GTCTTTATTT TTGTCAATAC TGTAAATCCA AACGTCAACG ATATCACCAA CACTGACAAT        480

ATCCATTGGA TTTTTTACGA ACTTCTTAGA AAGTTTCGAA ACATGGACAA GTCCATCTTG        540
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TTTCATTCCT TCTTGTAAAT CTTCAATTGA TAGCACATCG GATTTAAGGA TTGGTGTTTC   660

AAACTCGTCC CTTGGATCTC GATTAGGTGC GTTCAAGGAT TTAATAATAT CCTCTAATGT   720

AGGTACACCG ACTTGTAATT CAATCGCCAG T   751

(2) INFORMATION FOR SEQ ID NO: 41:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1076 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCTCCAGCTT TAACTTGATC TGGCACTTTA ACAATTGTCT GATCCATACA TACGCGACCA   60

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CCATCTGCAT ATCCAATAgG TAACAATGCT ATTGTAGTTG GGTCAGTAGC TGTATAAGTT   180

GCACCATAAC TTACAGACTC ACCCGCTTGT AGCGTCTTTG TTTGAACTAC ATTAGCAATT   240

AATTGCACAC TTGGTTTAAG GTGTACTTTA ACTTTTTGCT GTACATACTC TGATGGATAA   300

TATCCATAAA GGGAAATTCC TGGTCTTATT GCATTACAGA ATTGGCAATC CATTAATAGA   360

GAGCCTGCTG AGTTCTGACA ATGTATATAT TCAGGTTTAA TTGCTTCATT GACCATATCT   420

TTAAAACGTT GATATTGTTC AGTTGTCATA TCTCCTGGTT CGTCAGCACA GGCAAAGTGT   480

GTAAACACGC CTTCAAATAC AAGTTGCTCA TATTGTTGAA TGATTTCAAT CACTTCTTGA   540

TACGTTTTAG TATCTTTAAT ACCTAAACGT CCCATTCCTG TATCTAATTT AATGTGCAAC   600

CATAACTTTT TCTCTTGCTC ACCAGAAATG TTTTTAATTG CTTCTTTCAA CCACTGTTTA   660

GACGGAACCG TTAAGGCAAC TCGGTGTTGT ATCGCTTTAT CAATATCTTT AGCTGGTAAC   720

ACACCTAAGA CTAAAATTTT AGCAGTAATC CCATGCATTC TAAGTTCTAT CGCTTCATCT   780

AACGTTGCTA CAGCAAAAAA TGTGGCGCCA TTTTCCATTA AATGACGTGC TACTTTAACA   840

CTACCTAGTC CATAGGCATT GGCTTTAACG ACAGCCATCA CTGTTTTATT TGGATGCAAT   900

GTACTGAATA CTTTGAAATT TGATGCAACA GCGTTTAAAT CTACATTCAT ATACGCAGAT   960

CTATAATATT TATCCGACAT ATTACTTCCT CCTGTAATTC CCACACGTTT TAAAACTAGA   1020

TCTTAATTAT CATTGTATAA CAAATTTAAA ATGCTGACTT TTCTAAAACA ACTTGG   1076

(2) INFORMATION FOR SEQ ID NO: 42:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2930 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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TGACCACAAT GCCCAATACA ACCATCCCAT GGTAAAGCCA AGAGATGAGT CAATAAAGCG      60

TGTTGAATAA GAGCTGAATG AACCTGATAC TGGATAAAAT GTTGCCAACT CTCCAATTGA     120

TGACATTAAG AAATATAGCA TGACACCAAT AACAAGATAA GCGAGTATAG CGCCTCCAGG     180

ACCAGCTTGA GAAATGATAT TACCAGTAGC TACAAATAGA CCAGTCCCAA TTGCACCACC     240

TATAGCAATC ATGGAAATGT GTCTTGAGTT AAGACTACGG TTCATTTTAT TATCTTCCAT     300

ATTTAGTCTC CCATCTATTT AAATATACCC ATTATTGTAA GCTTTTTAAG TGTACTATTC     360

AATAACTATT TAGTACTGTA AAGCGAAAAA ATTAAAATTT TCTGATTTTT TAATCATCTT     420

GAGCATGTTT AATTGTAATT TTGATGGGGT TAAATTATAA TATGTATTAA ATTATAATTA     480

TnATAAATTG TGGAGGGaTG ACTATGTCAC AACAAGACAA AAAGTTAACT GGTGTTTTTG     540

GGCATCCAGT ATCAGACCGA GAAAATAGTA TGACAGCAGG GCCTAGGGGA CCTCTTTTAA     600

TGCAAGATAT TTACTTTTTA GAGCAAATGT CTCAATTTGA TAGAGAAGTA ATACCAGAAC     660

GTCGAATGCA TGCCAAAGGT TCTGGTGCAT TTGGGACATT TACTGTAACT AAAGATATAA     720

CAAAATATAC GAATGCTAAA AtATTCTCTG AAATAGGTAA GCAAACCGAA ATGTTTGCCC     780

GTTTCTCTAC TGTAGCAGGA GAACGTGGTG CTGCTGATGC GGAcGTGACA TTCGAGGATT     840

TGCGTTAAAG TTCTACACTG AAGAAGGGAA CTGGGaTTTA GTAGGGAATA ACACACCaGT     900

ATTCTTCTTT AGAGATCCAA AGTTATTTGT TAGTTTAAAT CGTGCGGTGA AACGAGATCC     960

TAGAACAAAT ATGAGAGATG CACAAAATAA CTGGGATTTC TGGaCGGGTt TCCAGAAGCA    1020

TTGCACCAAG TAACGATCTT AATGTCAGAT AGAGGGATTC CTAAAGATTT ACGTCATATG    1080

CATGGGTTCG GTTCTCACAC ATACTCTATG TATAATGATT CTGGTGAACG TGTTTGGGTT    1140

AAATTCCATT TTAGAACGCA ACAAGGTATT GAAAACTTAA CTGATGAAGA AGCTGCTGAA    1200

ATTATAGCTA CAGATCGTGA TTCATCTCAA CGCGATTTAT TCGAAGCCAT TGAAAAAGGT    1260

GATTATCCAA AATGGACAAT GTATATTCAA GTAATGACTG AGGAACAAGC TAAAAACCAT    1320

AAAGATAATC CATTTGATTT AACAAAAGTA TGGTATCACG ATGAGTATCC TCTAATTGAA    1380

GTTGGAGAGT TTGAATTAAA TAGAAATCCA GATAATTACT TTATGGATGT TGAACAAGCT    1440

GCGTTTGCAC CAACTAATAT TATTCCAGGA TTAGATTTTT CTCCAGACAA AATGCTGCAA    1500

GGGCGTTTAT TCTCATATGG CGATGCGCAA AGATATCGAT TAGGAGTTAA TCATTGGCAG    1560
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GGTCAAATGC GCGTAGTTGA CAATAACCAA GGTGGAGGAA CACATTATTA TCCAAATAAC    1680

CATGGTAAAT TTGATTCTCA ACCTGAATAT AAAAAGCCAC CATTCCCAAC TGATGGATAC    1740

GGCTATGAAT ATAATCAACG TCAAGATGAT GATAATTATT TTGAACAACC AGGTAAATTG    1800

TTTAGATTAC AATCAGAGGA CGCTAAAGAA AGAATTTTTA CAAATACAGC AAATGCAATG    1860

GAAGGCGTAA CGGATGATGT TAAACGACGT CATATTCGTC ATTGTTACAA AGCTGACCCA    1920

GAATATGGTA AAGGTGTTGC AAAAGCATTA GGTATTGATA TAAATTCTAT TGATCTTGAA    1980

ACTGAAAATG ATGAAACATA CGAAAACTTT GAAAAATAAA TTTGATATGT AGTTTCTATA    2040

TTGCGTAGTT GAGCAGTTTA TGATATCATA ATAAATCGTA AAGATTCCTA ACAAGAGAGG    2100

GTGTTTAACG TGCGCGTAAA CGTAACATTA GCATGCACAG AATGTGGCGA TCGTAACTAT    2160

ATCACTACTA AAAATAAACG TAATAATCCT GAGCGTATTG AAATGAAAAA ATATTGCCCA    2220

AGATTAAACA AATATACGTT ACATCGTGAA ACTAAGTAAT TCTTATCATT CAAATACGAC    2280

GATTTGAAAA TAAAGCGGGC TTACCTATTA TATTGGGGAG CTCGCTTTTT TATGAAATTT    2340

TTGTGAAGAG TGATTAATGG ATTGAGTTTC ATCGGTAGAA CAATATATGA TTATATTAGT    2400

TGTTACTTTA TTAAAaTTTG AGAATATTTA TAGAAGGAAA TAGATTACTG ATTTTATAAA    2460

GTCACTTTGT TAGCGAATGC TTGAAAGAGT ATTTAATATA GTAGAATTTA AAATTTCAAA    2520

GCGGAATTTA ATAAGTACGA AGTAGTTCTG GGTATGTTTT ATAAATGTTC GATAATACAC    2580

TTTAATCTTA AATATGATGG TTTAGAAAAT GATTTAACAA AGAAATGAaA CTTTACTGTT    2640

GAATTATGTG AGGATTGTGT TATTATATAA ATCGTAATAA TTACGATTTG ATAAAAAGTG    2700

AGGTAACTAT ATATGGCTAA GAAATCTAAA ATAGCAAAAG AGAGAAAAG AGAAGAGTTA    2760

GTAAATAAAT ATTACGAATT ACGTAAAGAG TTAAAAGCAA AAGGTGATTA CGAAGCGTTA    2820

AGAAAATTAC CAAGAGATTC ATCACCTACA CGTTTAACTA GAAGATGTAA AGTAACTGGA    2880

AGACCTAGAG GTGTATTACG TAAATTTGAA ATGTCTCGTA TTGCGTTTAG             2930
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(2) INFORMATION FOR SEQ ID NO: 43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3606 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

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CTTCTTGCCA TGGCTCTCTT TATTTAAAAA TGCTTCCAAC TTGTCCATTT GATTGTTTCT    60
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TTATAAAAAA CTAATTTTAC AAATGCTTTT GCGTTCTTAC AAAAAATGCA TTTGACTATT      180

ATTATAATAA GCGTATAATT GTCGCATATT ATTTTTTGTA TTTTTGGCAA TAACGAAGGA      240

GTATTTATGA ATAAAGACAA GCAATTGCAC AACGACAAAA TCAATCTATC CCAATTAGTC      300

TTATTAGGGT TAGGCTCTTT AATAGGATCT GGTTGGCTAT TTGGTGCGTG GGAAGCATCA      360

TCAATAGCTG GACCAGCAGC AATCATATCA TGGGTTCTTG GATTCCTAGT CATTGGAACC      420

ATTGCCTATA ACTACATTGA AATCGGCACA ATGTTTCCTC AATCAGGTGG CATGAGTAAC      480

TATGCCCAGT ATACACATGG CTCATTATTA GGCTTTATTG CTGCTTGGGC GAATTGGGTG      540

TCTTTGGTGA CAATAATACC TATCGAAGCT GTGTCAGCTG TTCAATATAT GAGTTCTTGG      600

CCGTGGCATT GGGCGAAACC AATGAGATAT TTAATGGAAA ATGGCTCTAT TAGCACATAC      660

GGATTGCTAG CTGTATATCT CATCATTGTT ATTTTTTCAT TATTAAACTA TTGGTCCGTA      720

AAACTTTTAA CATCATTTAC GAGTTTAATT TCTGTATTTA AATTAGGCGT ACCCATGTTA      780

ACCATCATCA TGTTGATGCT ATCAGGATTC GACACTTCAA ATTACGGCCA TTCGGCAAGC      840

ACATTTATGC CTTACGGAAG TGCACCGATT TTTGCTGCAA CAACAGCATC AGGGATTATT      900

TTTTCATTCA ATTCATTCCA GACAATTATT AATATGGGTT CAGAAATTAA AAATCCTGAA      960

AAAAATATCG CAAGAGGCAT CGCTATCTCA CTGTCAATCA GTGCAGTGTT GTACATCATT     1020

TTACAAAGTA CGTTTATCAC TTCTATGCCT CAATCAATGT TACAACATAG TGGATGGAAT     1080

GGCATCAACT TCAATTCACC ATTTGCTGAT TTAGCTATCT TATTAGGAAT TAATTGGCTC     1140

GCAATTTTAC TATACATTGA AGCTTTTGTA TCACCATTCG GTACTGGCGT GTCATTTGTC     1200

GCCGTTACAG GTCGAGTTTT ACGAGCAATG GAGAAAAATG GACATATCCC TAAATTTCTT     1260

GGGAAGATGA ATGAAAAATA TCATATCCCA CGTGTAGCAA TCATCTTTAA TGCCATCATT     1320

AGTATGATTA TGGTTACATT ATTTAGAGAT TGGGGTACGC TAGCAGCAGT TATTTCTACT     1380

GCAACTTTAG TAGCCTATTT AACTGGCCCA ACGACAGTGA TTGCATTAAG AAAAATGGGA     1440

CCAACAATGA CTCGTCCATT TAGAGCAAAA ATTTTAAAAG TAATGGCACC ATTATCATTT     1500

GTATTAGCTT CATTAGCTAT ATATTGGGCA ATGTGGCCAA CAACGGCTGA AGTTATTTTA     1560

ATCATTATAC TTGGATTACC AATCTACTTC TTCTATGAAT ATCGTATGAA TTGGCGTAAT     1620

ACAAAGAAAC AAAATTGGTGG TAGCTTATGG ATTATTGTAT ATTTAATCGT GCTATCAATA     1680

CTGTCATTTA TAGGAAGCAA AGAATTTAAA GGCTTAAATA TGATTCACTA TCCATTTGAC     1740

TTTATCGTTA TTATTATTGT GGCACTTATC TTCTATTACA TCGGTACAAC GAGTTCATTT     1800

GAAAGCGTCT ATTTCCGTCG CGCAACACGA ATCAATACGA AGATGCGTGA GTCACTAAAT     1860
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CACACACATT AACCAACCAT TGATTTCAAC ATCTTGGTTG GTTTTTTATT TTGAAAATCG      1980

GTTATAAATA ACTAACATAA CAAGATGATG ATCAGGCTGG GACATAAATC AATGTTCTAT      2040

GCTCTACGAA gTTATATTGG CAGTAGTTGA CTGAACGAAA ATGCGCTTGT AACAAGCTTT      2100

TTTCGATTCT AGTCAGGGGC CCCAACACAG AGAATTTCGA AAAGAAATTC TACAGGCAAT      2160

GCAAGTTGGG GTGGGACGAC GATAAAGAAA TACTTTTTCT ATAGAAATTA GTATYtCTTA      2220

TGCATGAGTT TTACTCATGT ATTCATATTT TTAAGTACAC ATTAGCTGTG GCTAATGTAT      2280

AAGAACCACT ACATAATAAA TCATTTGTGG CTCTTTATCA TTTCTGTCCC ACTCCCGTAG      2340

AAGTACATCA TATAATGCTG AAAATGGTTT GAGTTAAAAC AGATATCAAG CTCGTCTGAT      2400

TCAGTCACAA AATTGTCTTG TTATACTTGT CACCTATCAT CTATAGACCG TGGTATGATT      2460

AAATTGGGGA TGATAAAGGA GGTTAATAAA TATGAAGATT AATACTACAG GTGGTCAAAT      2520

TCATGGTATT ACACAAGATG GTTTAGATAT CTTCTTAGGC ATTCCTTATG CAGAACCACC      2580

AGTTCATGAC AATCGCTTTA AACATTCTAC GTTAAAAACA CAATGGTCAG AGCCAATTGA      2640

TGCAACTGAA ATACAACCCA TCCCACCGCA ACCAGACAAC AAATTAGAAG ATTTTTTCTC      2700

CTCACAATCT ACAACTTTTA CTGAACATGA AGACTGTTTA TATCTAAATA TTTGGAAACA      2760

ACATAATGAT CAGACGAAGA AACCTGTCAT CATTTATTTT TATGGTGGTA GTTTTGAAAA      2820

TGGTCATGGT ACAGCCGAAC TCTATCAACC GGCACATTTA GTACAAAATA ACGACATTAT      2880

CGTTATTACA TGCAATTATC GTTTAGGCGC ATTAGGATAT TTAGACTGGT CATATTTTAA      2940

TAAAGATTTT CATTCCAATA ATGGCCTTTC AGATCAAATC AATGTCATAA AATGGGTGCA      3000

TCAATTTATT GAATCCTTCG GTGGCGACGC TAATAACATT ACTTTAATGG GTCAGTCTGC      3060

AGGCAGTATG AGCATTTTGA CTTTACTTAA AATACCTGAC ATTGAGCCAT ACTTCCATAA      3120

AGTCGTTCTA CTAAGTGGCG CACTACGATT AGACACCCTT GAGAGTGCAC GCAATAAAGC      3180

ACAACATTTC CAAAAAATGA TGCTCGATTA TTTAGATACA GATGATGTTA CATCATTATC      3240

GACAAATGAT ATTCTTATGC TGATGGCGAA gcTAAAACAA TCTCGAGGAC CTTCTAAAGG      3300

GCTTGATTTA ATATATGCGC CTATTAAAAC AGATTATATA CAAAATAATT ATCCAACAAC      3360

GAAACCAATT TTTGCATGTT ATACAAAAGA TGAAGGCGAT ATTTATATTA CTAGTGAACA      3420

GAAAAAATTA TCGCCGCAAC GCTTTATCGA CATTATGGAA TTAAATGATA TTCCTTTAAA      3480

ATACGAAGAT GTTCAGACGG CGAAGcAACA ATCTTTAGCG ATTACACATT GTTATTTCaA      3540

ACAGCCGATG aAGCAATTTT TACmACmACT CAATATACmA GATTCCAACC GCACCAACTA      3600

TGGCTT                                                                3606
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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 15109 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

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GAAATTAAAA AAGCAATTGG nACAAGATGC AACAGTGTCA TTGTTTGATG AATTTGATAA        60

AAAATTATAC ACTTACGGCG ATAACTGGGG TCGTGGTGGA GAAGTATTAT ATCAAGCATT       120

TGGTTTGAAA ATGCAACsAG AACAACAAAA GTTAACTGCA AAAGCAGGTT GGGCTGAAGT       180

GAAACAAGAA GAAATTGAAA AATATGCTGG TGATTACATT GTGAGTACAA GTGAAGGTAA       240

ACCTACACCA GGATACGAAT CAACAAACAT GTGGaAGAAT TTGAAAGCTA CTAAAGAAGG       300

ACATATTGTT AAAGTTGATG CTGGTACATA CTGGTACAAC GATCCTTATA CATTAGATTT       360

CATGCGTAAA GATTTAAAAG AmAAATTAAT TAAAGCTGCA AAATAATTCA GCTATATAAG       420

TTAGTGAAAT GAGAGTCTGA AACATATCAA TCTTTTGATA TTGTATTAGG CTCTTATTTT       480

TATAGCTAGA AAGTTAGATA TTTGTATTTT TTTAAATAAT AAGTGCCGTT GTTATCGTTC       540

AATTTAATTA ATGATAGATT AGTATTATTA TAGCTAAAGT AGTATACCTG AGAAAATAGC       600

TCAATGTATC TCTTTATTAA TAAGTTATAT CATAATTATT TTAGTGCATA CTTTATGGAA       660

GGGATATCAG GGAATGGCTT TCAATTAAAG AAGAGGTTTA AAAGGATTAC AACAGAATGT       720

TATGATTTTG TAGAAAGATA TATAACAACG TTTTATAAAA ACATAATATT GTTAATGGAA       780

AATGAAATGT AAGGGGGATT TCGAGTGACT AAGAAAGTTT ATTTTAACCA CGATGGTGGT       840

GTAGATGATT TAGTATCTCT ATTTTTATTA TTACAAATGG AAAACGTTCA ATTGATAGGG       900

GTCAGTACAA TTGGTGCTGA TTGTTATTTA GAGCCATCTT TGAGCGCATC AGTAAAAATT       960

ATTAATCGTT TTTCAAATGA AGATATTCAA GTTGCGCCAT CATATGAACG AGGAAAAAAT      1020

CCATTTCCTA AAGAATGGCG TATGCATGCC TTTTTTATGG ACGCATTGCC AATTTTAAAT      1080

GAGCCAGTCA AACATGTTGC TTCAAATGTG AGCGACAAAG AAGCCTTTGA AGACATTATT      1140

CAAACTTTAA AGAGACAATC AGAAAAAGTA ACATTATTAT TTACAGGCCC GCTTACAGAT      1200

TTAGCAAAAG CACTACAAAA AGATTCATCT ATCGTTCAGT ATATAGAAAA ATTAGTTTGG      1260

ATGGGTGGCA CCTTTTTACC AAAAGGAAAT GTTGAAGAAC CTGAGCATGA TGGTTCTGCA      1320

GAATGGAATG CATATTGGGA TCCAGAAGCG GTTAAAATTG TTTTTGATAG CGATATAGAG      1380

ATTGATATGG TTGCTTTAGA AAGTACGAAT CAAGTACCGC TAACGTTAGA TGTTAGACAA      1440
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GTACCACCAT TAACACACTT TATAACAAAT TCTACTTACT TTTTATGGGA TGTTTTAACG      1560

ACTGCTTATA TTGGTAACAA GGACTTGGTT CATTCAATTG AGAAAAAAGT CGATGTAATA      1620

AGTTATGGAC CAAGTCAAGG TAAGACATTT GAGTGTAAAG ATGGGCGCAA AATTAATGTC      1680

ATAAATCATG TAGATAACAA CGCATTTTTT GATTATATAA CTGCACTTGC TAAAAAAGTA      1740

AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT TATTGTAAAC      1800

TTTTCATTTC TTAAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA CGAAAGGAAG      1860

TAAAAAATGA CAACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT TATCGCTATT      1920

TTAGGATTGG TACCGGTAAT TCCACTACCA TTTTCTTCAG TACCAATTGT ACTTCAAAAC      1980

ATTGGTATTT TCTTAGCAGG TGCGATTTTA GGACGTAAAT ATGGCACATT AAGTGTTATC      2040

GTCTTTTTAT TATTAGTAGT TGCTGGCTTG CCATTGTTAT CAGGTGGTCG CGGTGGCATC      2100

GGTGTATTCG CAGGTCCTTC AGCAGGGTTT TTACTATTAT ATCCAGTTGT AGCATTCATG      2160

ATTGGGGCGA TTCGAGATAG ATTCATCAAT GAAATTAATT TCTGGATTTT ATTCGTTGGT      2220

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TTAAAAGCAA TTGTAGCAAG TTTGATTGGT ACAGCTTTAC TTAATCACTC GCAGTTTCGT      2400

CAAATTATGG GAATAAAATA ATCATATTTA AGATAGTAAA GTAATTGAAT AAGTTGCTTT      2460

GAAATTTATA AAAGTGAAAG GAGTAGGTGT CAATGGCTAG TATAAGTATG TCAGATATAT      2520

ATTGTAACGG CACTATATTT GAAAATGACG ACGAGCAGTT GATTTATTTA ACGCCTTCTT      2580

TTCCACAACG ATACACAAGT AACACATGGA TATATAAAAA GACGCCTACC CAAGAGCGAT      2640

GGCTGAAAGA CTTAGAACGT CAACATCAAT TACATACAAA TCAAGGTTCA AATCATTATG      2700

CGTTTAGTTT CCCGGAAAAT GAACAACTTG ATAATCATTG GATGGCTATG TTTAAAGATA      2760

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ATGAACCTAT TGGCGTTGTA GATGTCATTG AAAGTGAAAA TTACATTGAA TTAGATGGAT      3060

TTGGTGTATT AGAACAATTT CGGCACCAAG GAATTGGATC TACAATTCAA TCGTTGATAG      3120

GTGAATACGC CATATCAAAA AATCACAAAC CAATCATATT AGTTGCAGAT GGTGAAGATA      3180

CAGCAAAAGA TATGTATGCA AAGCAAGGTT ATGTCTATCA ATCGTTTTGT TATCAAATAT      3240
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TAAGCTGGTT TCGAGTAGAA ATCAACTTAC TGCTTTTTAA ATTGTTTTGA GCTACTTATA      3360

CTTATAAAAA TAGTGCGTTT AAATTGTTGA TTCATGTAGA ATATCGTTCA TTATGACACA      3420

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AAGCCACCAT TTCGAATAAA TCCAACTGCC GTAATATTTA GGTCATTAGC TAAGGTTACA      3540

GCAAGCGTTG TCGGAGCTGA TTTAGATAAA ATGACGCCAA CACCAATTTT TGCGGCTTTA      3600

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TGTCGCTGAA TACAAAATCC ATATAATTTA TCTAGAGCGT TATGTCTACC AATGTCTTGT      3720

CGATGTACAA AAAATGTCAA ACCATCGCTT ATAGCAGCAT TATGTAAGCC ACCTGTTTCT      3780

TGGTAAATAT GACTTGCACT TTGTAATCGA GTCATCATGT TAATAATTTG CATTGGAGTT      3840

AAAGTGATTT TAGACATAGA TGTTTTAGCG ATAGCAGCAT CATTTTGAAA ATAAAACTCA      3900

CGACTCTTTC CGCAACAAGA TGCAATCATT CGTTTTGTGG AATATTGAAA GCGATCGCCT      3960

AAATCTTTAT TAAGTTCAAC ATGGGCAAAA CCTTTACTAT CATCAATCAG TACAGATTTT      4020

AATTCATCTC GCTTTAAAAT GGCACCTTCC GAAGCCAGAA ATCCAATGAC TAACTCCTCA      4080

AGGTTTGTTG GACTGCATAT AACAGTCGCA AATTCTTCAC CATTCACCAT AATTGTAAGT      4140

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ACCAAGAAAT TAGCTTCAGA ATTTAAAAAA GAGCATAAAA ATGCTGATAT TAAATTTAAC      4740

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CGAAATATG CGAACAGTA TTTAGATAAC AATAACTTAT TTAAAGAAGT CGAAAGTAAA      5040
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CAAGGTTTTG TGTATAAAAC TGACTTATAT AAACAAAATA AAAAAATTGA TACTGTAAAA   5160

GTAATTAAAG AAGTAGAACT TAAGAAGCCA ATCACATACG AAGCTGGTGC TACATCAGAT   5220

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CAATGTGAAA TATCAATTAA AGAACACTTT AATTCGCATC AATATAGATG ATACTGAACC   6060

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TGCCGGATTA CGTAAAGCAG ATGAAGCTAT TATCGAAGTG AATGGGCAAT TACTTACTGA   6180

TACGGCAAAA AACGTGAATG TTAAAATTCA ACAACGACGT ATTGGATATC TGTTTCAAGA   6240

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TGAACACATC GATCAATTAA TTCAAACTTT AAACATTGAT CATTTGATGA AACAATATCC   6360

TATGACATTG TCAGGTGGAG AGGCACAACG TGTAGCACTT GCACGTGCAC TTAGCACrAA   6420

ACCAGATTTA ATTTTATTAG ATGAACCTTT TTCTAGTTTG GATGATACTA CAAAAGATGA   6480

GAGTATTACA TTAGTTAAAC GTATTTTCAA CGAATGGCAA ATACCAATCA TATTTGTGAC   6540

ACATTCAAAC TATGAAGCAG AACAAATGGC TCATGAAATT ATTACAATTG GGTAATCATT   6600

TATTTGCCAT TAAAGAGTTT AGAACGTATT TAAAATTGTA GAAGTGAATG CTTCTATCAG   6660

CATTTTAATG ATGTTTTAAA CTCTTTTTTA GGGGCAGTTT TTTTGAGAGA CATTGACGCG   6720

CGTCATATAA TGAAAGTAAT GATAAAAAGA AAGGATAACT TAATGTGAGT CAAGAACGTT   6780

ATTCAAGGCA AATTTTATTT AAACAAATAG GTGAAATAGG TCAAAGCAAA ATAAATCAAA   6840

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GAGCAGGCAT TGCCAAACTA ATCATTGTTG ATAGAGATTA TATTGAATTT AGTAATTTAC    6960

AAAGACAAAC ATTGTTTACT GAAGAAGATG CTTTGAAAAT GATGCCTAAG GTGGTTGCAG    7020

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TGGATTATTA TTTTTTGGAA ACACATGGAC AGGACGTTGA CGTTATTATT GATGCAACCG    7140

ATAACTTTGA AACACGACAA CTGATTAATG ATTTTGCATA TAAATATCGT ATACCTTGGA    7200

TTTATGGTGG TGTTGTACAG AGTACATATA CAGAAGCTGC ATTTATACCT GGTAAAACAC    7260

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TATTAACGGA ACAACCAATT GACACAAAAA TAACTTATGG CGATATTTGG GAAGGTAGTC    7440

ATTATTCATT TGGTTTCAGT AAAATGCAAC GTTCAGACTG TACAACTTGT GGAGATGTAC    7500

CAAGTTATCC GTATTTAAAC AAGAATGAAC AACGTTATGC AACATTGTGT GGTAGAGACA    7560

CTGTACAGTA TGAAAATGCA TCAATTACAC ACGACATTCT TGTTCAATTT TTAAAACAAC    7620

ATCAGTTAAA TTATCGCAGT AATTCGTATA TGGTTATGTT TGAATTTAAA GGACACCGCA    7680

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CAGGATCAAC AGGCGCAGTT AAATTAGCAT TAGAAAAGCT CATTAAACCA GAATTAAATC    8280

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TTTCGTCATG TCGTAAATGG TTAAAGCCGT TGCTGATGCA GCGGTTAAAG CTTCCATTTC    8460

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ATTTGTTTCA TCCCAGCTGA AGTGAACATC TATGCCAGTC AATGGTAATG GATGGCACAT    8580

CGGAATAAGT GTTGATGTAT TTTTGGCAGC CATAATACCA GCGATTTGAG CAGTGTTCAA    8640
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TGATAAAGGT CCATTAGCAG GAATTTATAC AATCATGAAG CAACATCCTG AAGAAGAATT      11580

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GATGGGATTT CAGTAAAGTT GTAACTAAAG ATGAAATGCT TACAATGATA GAGCAGCACT      12600

TTGAAATCGA TCCTGTAGAA CCAAAATATT TTGGGGAAGT AGCAAAATAT TATCGCCATA      12660

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GGGAGTTAAG TCAGTTAAAG CACTGGTTAA AAACAACACA TAAGATTTCA ATTGAAGAAT      13740

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TCTATAGTAC TTCTCAAAAG AAAATTGTTAG ATAAAATTAC TAAAGAAATA GAAGTGTTAA     13980

GCGTTACAAA CTAAAAACTT aAAAAgcaTG CCAATCTCTA TTCATCATAA TTGCGTCTTG      14040
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    GATTGCTAAA GCGGCCATAA AGCCGAAGAT TTCACTATAT GAAAACATAT GAGTAAATAA      14220

    CCCAAGGAAT GATGGACCGA AGCCGACACC TGCATCTAGA CCAACGTAAA AAGTAGATGT      14280

    CGCGATACCA TATTTAATCG GGGGTGAGAC TTTTATCGCA ATAGATTGCA TTGCAGATGA      14340

    TAAATTTCCA TACCCTAAAC CTAGGCAAGC ACCAGCAAGT AATATTAACC AGCTTTGATA      14400

    GCTTGAAATT AAGCATACAA ATGAAAGGAA AAGCATGATA AATGCTGGGT AGACAATAAT      14460

    ATTTTCATTT TTATCATCCA TCAATCTACC AGCAATAGGT CTAGTAATTA ACGATGCTAT      14520

    AGCATAGCAA ATAAAGAAAT AGCTTGCTGC AGTGACTAGG TGTCGCTCTA AAGCAAATGC      14580

    TTGTAAATAA GTTAGGATGG ACGCATAGGT AACGCCAATT AAAAGCATAA TTACAGCAAC      14640

    AGGAATGGCC TCTTTTGCAA TAAATTGATG AATACTAAAT CTTGGTTTAT CAATGACATT      14700

    AGTTTCAGTT TTGTTATTTG TTACTTCGAA ATCAACTTTT ATAAATAATG AGATAATGAG      14760

    TCCGAGTATG CCTAATATGA CACAAATAAT AAACAGTAAG TCAATTGCGT ATTTTGTAAT      14820

    AAGTAACATG CCTAGAAATG GGCCAATCGC TGTACCTAAT ACTAAACTTA AGGAAAATAA      14880

    ACTGATGCCT TCACTTTTTC TATTAACAGG GGTAACGTAT GCCGCAATAG TACCTGTTGC      14940

    AGTTGTCACA ACTGCAGTTG CGATACCGTT TATGAGACGT ACAAAGATTA AAAAAGCTAA      15000

    AGATCCATCA ATAAAATAAA GTAATTGCGT GATAATTAAA GCAATTAAAC CAATAAATAA      15060

    TAATCGTTTA GGTCCrATTT sATTTACAAA TTTACCTGTA GCAAATCGA                  15109
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(2) INFORMATION FOR SEQ ID NO: 45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9072 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

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    GAGAGTCAAT GGCAAGAAGA ATATAAATAT TTGAGAGCGT TAATCTTTAA TGAAACAGAA       60

    TTAGAGGAAG CGTATAAATG GATGCATCCT TGTTACACGT TGAATAATAA AAATGTAGTA      120

    CTTATCCATG GCTTCAAAAA TTATGTTGCA CTATTATTTC ATAAAGGTGC CATTTTGGAG      180

    GATAAATATC ATACACTCAT TCAACAGACT GAAAAGGTGC AAGCAGCTCG TCAGTTACGA      240

    TTTGAAAATT TAACAGAGAT TCAAGCACGT ACCGAAGAAA TTAAATATTA TCTAGCCGAA      300

    GCAATTAAAG CTGAAAAAGC TGGTAAAAAA GTTGAAATGA AGAAAACAGA GGAATATGTT      360
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AAAATTAACGC CAGGCAGACA ACATCAATAT ATATATCATA TTGGACAAGC TAAACGCAgT    480

GgAACAAGAC AAAAGCGTGT TGAAAAGTAT ATTAACCAAA TACTAGAAGG TAAAGGGATG    540

CATGATAAGT AATTAATGAG TAAAGCATAC CGGTTATACA ACAACATACA AGATGACACG    600

AAACAACCAA TGGCTCATGC TGTTGGTTGT TTTTTAGGT GTGTCTGTCA TGGGCAACAC    660

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GTCTACAATG AATGATGAAG ATATTAAAAT ATAAGGATGA CTTTGTGAGT GGCGGATGGG    780

CGGTTGTCCG TCTGTAACAA TGGATGCGTG TGCATTATTA CAAAAATTCG ACTTTTGTAA    840

TAATATTTCA CATTTTCGAC ACTTTTTTGC TATAAAACAA CCAATTGAGC GATAATAAAT    900

TCGCTTTTAA AAAATATGAG TTATCTATTT AGTTGCCAAA GATAAAATAA TAATGTTTAA    960

TAACATCATA TAGAGTATGT TAGTTTTAAA TGTCGAATAT ACGAATGTGc AAACAAAGTA    1020

ATCGGTAGAA ATTCAACATA CATAGCGCCG TTTACTGTTA AGTATTCACA TTACAGATGA    1080

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GATTTTATAG GACAAAATAG ACTGATTCAA GACCGTCCCA ATGACAAGAC TGTAGAAGGT    1980

GTAATGATTA AACCAATCAC GATACAAGCA GAAGCAACAC TGAATGACGC CGTTCATATT    2040

ATGAGACAAA AACGTGTTGA TACTATTTTT GTAGTAGATA GTAATAACCA TTTACTAGGT    2100

TTCTTAGACA TTGAAGATAT AAATCAGGGT ATACGTGGAC ACAAAAGTTT ACGAGACACC    2160
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ATTTTAAAAA GAAACGTTAG GAATGTACCT GTCGTAGATG ATCAACAGCG TTTAGTAGGA     2280

CTGATTACGC GTGCCAATGT TGTTGATATT GTATATGACA CGATTTGGGG CGATAGTGAG     2340

GATACAGTGC AAACAGAACA TGTGGGGGAA GACAcTGCGT CCTCAAAAGT GCATGAGCAA     2400

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CGTTATTGGT TTAGTCATTT TAGTAGTGAC GATGTTAAGT TTAAATGTAA TCATCACACA      5700

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ATTAAATATA ACGATTAATG GAGAGGCATT CGAGTTAAAC ATTCCGATGT ATCATTTTAA    6840

TGATCAACCG GACGAAAGCA TTTACGATGT TGTCTTTCTA TTTCCAAAGT CTATGCAATT    6900

AAAAGAAGTG ATGGAAGATA TGAAGCCACA TATTGATAAT GAAACGATCG TCGTATGTAC    6960

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AGAAATAGTG CATGTAGCGA CGATTGATAA TGTTCATTTA AATGTTGATG AAGTATTTGA    7380

ATATTTAGTT GATTTAAATG AAAAAGTTGG TGCGCATTAT CCATCCATGT ATCAAGATTT    7440

AATTGTTAAT AATAGAAAAA CTGAAATTGA TTATATTAAT GGCGCAGTTG CAACATTAGG    7500

TAAACAACGT CaTATTGAAG CGCCAGTCAA TCGCTTTATT ACTGATTTAA TTCATACTAA    7560
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CAATCACGTG ATATTACGGT CATTATTAAG ATTGAAATGT AATAAATAAA GAACAGCAGT          7680

AAGGTACTTT CAAATTGAAA TGATCTTGGT GCTGTTTTTC TTGATTGATC TTCGTCATAA          7740

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TAATTTCTAT TGGTAGCCAA GTCAGTACAA AAGACCAATT ATTGCTACCG AGAATGAGAT          9000

ATGGTAATGC ATATAATATG AGCGCTAAAG CGATACATAT ACATAATGAT AACCAACTCA          9060

ATACAGCAAT CC                                                             9072
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(2) INFORMATION FOR SEQ ID NO: 46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16826 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

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GTGGAACAGC TGTAACTATA TCATTTCTTT CAACATTTAT TGGGAAAATG TTAGCTACAT      60

TTCTATATCC GATTAATAAT GTAGTACTTT CATATATnTC TGTAAATGAA AGTGACAATA     120

TAAAGAAGCA ATATTTGaAA ACTAATCTAA TTGCTATAGC TGCCCTATGT TTAGTCATGA     180

TTATATGTTA TCCAATTACA ATAATTATTG TCTCTTTACT GTATAACATT GATTCAAGTT     240

TATATTCGAA GTTTATTATT TTAGGTAATA TAGGTGTTTT ATTCAATGCA GTGAGTATTA     300

TGATCCAAAC TTTAAATACA AAACACGCAT CAATAACATT ACAAGCGAAT TATATGACGC     360

TTCACACGAT TACATTTATA TTCATAACTA TTTTAATGAC AATTGCGTTT GGTCTAAATG     420

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TGGCGGAAGA TTTAATTGCG AATCACATTA ATGTCGATGT CATGTGTGGA TGGCCATATG     660

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GGTGTGCATC ACTAATGAGA AAAAATATTT TAATTACAGG CGTACATGGA TATATCGGTA   2340

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TCAAATTAGT ATTGAAGAAC CTGGATTACA AGAGGTTTAT GAAGAGGTAC TGTCATCGGG   3420

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AGACGCATCG CTAGTATTGA TTTTAAGTGA CCACTCAGAA TTTAAAAATT TATCGGACAG      4380

TCATTTTGAT AAAATGAAGC ATAAAGTGAT TTTTGATACA AAAAATGTTG TGAAATCATC      4440

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AGTGAGTGAC GATGAAAAGG TTAAGCATAA TCGTCATCAT TGGAATCTTT ATAATTACAG   12120
GATGTGATTG GCAAAGGACG TCTAAAGAAC GGTCTAAAAA TGCCCAAAAT CAGCAAGTGA   12180
TTAAAATTGG ATATTTGCCG ATTACACATT CAGCTAATTT GATGATGACT AAAAAATTAT   12240
TATCACAATA CAATCATCCG AAATATAAAC TAGAATTAGT TAAATTCAAT AATTGGCCAG   12300
ATTTAATGGA CGCATTAAAC AGTGGTCGTA TTGATGGTGC ATCAACTTTA ATAGAGCTAG   12360
CGATGAAATC AAAACAGAAG GGCTCAAATA TAAAGGCTGT GGCATTGGGC CATCATGAAG   12420
GCAATGTCAT TATGGGACAA AAAGGTATGC ACTTAAATGA ATTTAATAAT AATGGCGATG   12480
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GTAAACAATT AAAGATTAAA CCGGGGCATT TTAGCTATCA TGAAATGTCG CCAGCAGAAA    12600

TGCCAGCCGC ATTGAGTGAA CACAGAATTA CAGGGTATTC TGTAGCCGAA CCATTCGGTG    12660

CACTGGGTGA AAAGTTAGGC AAAGGTAAGA CTTTGAAACA TGGTGATGAC GTTATACCTG    12720

ATGCGTATTG CTGTGTGCTA GTACTGAGAG GGGAATTGCT TGATCAACAC AAGGATGTAG    12780

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TAATATTCAA GAAGACCATT ATTTTGGTGC GATTTCGAAA CATGAATCAT CAGATGAATT    14280
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TTCACATTTA AATGAATTAA TATCATTGAA GAAGGACATC GGCTATTTAT TGTTAGATGT      14700

AAATCAAGCT TCTGTTGTCA ATGGTGGTTC TAGAGCGTAC ACACCATATT CGCCACAAGT      14760

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GTTATATCCT TTTAACTAGG AAAATATACA TTTCGTAATA ATAATAATCG TTATCATTGA      15000

AAAAGTGTTA ATAAGGTGTA TAATGAAAAT GTGAACAATT AATGAACTTC TTATTTTAAA      15060

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CAGATAATGG TGAAGACTTA GATAAACATT TACCAGATAT GGATGTGATT ATTAGTGCGC      15780

CATTTTATCC TGCATATATG ACTCGTGAAC GTATTGAAAA AGCACCGAAC TTGAAATTAG      15840

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ATTTATTAAT ACTTCTTAGA AACTATGAAG AAGGTCATCG TCAATCAGTA GAAGGTGAAT      16020

GGAACTTGTC TCAAGTAGGT AATCATGCGC ATGAATTACA ACACAAAACA ATTGGTATTT      16080
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TACAAGGATA TGCTGGTGAT GTTTGGTATC CaCAACCtGC ACCTGCTGAT CATCCATGGA       16440

GAACAATGCC TAGAAATGCT ATGACGGTTC ACTATTCAGG TATGACTTTA GAAGCACAAA       16500

AACGTATTGA AGATGGAGTT AAAGATATTT TAGAGCGTTT CTTCAATCAT GAACCTTTCC       16560

AAGATAAAGA TATTATTGTT GCAAGTGGTC GTATTGCTAG TAAAAGTTAT ACAGCTAAAT       16620

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GCACTACTGC TGTTGTAAAG ATGGCAGTAG TTTTTTTATG ATTACATCTA AGTATAGTCA       16740

CGGCTATGTT AGGACAATGA TTTAACATTT ACGCACATAT GTGTTCACTT ACGCAATTAT       16800

TGAnAAATnT CATTCATGTG GnAATC                                           16826
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(2) INFORMATION FOR SEQ ID NO: 47:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 4012 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

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TTCAATGAGA GTAGTGGGCT GATGTTTAGC GATATCGCGT AAGATTAACC ATTGGCCATA         60

ATATATATTG TGTTTTTCTA AAATCGGCTC GGCTAATTTT AAATAGGGGC GATATATTGT        120

TATAAAACTA TTGAAAAATT CTTGTGATAG CATAGTGACA TCTCCTAAGA CAAAATAGTT        180

AGCTTAGCTA mCCTTTTTAC AACAATAGTA ATTATAAAAC GGGAGCAATT AGAAATCAAT        240

ATATAATTAT TAAGAGCAAA AATAATTATA CTTTGTTAAA ATAAGCGTAA TTACATGTAA        300

ATAGGGGGAT ACTAATGATA TTGAAATTTG aTCACATCAT TCATTATATA GATCAGTTAG        360

ATCGGTTTAG TTTTCCAGGA GATGTTATAA AATTACATTC AGGTGGGTAT CATCATAAAT        420

ATGGAACATT CAATAAATTA GGTTATATCA ATGAAAATTA TATTGAGCTA CTAGATGTAG        480

AAAATAATGA AAAGTTGAAA AAGATGGCAA AAACGATAGA mGGCGGAGTC GCTTTTGCTA        540

CTCAAATTGT TCAAGAGAAG TATGAGCAAG GCTTTAAAAA TATTTGTTTG CGTACAAATG        600

ATATAGAGGC AGTTAAAAAT AAACTACAAA GTGAGCAGGT TGAAGTAGTA GGGCCGATTC        660
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ATCAGGATGA TGATGAAATT AAGCCACCAT TTTTTATTCA ATGGGAAGAA AGTGATTCCA      780

TGCGTACTAA AAAATTGCAA AAATATTTTC AAAAACAATT TTCAATTGAA ACTGTTATTG      840

TGAAAAGTAA AAACCGATCA CAAACAGTAT CGAATTGGTT GAAATGGTTT GATATGGACA      900

TTGTAGAAGA GAATGACCAT TACACAGATT TGATTTTAAA AAATGATGAT ATTTATTTTA      960

GAATTGAAGA TGGTAAAGTT TCAAAATATC ATTCGGTTAT CATAAAAGAC GCACAAGCAA     1020

CTTCACCATA TTCAATTTTT ATCAGAGGTG CTATTTATCG CTTTGAACCA TTAGTATAAA     1080

TATACGTAAG TGCTATGAGC GAGAATGCCC ATATGAATAA TGACAAGCAC AATGGAAAGA     1140

ATCGTTAATA TATTATTTAA TCGTGATGAC TTAATTAAAA TGAAAAGAT TGATAATATA      1200

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TATATTTCGC GTGGTTTTGT TGTTGATTAT AGTAATAAAG AAGCGTTAAA TGCATTGTTA     1980

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GTAAAGTTGG ATCCAAAAGA AAATATAGCG AAAGTAAATC AAGAATTGAA TGAACTTCAT     2460
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CTAGAAGCTT TAGAAAAGGA ACATCCTGAA GGTATTTATC TTTCTGGTGC ACTATTAATG      2640

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ACTTACGATT TCGGTGGTAC AGATAATGAT CCAGATAAAG ACTCAGAACA TTATGGATTA      2820

TGGGCATTTA AAAAGTGTG GGGAACATAC TTAAGTGAAA AGATTGGTGA ATTTGATTAT      2880

GTATTGAATC AGCCATTGTA CCAATTAATT GAGCAAGTTA AACCGCGTTT AACAAAAGCT      2940

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TTATCAGGCA TCACCACAGC AAAATTCAAAG CGTCAGCnCC AATATATAGT GGATGCCGCA      3960

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(2) INFORMATION FOR SEQ ID NO: 48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7778 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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TAAGACAACA GTAGCGCTTC ACGCTATTGC TGAAGTACAA AGTAATGGCG GGGTGGCAGC         180

ATTTATCGAT GCTGAACATG CTTTAGATCC AGAATATGCT CAAGCATTAG GCGTAGATAT         240

CGATAATTTA TATTTATCGC AACCGGATCA TGGTGAACAA GGTCTTGAAA TCGCCGAAGC         300

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CATCAACCAA ATTCGTGAAA AAGTTGGTGT TATGTTCGGT AATCCAGAGA CTACACCAGG         540

TGGACGTGCA TTAAAATTCT ATAGTTCAGT AAGACTAGAA GTACGTCGTG CAGAACAGCT         600

TAAACAAGGA CAAGAAATTG TAGGTAATAG AACTAAAATT AAAGTCGTTA AAAATAAAGT         660

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GGATCAATAT TAATAGACAT GTATTTATTT ACAACTCCTA TTTATTTTGA TGTCTTAATA    3420

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5     AAATGCTGAA AATGCAGCAC ATGGTAAAGG TTTGACTGAA AAAATATATA AACAATTACT          3720

      AAGAAATGGT GTAGATTTCA TGACTATGGG TAATCACACA TATGGTCAAC GTGAAATTTA          3780

      TGATTTTATA GATGAAGCAA AACGACTAGT AAGACCAGCG AATTTTCCGG ATGAAGCGCC          3840
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      GGGAATTGGT ATGAGATTTA TACAAATTAA TGATATTAAA CTTGCAGTTA TTAATCTGCA          3900

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      AAAGTATGCA ATGGGATGGC ATTTAGATGG TAGAsTAGCG CTGTTGTTGG AACGCATACA          4080

      CACATTCAAA CAGCAGATGA ACGTATTTTA CCAAAGGGGA CAGGGTATAT AACGGATGTT          4140

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      GGTGTTGTTA TTGATTTAGA CAAAGAAGGT AAAACAAAGC ACATCGAACG TATATTGATA          4320

25    AATGATGACC ATCCATTTTC AACATTTTAA AATTACGTAA GTAAACATTC GAATTGGACC          4380

      CTATCGTCCA TTAGTATGAA TTTAATATAG TACCACTGTT TACATAGTAA ATCGGTGGTT          4440

      CTTTTTGTTA TCATTTAATA TGAAATATAT CCATAGGAGG CATATAACTA TGAAACCACA          4500

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      CGCTACGGCT ATGAATAGAA AAGGATATTA TTTATATGGA TATAGACATT TTTCAAGTCC          4620

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      TGAAATGAGA GAAGACAGTA TTATTTTArC TGATGCCAAG GCTAAACCTG TGAAaCCAGA          4800

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      AAATACATTT GAAGAACTTA TTACTAATAT GTTTTCTAAA AAAGGTGACA AGGTAGTTGA          4980

      AGTCAATATC CAAGCATTAA ACGAAGGTTA TCAATTAATG CAATCTCGCT TACCTGAAAT          5040
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      CTACGGGGAC TTTGAATTAG AGTCAACAGA TGCACTACCA CATCTATATA TGATTGGTAA          5100

      CGATGCCATT GGATTAGGTG CAATTGCTGC AGGTTCACAA TTTATGGCGG CATATCCTAT          5160

      TACACCTGCG TCTGAAGTTA TGGAATATAT GATTGCCAAT ATATCTAAAG TAAACGGAGC          5220
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      GGTTATTCAA ACAGAAGATG AAATTGCTGC TGTAACTATG GCTATTGGTG CAAATTATGG          5280
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TGGATTATCT GGTATGACTG AAACGCCATT AGTCATTATT AATACCCAAC GAGGTGGACC          5400

TTCTACTGGA TTACCTACGA AACAAGAACA GTCAGATTTA ATGCAAATGA TTTATGGTAC          5460

ACATGGTGAT ATTCCAAAAA TTGTTGTAGC ACCAACAGAT GCAGAAGATG CATTTTATTT          5520

AACTATGGAA GCATTTAATT TAGCAGAACA ATATCAATGC CCTGTTATAG TTCTAAGTGA          5580

TTTGCAATTA TCTTTAGGTA AACAAACTGT TGAAAAATTA GATTATAATC GTATTGAAAT          5640

TAAACGTGGT GAAATCATTC AATCTGATAT TGAACGTGAA GAAGATGATA AAGGTTATTT          5700

CAAGCGTTAT GCGTtAACAT CCGATGGTGT TTCTCCTAGA CCTATCCCCG GTGTTAAAGG          5760

AGGTATTCAT CATATAACTG GTGTGGAaCa CAATGAAGAA GGTAAACCTA GTGAATCTGC          5820

GTCAAATAGA CAACAACAAA TGGAAAAACG AATGCGTAAA ATTGAGCAGT TACTAATTGA          5880

ATCGCCAGTA GAAGCTAACT TACAACATGA GGATGCAGAT ATTCTTTATA TCGGTTTTAT          5940

TTCTACAAAA GGTGCAATTC AAGAAGGTAG TAACCGTTTG AATCAACAAG GCATAAAAGT          6000

TAACACTATA CAAATTAGAC AATTGCATCC ATTCCCAACA AGCGTTATTC AAGATGCAGT          6060

TAATAAAGCG AAGAAAGTCG TTGTAGTGGA GCACAATTAT CAAGGACAAT TGGCTAGTAT          6120

TATAAAAATG AATGTCAATA TTCATGATAA GATTGAAAAT TATACAAAGT ATGATGGGAC          6180

ACCTTTCCTA CCACATGAAA TCGAAGAAAA AGGCAAAATA ATTGCTACTG AAATAAAGGA          6240

GATGGTATAG ATGGCGACAT TTAAAGATTT TAGAAATAAT GTTAAGCCTA ACTGGTGCCC          6300

CGGATGTGGC GATTTCTCAG TACAAGCTGC AATTCAAAAA GCAGCCGCAA ATATAGGGTT          6360

AGAACCTGAA GAAGTAGCTA TCATCACCGG TATAGGATGT TCTGGCCGTC TTTCAGGATA          6420

TATTAATTCT TATGGCGTTC ATTCTATTCA CGGACGTGCA TTACCTTTAG CTCAAGGTGT          6480

AAAAATGGCG AATAAAGATT TAACTGTTAT TGCATCGGGA GGAGATGGTG ATGGTTATGC          6540

TATAGGTATG GGGCATACAA TCCATGCTTT AAGAAGAAAT ATGAACATGA CGTATATAGT          6600

CATGGATAAT CAAATTTATG GTTTGACAAA GGGACAAACA TCGCCGTCAT CAGCAGTAGG          6660

ATTTGTTACT AAAACAACGC CAAAAGGTAA TATAGAAAAA AATGTTGCGC CTTTAGAATT          6720

AGTATTATCA TCTGGTGCCA CATTTGTAGC CCAAGGTTTT TCAAGCGATA TTAAAGGATT          6780

AACAAAACTA ATTGAAGATG cAATTAATCA TGATGGATTT TCATTCGTTA ATGTCTTTTC          6840

ACCATGTGTG ACTTATAATA AAATTAACAC ATACGATTGG TTTaAAGAAC ATTTAACAAG          6900

TGTTGATGAc ATTGAAAATT ATGATTCTAC AGATAAACAA TTAGCGACTA AAACTGTTAT          6960

TGAACATGAA TCTTTAGTAA CTGGTATTGT TTATCaAGAT AAAGAAACAC CATCATATGA          7020

ATCtCAAATT AAAGAGTTAG ATGATmCACC ACTTGCTAAA AGAGATATCa AAATTaCTGA          7080
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TGTATTTATA ACAGATCCAT TTATGCTACT CAGTTTTTTA CTATTACAAA AAATAAAGGA        7200

GTTTTTAAAA ATGAAAGACA CATTAATGAG TATACAAATA ATTCCTAAAA CACCAAACAA        7260

TGACAATGTT ATACCTTACG TAGACGAGGC GATTAAAATA ATTGACGAAT CTGGTTTGCA        7320

TTTTAGAGTA GGTCCGTTAG AAACGACAGT ACAAGGAAAT ATGAATGAAT GTTTAATTTT        7380

AATACAATCA TTAAATGAAC GAATGGTGGA ACTTGAATGT CCAAGTATTA TTAGCCAAGT        7440

TAAGTTTTAT CATGTGCCAG ATGGCATCAC TATTGAAACT TTAACTGAAA AATATGATGA        7500

ATAACATTAA AAGTGAAGTA AACTGGATTT GAATTGGCTT GTTAGAGATG ACGTATAACT        7560

TTAACTGTTT TTGCACTTTA TAGTTAAATT TAATATAATT ATTAAATGAT ACGGGCAAAT        7620

AGAAAGGATT TTGTAAAGTG AACGAAGAAC AAAGAAAAGC AAGTTCTGTA GATGTTTTAG        7680

CTGAGAGAGA TAAGAAAGCA GAAAAGATT ATAGTAAATA TTTTGAACAT GTTTATCAGC        7740

CGCCTAATTT AAAAGCAAGC GCAAAAAAAG AGGTnAAA                               7778
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(2) INFORMATION FOR SEQ ID NO: 49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1128 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

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AGATGAAGTT GTTACgAAAA TTGCGTACGC TGTTTCAGAA CATGTCAAAA TAGAAACAGG         60

TAATCCATTC TTTCAAACAT CACATAGTGG TTGTGCGACG GGCGGATCCT GTAATTGTTC        120

ATTATAAAAA ACATCGAGTC AGAAAAAGGT GGTTATTGAA cCACTAACTA GCATCTGACT        180

CGATGTTTTT ATTTATTCGG GATTGTTTGT TTGAATTGTT GTGCTAAATC TGGTCGATCT        240

GTCACAATCG TGTGTGCACC TTTTTGGTAT AAATCATTCA TCAGATTTAT ACTATTTACG        300

CCATAATAGC CTGGAATGAT ATTCATATCA TTTAACCATT TGATAAAACG AGATGAAGTC        360

AAATCAATGC CTTTAAAATG AGTAGGCATT TGGAACGTTT GTGCTAATGG TTGGTAGTAC        420

CTACCACCTA ATAAATGATA TTTTAAAAAT GCTTCTGTAA CTTCCTGTTG GCTAGCACCA        480

ATTGCGACGG ATCCTTGTGC AATTTTATTA AAACGAACGA TTTGTTCTTT ATAAAAACTT        540

GTCACAAGAA CGCGGTCAAA TGCTTGATTT CTGCAATTG TATCAAACAT AATTTGTGGT        600

nCCATTCAGC CTTCATAGGA TTCAGGAGCA TCTTTTAAGT CTACGTTTAT ATACATATCA        660
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AATGTATGGG CACTAACTTT TCCAGAGCCG TTCGTCGTTC TATCAACAGT TGCGTCATGA          840

AAAACGATAA GCTGTTGATC TTTTGTGAGT CTCACATCTG TTTCAAAGCC ATCAACGCCT          900

AATTGTTTAG CATAGTCAAA TGCAAGTTGC GTTTGCTCTG GTCTTAAAGC CATACCACCG          960

CGATGCGCAA ATATATATGG TGCATTGCCT TTGAAAAAAG CAGGGATGGT TTGCTTTTTA         1020

GTAATCACTT TATTTTTATT GATCATTAAT AGACTACTTA AAAATCCAGC ACCGACTAGT         1080

ACCGCATTTA AAATGTTTCT GTTTACnTTT TTCATAAAAA ATTCCTCC                     1128
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(2) INFORMATION FOR SEQ ID NO: 50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6252 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

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CAAGCAAACA ATCGTCGATA AAATTGCTAA AATAATAAAA GTAATTCGAA CTTTCATCAT           60

GATCATCCTT TGTTTATAGA GTCAATATAA GTATGGAATA TGTTAGGTAT ATAGTCAAAT          120

GCGTCAACTA ATGGGAATTT TGGCATAGAT AGAGAATTTA AGGCAATTAA AAAGGCATCA          180

AACAGTAATA TGCTGCTTGA TGCCCAAATG ATGACTTTAG CTAAATTGAT TAGTCACTTT          240

TAAAGATAAA GAATTGTCAT GAATTAAAAC TCATGTAATG ATGTGTTACA TTTCGCAATG          300

ATGGCTTTCA GTTATTTATC GATAACATCA CTCTTGATAC CTTTAGATTT TAAGAAATCT          360

TTAATTTTAT CTTGTTGCTT TTTATTAACA TCACCGGCAT ATTTTGTTGG CACGTCGACA          420

ACATTGATTT TATTTTGCGG TTGATAGCTA AGCTTTTCAA TATCTTCATC AACATTGGCG          480

ATTGTACTAT TTAAAGCTTT GAAGTAATTC ATCATTAATT CAACGGGTTT CTTATATTCT          540

TTAGGAATAT TGTTTTCAGT GACAAATTTC TTGAAATGCA AATCGTTTTT AACAGCTAAG          600

TTAGATAAGT GGCTAAGTGT TTCTGCTTGT TTTTCAGTCA CTTTTGTTTG ACTGTCAATT          660

TGTTTATCTA GTTTATGTTG CATAATATAT TTGTTATCAA GTATATCGCT ATTTACAGAC          720

AAATACTTTT CTATAGCTTG CTTCATCTCT GCATCACTAA TATCACTATT TTTCTTATCT          780

GAGTTAAAGA TATCTTTTGT tTCTAATTTT TTAGCGCTTT TAGGTGCATG GATGCCAGTA          840

CTTGTATGAT GATCTTCGTT ATCAGATTGA TCGGACGCGC AACCTGTAAG AATTAATGTC          900

GATGCTAAAA ATGTACTTAG TAGTAATCTC TTTTTCATAA TGTAATATAA CTCCTTAGTT          960

TATCTTTAAT TGAAAAAATA TGTATTCATG TTTAATAGAG TAACATTGAA TTAGTTTGGA         1020
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TCTATCAATA ATGCATCATT TTGGACGTTG TTAAGGATAG CTTTATCTAT AAATAACTGC      1140

ATAATTGGTT GTACTAATTT AGACGTAGGT ATCGTACGTA AAAGCATAAT AATTTCGTTC      1200

ACATACTTTT CTTTCTCAAT ATCATTTTTC ATATTGATTT GTTTGCGAGA GGTACATACT      1260

TTAAGCATTA TCGCACATCT CGTTGTATAT ATTAAGTTTA TCATAACATG ATTTTATGTC      1320

GGGATAAAAA AATAACAGCA TCTTAACAAA TGTAAGATAC TGTCAGTGAA ATGAATGAAA      1380

CTTTAGTTTC TGaTAATATA GTCAAAGGCA TTTAATGCTG CATTTGCACC AGCGCCCATT      1440

GAAATGATAA TTTGTTTGTT CTTCTGATCT GTGACATCGC CAGCAGCAAA TATTCCAGGA      1500

ACATTCGTAT TATTGTTACG ATCAATCACA ATTTCACCAC GTTCGTTTAA TTCAACAGCA      1560

TCGTTTAACC ATGATGTGTT TGGAAGTAAA CCAATTTGAA CAAAGATACC ATCTAAGTTA      1620

AGTAGATGTT CTTCGCCGGT GTTCATGTCT TCGTAACGTA TACCTGTAAC ATGGTCTTCT      1680

CCGACAACTT CAGTAGTTTT GGCATTTGTT TTGATATCAA CATTTGATAA AGAACGTAAA      1740

CGATCTTGTA ACACGTTGTC TGCTTTTAAT TCGCTAGCGA ATTCGAATAA TGTAACATGA      1800

TTAACGATAC CAGCAAGGTC AATTGCTGCT TCAACCCCAG AGTTACCGCC ACCGATAACT      1860

GCTACGTCTT TATTTTCAAA TAGAGGTCCG TCACAGTGAG GGCAGAATGC AACACCTTTA      1920

TTAATCAATT GCTCTTCACC TGGAATGTTT AGCTTACGCC AACCTGCACC AGTAGCAATA      1980

ATGACTGTTT TACTTTCTAA GACAGCACCG TTTTCTAACG TAACTTTAAT TGCTTCGTCA      2040

GTCTTTTCGA TATCTGTAGC ACGTATACCT GTCATTGCAT CAATGTCATA TTGATCAATG      2100

TGCGCTGCTA AGTTAGAAGA AAAATTCAGAA CCAGTTGTTT CTTTAACAGT AATGAAGTTC     2160

TCAATACCAG CAGTATCATT AACTTGGCCA CCGATACGAT CAGCAACTAT ACCAGTACGT      2220

AAACCTTTAC GTGCTGTGTA AATCGCTGCA CTACCACTAG CAGGACCACC ACCAACGATT      2280

AAGACATCAT AAGGTTCTTT ATTTTCAAAC TCAGATGCAT CTGCCGTACT GCCTAGTTTC      2340

GAAAGAATAT CTTGGATTGT CATACGACCA TTGCCAAATT CTTCGCCATT TAAAAAGACA      2400

GCAGGGACTG CCATGATGTT TTCAGATTCT TCACGGAACA CTGCACCATC AATCATAGAA      2460

TGCGTGATGT TAGGGTTGAT CACACTCATT AAGTTAAGTG CTTGAACGAC ATCAGGACAT      2520

TTTTGACACG TTAAACTAAT GAATGTTTCA AAATGGAATG AACCTTCTAA TTTTTTAATT      2580

TGGTCAATGA TTGACTGTTT TTCTTTAGGT GCACGACCAC TAACCTGTAA AATTGCTAAA      2640

ACAAGTGAGT TAAACTCGTG ACCTAATGGA ATACCTGCAA ATGTTACACC TGTTTCTTCG      2700

CCAGGACGAT TGACTGAGAA ACTTGGTGTA CGTTTTAAAG ATTTTTCAGA AAGAGATAGT      2760
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TGTTGTTTTA AATCAGCATT AAGCATGGTT GTAATGCCTC CTTAGATTTT ACCTACTAAA      2940

TCTAAACCAG GTTGCAATGT TTTAGCGCCT TCTTCCCATT TAGCTGGGCA TACTTCGCCA      3000

GGGTTTTTAC GAACATATTG AGCTGCTTTG ATTTTGTGAG CTAATGTACT AGCGTCACGG      3060

CCAATTCCGT CAGCGTTAAT TTCAGATGCT TGTACAACAC CGTCTGGGTC GATAATGAAT      3120

GTACCACGTT GAGCTAAACC AGTAGCTTCA TCTAATACAT CAAAATTACG AGTGATTGTT      3180

TGTGATGGGT CACCAATCAT AGTGTAAGTG ATTTTGCTAA TTGCATCTGA ATGGTCATGC      3240

CATGCTTTGT GTACGAAGTG AGTATCAGTT GATACTGAGA ATACATTTAC GCCTAATTTT      3300

TGTAATTCTT CATATTGGTT TTGTAAGTCT TCTAATTCAG TTGGACAAAC GAATGAGAAG      3360

TCAGCAGGAT AGAAGCATAC TACGCTCCAA GAACCTTTTA AATCTTCTTG TGTAACTTCT      3420

TTAAATTGAT CTTTTTTTGG ATCGAAArCT TGCGCTGTAA ATGGTAAGAT TTCTTTGTTA      3480

ATTAATGACA TAAATATCTT CCTCCTAAGA ATTTAAGTAT GAATTAGAAC TATCAATTGA      3540

TTGCGCTTAA TTATAATAAT TCTAATCTCT TAGTTAGCAT TATTACATTT TGATCCAGAA      3600

TAGTCAACTG GATAACTTTG TAAAGTGAAT GATTACTTTT AAAATAAAGA AAGATAATAT      3660

AAAGTGCTTT GATAATGGAT TTTGTAGTTG ATGATTTAAA AGGTTGTGTC TATATTTAAT      3720

ATCTTGATTT TAATGTAAAA AATGTAAAAA AAGAAGATTT GTATTCTCAA CTAAGTCAAC      3780

CTTATTGATA ATGGTATGAG AATATTTGTT CGAGATGGAT GAAGGTAATG AGTGAGAAAC      3840

TGGATTTTTA AAGTATGAGA CAATATTTTA AAAAGTTCAA TTATTAACTT ATAAGCAAAT      3900

AATTGCTATA AAAAAGTTTG GACGTGTACA ATTGCAATAT GAAGATTTTA AATTAATTGT      3960

AAAGTATCGA GGAGTGGGTA ACGTGTCAGA ACATGTATAT AATCTTGTGA AAAAGCATCA      4020

TTCTGTTAGA AAATTTAAGA ATAAACCTTT AAGTGAAGAC GTTGTTAAGA AATTGGTAGA      4080

AGCTGGACAA AGCGCTTCGA CGTCAAGTTT CCTGCAAGCA TACTCAATTA TTGGTATCGA      4140

CGATGAGAAG ATTAAAGAAA ATTTACGAGA AGTTTCTGGA CAACCTTATG TTGTAGAAAA      4200

TGGCTATTTA TTCGTCTTTG TTATTGATTA TTATCGTCAT CATTTAGTTG ATCAACATGC      4260

TGAAACTGAT ATGGAAAATG CATATGGTTC AACGGAAGGT TTGCTAGTAG GTGCAATCGA      4320

TGCAGCATTA GTTGCCGAAA ATATTGCGGT AACTGCTGAA GATATGGGGT ATGGCATTGT      4380

CTTTTTAGGA TCATTAAGAA ATGATGTTGA ACGCGTTCGA GAAATTTTAG ACTTACCTGA      4440

CTATGTCTTC CCGGTATTTG GTATGGCAGT AGGGGAACCc GCAGATGACG AAAATGGTGC      4500

AGCCAAGCCA CGCTTACCAT TTGACCATGT CTTCCATCAT AATAAGTATC ATGCTGATAA      4560

GGAAACACAG TATGCACAAA TGGCAGATTA CGACCAGACA ATCAGCGAGT ACTATGATCA      4620
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CAAAGCAAGA TTAGATATGT TAGAACAATT GCAAAAATCA GGCTTAATAC AGCGATAgCA        4740

AGATACCAAA ATAACCCGCC CCCCTCTAGC TTAAAATGAT AAGTATAGCT AGAGGGGGCG        4800

GGTATTTCTT GCAATGAATT AGTGTGAAGT TAATGCAGCA TTATCATTTG AATCGAAAGT        4860

ATCTTTATCC CAATGTTTAG TTAACTTGGC GGTACCTGTA CCAGCTAGCA TTGAATCGTT        4920

CACGTTTAAT GCTGTTCTAC CCATGTCAAT CAATGGTTCA ACGGAGATGA GCACGCCGGc        4980

TAAAGCGACT GGCAAGTTTA ACGTTGACAA CACCAATATG GATGCAAATG TAGCCCCGCC        5040

ACCGACGCCA GCAACGCCGA ATGAACTAAT AATCACGACA GCGATTAACG TTACAATAAA        5100

TTGTAAATCA ATTTCTACAT TAGCGACGGG TGCGACCATA ATTGCAAGCA TGGCAGGGTA        5160

AATGCCTGCA CAACCATTTT GTCCAATCGA CAATCCAAAT GTCGCAGCGA AATTGGCAAT        5220

ACCTTCTGGC ACGCCTAGAC GTCTTGTTTG TGTTTGTACA TTCAATGGTA AGGCACCCGC        5280

GCTTGAGCGT GATGTGAATG CAAAGATTAA TACTTCCAAA GTCTTTTTAA CATAGCGAAT        5340

TGGGCTAATA CCTAACAGGC TTAAAATAAT TAAGTGAATG ATATACATCG TAATTAATGC        5400

AGCGTACGAT GCGATTAAGA ATTTTCCTAA AGTCCAAATG GCGCCAAAGT CACTTGTCGA        5460

TAATGTGTTG GCCATAATTG CTAATACACC GTATGGCGTT AAACGTAAGA CGAACGTCAC        5520

AATCGCCATT ACTAGTGAAT AGATAGCGTC AATCGCACGC TTAAGCAATT CACCATGATC        5580

AGGTTGTTTG CGTnTACGCG TAAATAAGCA AATCCTATAA ACGAAGCAAA TATCACGACA        5640

GCAATCGTGG aAGTTGCACG TTGTCCaGTG AAATCTAAGA ATGGATTTTT AGGCAATAAT        5700

TCCAAAATTT GTTGTGGTAA CGTATGTGCT GTTAAATCTT TCGCTTGTTT AGCAATTTCG        5760

CTTCCACGTG CTTGTTCAGC GTTACCAAGG TTAATTGTTG ATGCATCTAA ACCAAACACC        5820

AAGGCATACA CAACACCAAC AATCGCAGCA ATGGTGACAG TGCCAATTAA AAAGATAAAA        5880

ATGAGACTAC CAATTTTAGC AAACTTTTCT CCGATTTGAA TTTTAGTGAA TGCAGCTACA        5940

ATAGAAATGA AAATTAAAGG CATAACAATC ATTTGCAACA ATGCAACGTA ACCTTGTCCG        6000

ACAATGTTGA ACCAGTCACT TGTTGATGTA ATAACATTCG AATGTGTGCC ATAAATAAGA        6060

TGCAATAACA CACCGAATAC TATACCAATC CCTAAAGCTG TAAACACACG TTTCGCAAAA        6120

GATATATGTT TGCGAGCCAT CATGTGCAAT ATTACGATGA AAATCACCAA TACAATAATA        6180

TTAATCAGTG TAAGAAAAGC ATTCATGAAC GTCACTCCTT AAATTTTTGA ATATAATTCC        6240

GACTAGTATG CT                                                          6252
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(2) INFORMATION FOR SEQ ID NO: 51:

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

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ATCAAATCnC AAAATATTTA TTAATnAnAA GGGGATTATC CaTGTgAGAA ACAAAGTAAT      60

GCTCTTTTTT TACCTCTTGT GGGTTGAAAA aTGGATCATC AGAGATAGAC TTCTTCTTTT     120

TCGAAGATGA CATTTGATAC TTTAATCTTC TAAAACCATA ACTTGTCGCA TCAAAAATGC     180

CTTCTTGTAC AAGTAAAATC AAAAATATGC TAATAAAAAT AATTAATGAA ACATAAAACA     240

ATATATTTAA ATATGTAATG ATAGTATGGC TATTAAAAAG CCATATAATA AACGTTAATA     300

TTGGCGTTAT TAGTGCCATT CCAAGCCATT TTTTCAACAT TTGATCACTC CCACTTATAG     360

AAAACTCTTA CGCATAGTTT ACATTAAAAT CAGACATTGA GGAATGATTT TTTAATTTCT     420

TCAGCTTTAT TGAAATTCTA AAATCAATCA TTCTTCATTA GTTTAAAGCA AAAAAATATT     480

GATATATAGT AAATATTGTA TATATAATAT TAGTTAAGAT TTCaGAAAAT TTTGAAGGGA     540

ATGGAAATTT AGAAATCGGA ATTTGTTAGA GGAGGGGATT AGATGGGGAA ATATATTTTC     600

AAACGATTTA TTTATATGCT TATTTCTTTA TTTATTATTA TTACAATTAC ATTTTTCTTA     660

ATGAAATTAA TGCCAGGTTC GCCATTTAAC GATGCTAAAT TAAATGCTGA ACAAAAAGAA     720

ATTTTAAATG AAAAATATGG ATTAAATGAT CCTGtAGCTA CGCAgTATTT ACATTATTTA     780

AAAAATGTTG TTACAGGCGA TTTTGGTAAT TCATTCCAGT ATCATAATCA ACCTGTGTGG     840

GATTTGATTA AACCGAGACT ACTACCTTCT TTTGAAATGG GTCTTACAGC AATGTTCaTC     900

GGTGTGATAC TGGGACTTAT TTTAGGTGTT GCAGCAGCTA CTAAACAAAA TTCTTGGGTT     960

GACTATACAA CTACAGTTAT TTCAGTTATT GCAGTATCTG TACCATCTTT TGTACTTGCT    1020

GTACTTTTAC AATATGTATT TGCAGTTAAA TTAAGATGGT TCCCAGTAGC TGGATGGGAA    1080

GGTTTTTCGA CCGCGGTATT ACCGTCACTT GCATTATCTG CAGCTGTTTT AGCAACTGTC    1140

GCCAGATACA TAAGAGCAGA GATGATAGAG GTATTAAGTT CAGACTATAT TTTATTAGCG    1200

AGAGCTAAAG GTAATTCGAC AATGCGTGTA CTTTTTGGAC ATGCACTTAG AAATGCTTTA    1260

ATTCCAATTA TTACAATTAT CGTTCCCATG TTAGCAAGTA TTTTAACAGG CACTTTAACA    1320

ATTGAAAATA TTTTTGGAGT TCCTGGATTA GGGGATCAAT CGTACGTTC AATTACAACA     1380

AATGATTTCT CAGTAATCAT GGCAATCACA CTATTATTTA GCACACTGTT TATCGTTTCT    1440

ATTTTTATTG TAGATATTTT GTACGGTGTG ATAGATCCAC GAATTCGTGT TCcAAGgAGG    1500

TAAAAAATAA TGGCTGAAAA TAAAAACAAT TTGTCGATTA ACGACGATCA TTCTAATGCA    1560
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TGAATCAGGA ACCTGAAATG CAACGAGAAA GCAAAAACTT TTGGCAAGAT GCTTGGGCTC     1680

AGTTAAAACG AAATAAGTTA GCTGTTGTCG GTATGATAGG TTTAATTATC ATTGTAATAT     1740

TTGCTTTTAT CGGTCCAGTT ATAAATAAAC ATGATTATGC TGAACAAAAT GTAGAACATA     1800

GAAATCTTCC GGCAAAAATA CCTGTATTAG ACAAAGTTCC ATTTTTACCT TTTGATGGTA     1860

AAGATGCAGA TGGCAAGGAT GCTTATAAAG CAGCAAATGC TAAAGAAAAT TATTGGTTTG     1920

GTACTGATCA GTTGGGTCGA GATTTATGGA CAAGAACATG GAAAGGTGCT CAAATTTCAT     1980

TGTTTATCGG TGTTGTTGCA GCGATGTTAG ATATTTTTAT TGGTGTTGTA TATGGTGCGA     2040

TTTCTGGATT CTTCGGTGGA CGTGTCGATA CGATTATGCA ACGTATACTT GAAGTCATAG     2100

CATCTATTCC GAATTTAATT GTCGTAATTT TATTTGTATT AATTTTTGAA CCATCCATTT     2160

GGACAATTAT ATTGGCTATG TCTATCACAG GCTGGTTAGG CATGAGCAGA GTTGTACGTG     2220

GAGAATTTTT AAAATTAAAA AATCAAGAGT TTGTCATGGC TTCGAAAACA TTGGGGGCTT     2280

CAAAATTCAA ATTGATATTT AAGCATATTT TACCTAATAC ATTAGGTGCT ATCGTGGTTA     2340

CATCAATGTT TACAGTACCT AGTGCTATTT TCTTCGAAGC ATTTTTAAGT TTCATTGGTA     2400

TAGGTGTACC CGCACCTCAA ACATCGTTAG GGTCATTAGT AAATGATGGG CGCGCAATGT     2460

TATTAATTTA TCCACATGAA TTATTTATAC CAGCAATGAT TTTAAGTTTA TTAATTCTAT     2520

TCTTTTACTT ATTTAGTGAT GGATTACGTG ATGCATTTGA TCCGAAAATG CGTAAATAAA     2580

AAGGGGGCAT AGCATATGAC TGAAAGAATA TTAGAAGTAA ATGATTTGCA TGTTTCCTTT     2640

GATATTACAG CAGGGGAAGT GCAGGCAGTG AGAGGCGTAG ATTTTTATTT GAACAAAGGG     2700

GAAACATTGG CAATTGTTGG TGAATCAGGT TCAGGTAAAT CTGTAACAAC AAAAGCAATT     2760

ACAAAATTAT TCCAAGGGGA CACAGGAAGA ATTAAAAAGG GAGAAATTTT ATTTTTAGGG     2820

GAAGATTTAG CAAAAAAACC TGAAAATGAG TTGATTAAAT TACGTGGCAA AGATATTTCA     2880

ATGATCTTTC AAGATCCAAT GACATCTTTA AACCCAACGA TGCAAATTGG TAAACAAGTC     2940

ATGGAACCAT TAATTAAGCA CAAAAATTAT AGTAAAGCAC AAGCTAAAAA GCGCGCATTG     3000

GAAATACTAA ATCTTGTAGG TTTACCAAAT GCAGAAAAAA GATTTAAAGC ATATCCTCAT     3060

CAATTTTCAG GTGGACAAAG GCAAAGAATT GTTATTGCAA CCGCATTAGC TTGTGAACCT     3120

AAAGTGCTCA TTGCTGATGA ACCAACGACT GCATTAGACG TAACGATGCA GGCACAAATT     3180

TTAGATTTAA TGAAAGAACT ACAACAAAAA ATCGATACAG CAATTATTTT TATAACGCAT     3240

GATTTAGGGG TTGTTGCGAA TATTGCTGAT AGAGTGGCAG TTATGTATGG TGGTCAAATG     3300
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GGAGCGCCAC CTGATTTATT ACACCCACCT AAAGGTGATG CATTTGCGAG ACGTAGcAAT      3480

ATGCATTAGA TATTGATTTT AAAGTAGAAC CACCGTGGTT TAAAGTTTCA CCGACACATT      3540

TTGTGAAATC TTGGTTATTA GACGCACGTG CACCAAAAGT TGAACTACCC GAGCTGGTAA      3600

AACAACGTAT GAAACCGATG CCTAATAATT ATGAAAAACC ACTCAAGGTA GAAAGGGTGT      3660

CGTTCAATGA AAAATGATGA AGTGCTATTA TCTATTAAAA ATTTAAAGCA ATATTTTAAC      3720

GCAGGAAAGA AAAACGAAGT GgaGCGATTG AAAATATTTC GTTTGATATA TACAAAGGGG      3780

AAACATTAGG TTTAGTAGGA GAATCGGGGT GTGGTAAATC TACAACTGGT AAATCAATTA      3840

TTAAACTTAA TGATATTACA AGTGGAGAAA TTTTGTATGA GGGTATTGAT ATACAAAAGA      3900

TTCGTAAACG TAAAGATTTG CTTAAATTTA ATAAAAAGAT ACAGATGATT TTTCAAGACC      3960

CATATGCGTC TTTAAATCCT AGGTTAAAAG TAATGGATAT AGTAGCTGAA GGTATTGATA      4020

TCCATCATTT AGCAACTGaT AAGCGTGACC GAAAAAAACG TGTCTATGaT TTACTTGaAA      4080

CTGTTGGATT AAGTAAAGAA CATGCCAATC GCTATCCTCA TGAATTTTCA GGTGGaCAAC      4140

GCCAACGTAT TGGaATTGCC CGTGcATTAG CCGTTGaACC AGAATTCATT ATCGCGGACG      4200

AACCAATATC GGCATTGGAT GTTTCAATCC AAGCTCAAGT AGTTAATTTA TTATTAAAAT      4260

TACAACGTGA AAGAGGGATT ACGTTCCTAT TTATAGCTCA TGATCTATCA ATGGTGAAGT      4320

ATATTTCAGA TCGTATTGCA GTCATGCATT TTGGGAAAAT AGTTGAAATT GGACCGGCAG      4380

AAGAAATTTA TCAAAATCCA TTACACGATT ATACTAAGTC TTTATTATCA GCCATTCCAC      4440

AACCTGATCC TGAATCAGAA CGCAGTCGCA AACGATTTAG TTATATTGAT GATGAAGCAA      4500

ATAATCATTT AAGACAATTA CATGAAATTA GACCGAATCA CTTTGTCTTT AGTACTGAAG      4560

AAGAAGCGGC ACAACTACGA GAAAATAAAT TGGTGACACA AAATTAAGGG GAAGGGGGAA      4620

ATGCAATGAC GAGAAAATTT AGAACACTTA TTTTAATTTT GATTGCTACA ATTGCATTAA      4680

GTGGTTGTGC TAATGACGAT GGTATTTATT CAGATAAAGG TCAAGTATTC AGAAAAATTT      4740

TGTCATCAGA CTTAACATCC CTTGATACAT CATTAATAAC GGATGAAATA TCTTCTGAAG      4800

TGAcTGCGCA AACATTCGAA GGTTTATACA CATTAGGAAA AGGTGACAAA CCGGTGTTAG      4860

GTGTTGCGAA AGCTTTTCCT GAAAAGAGTA AAGATGGTAA AACTTTAAAG GTTAAATTAA      4920

GAAGCGATGC TAAATGGAGC AATGGTGACA AAGTGACTGC ACAAGACTTT GTTTATGCTT      4980

GGAGAAAAAC AGTTGACCCT AAAACAGGTT CTGAATTTGC ATACATTATG GGGGACATTA      5040

AAAATGCGAG TGATATTAGT ACTGGTAAGA AACCTGTAGA GCAATTAGGT ATCAAAGCAT      5100

TAAATGATGA AACATTACAA ATTGAATTAG AAAAGCCGGT TCCATATATT AATCAATTAT      5160
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ACGGTACGGC AGCTGATAGA GCGGTATACA ATGGTCCaTT TAAAGTTGAT GATTGGAAAC          5280

AAGAAGATAA AACCTTACTA TCTAAAAATC AGTATTATTG GGATAAAAAG AATGTAAAAT          5340

TAGATAAAGT GAATTATAAA GTTATTAAAG ACTTACAAGC CGGTGCATCA TTGTATGATA          5400

CTGAATCAGT AGATGACGCA TTTATTACTG CAGATCAAGT AAATAAATAT AAAGACAACA          5460

AAGGATTAAA CTTTGTGTTA ACGACTGGGA CATTTTTTGT AAAAATGAAT GAAAAACAAT          5520

ATCCTGATTT TAAAAACAAA AATTTAAGAT TGsTATCGCA CAAGCAATAG ATAAAAAAGG          5580

ATACGTTGAT TCAGTGAAAA ACAATGGCTC AATTCCTTCC GATACACTAA CAGCCAAAGG          5640

AATTGCGAAA GCGCCTAATG GCAAAGATTA TGCGAGTACC ATGAATTCGC CTTTAAAATA          5700

TAATCCTAAA GAAGCAAGAG CACACTGGGA CAAAGCTAAA AAAGAGTTAG GTAAAAATGA          5760

AGTGACATTT TCAATGAACA CAGAAGATAC ACCAGATGCA AAAATATCTG CTGAATATAT          5820

CAAATCGCAA GTTGAGAAAA ATTTACCAGG AGTTACTTTG AAAATTAAGC AATTACCGTT          5880

TAAACAAAGA GTATCACTAG AACTGAGTAA CAATTTTGAA GCATCACTTA GTGGTTGGTC          5940

TGCAGATTAC CCTGATCCTA TGGCTTATTT AGAAACAATG ACCACAGGTA GCGCACAAAA          6000

TAATACAGAC TGGGGTAATA AAGAATATGA TCAATTACTT AAAGTAGCAA GAACCAAATT          6060

GGCACTTCAA CCGAACGAAC GATATGAAAA CTTGAAAAAA GCAGAAGAAA TGTTCCTAGG          6120

AGATGCACCG GTAGCACCAA TTTATCAAAA AGGTGTtGCA CATTTaACAA aTCCTCAAGT          6180

AAAAGGATTA ATTtACCATA AATTTGGTCC AAATAACTCA CTTAAACATG TATATATTGA          6240

TAAATCGATA GATAAAGAAA CAGGTAAGAA GAAAAAATAA TATGCTTTGT AAATTAGGCT          6300

GGAGACATAT CTCCAGTCTT TTTGTGTTGG ATAAAAaCTT TGGGAATAAA AATTTAAAAT          6360

AAGTCGTTTT TTAAATTACT GAAATTGATT AAATGCATAA ATAACTGAAT ATTCTAAAAA          6420

TAAACTTGTA ATAATTTTTT CTATGAGTAA ACTAAAAAGA AAAAATTAGA TTGAAAGTAG          6480

GAGGCATATG TATGGGGAAG CTAATTAAAT ATATTTCAAT ACTTCTTATT GTCGTTTTAG          6540

TGTTGAGTGC TTGCGGAAAA AGCAGTAATA AAGATGAAGG AGTAAAAGAT GCTACTAAAA          6600

CGGAAACCTC AAAACATAAA GGTGGTACCT TAAATGTAGC ATTAACAGCA CCGCCAAGTG          6660

GTGTTTATTC TTCGTTATTA AATAGTACAC ATGCAGATTC TGTAGTTGAG GGATATTTTA          6720

ACGAAAGCTT                                                              6730
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(2) INFORMATION FOR SEQ ID NO: 52:

  (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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AATTTTTGTC ATTATTAAAA ACCTCGCTTT TAAAAGATTG AAAAGTAAAT GAGTGAAATT      60

AAAGATTATG CACATTAAAA TCACGCCACA ATTTAATTGT GAAAAATATC ACAAATATAT     120

TATAACACTA AATTTCCCAA AATTCAAAAG TGTGTTTTAT TGCAGAAAAC TTATAACAyG     180

TGCACAAGTT ATAGTGAATT GCAAACGGAT TACTTTAGTC TTTTTAAAAC ATGAAGTATA     240

ATTTGTATAG CAATAAATAT AAAAATGGGA GGCTATGTTC AATGAGCAAT ATGAATCAAA     300

CAATTATGGA TGCATTTCAT TTCAGACATG CGACTAAGCA ATTCGATCCA CAAAAGAAAG     360

TTTCGAAAGA AGATTTTGAA ACAATATTAG AGTCAGGTAG ATTGTCTCCA AGTTCTCTTG     420

GGTTAGAACC TTGGAAGTTT GTCGTGATTC AAGATCAAGC GTTACGTGAT GAATTAAAAG     480

CGCACAGTTG GGGCGCAGCA AAACAATTAG ATACAGCGAG CCATTTGTG CTAATTTTTG      540

CGCGTAAAAA TGTAACGTCA AGATCACCGT ATGTACAACA TATGTTAAGA GATATTAAAA     600

AATATGAGGC ACAAACGATT CCAGCTGTTG AACAAAAATT CGATGCATTC CAAGCAGATT     660

TCCATATTTC TGATAATGAT CAAGCCTTGT ATGACTGGTC AAGTAAACAA ACGTATATTG     720

CATTAGGCAA TATGATGACG ACAGCCGCAT TGTTAGGTAT TGATTCATGT CCGATGGAAG     780

GTTTTAGTCT GGATACAGTG ACAGACATTT TAGCAAATAA AGGGATCTTA GATACTGAGC     840

AATTTGGTTT ATCAGTGATG GTCGCATTTG GCTACAGACA ACAAGAGCCA CCGAAAAATA     900

AAACACGCCA AGCTTATGAA GATGTTATTG AATGGGTTGG ACCAAAAGAA TAAATAGAAT     960

ACCGTATGTC TAAATATATA AAATTAAAAA GTTAGCAATA AAAAAGCCTG CGATTACATA    1020

AATGAATCGC AGGcTTTTGC GTGAAAAAAT TGTATTAATA AAGTATGGAT GATTATTTTT    1080

CTGGẮACAAG GTCAGTATTT GAATGAACTG TGATGTCAAA CCCTTCTGGT GCCGTAAATG    1140

TATGTGTTGA GGCGTCGGGT TGATAAATAT CAACATGTGT TAATCCATAA CTTTGTGAAT    1200

TGTTTTGTCT TGCTTGATTG GATTGCCAAG TATTAGCAGC AATATGATGG TGATAATGAT    1260

TCGTTGACAT AAATAGCGCA CGTGGAAAAT CAGACACATG TTGGAATCCT AATTGTTCAA    1320

TGTAACATTG ATATGCTGCG TCTAAATCAT GTGTTTTTAA ATGTAAGTGT CCAATCATGC    1380

CTTTTGCTGG CATTCCTTGC CAACCTTCAT CAGTACGATG TGTTAATAAG GTTTGGCTAT    1440

CAACTTCTAA AGTATCCATT TTAACTTTGC CATTTTGCCA TTCCCATGAA GATGAAGGTC    1500

TATCGCGATA GACTTCAATA CCATTACCTT CGGGGTCGTT GAAATATAAA GCTTCACTTA    1560

CTAAATGATC ACCAGCGCCG ATGCCCATAT TTTTTTGTGC CACGAAATAT AAGAAGTTAG    1620
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aAGTCTGACG GcCGTCTTCT AATAAATGTA ACGTTAGAGT ATGGcCACCA GTCCCAACAG   1740

ATAATACGGT TGTATTATCG TCAGAACTTT TAACGGATAG TCCTAAAATG TTTTTGTAAA   1800

ATGTTGTCAT TAAGTCTAAG TCTCTTACGT TCAGTACAAT GTTTGTCACT TGTGTTGCTG   1860

TTTTATCGTG AAATGCCATT ATGCATCGCC TCTTTTTCTA TTTTTCTATA AGTTAGTATA   1920

AAAAGTATAC CAGAAAAGAA AATGAATTGA TAGCATAAAG TTTGAAATGC AAAATAACTA   1980

GTCGTTTTGC AATTTTAtAT TGATGCGAAC AAAAAAGCGA TGGTACAGTT GCACCATCGC   2040

AAAATTTATT TAACCAAGAT ATACATCTTG ATATGAATCT TCTTTTTCTA ACATATGTTT   2100

GGCAAATGAA CATGAGGCAA TAATTTTCAA ATTATTTTCT CGAGCGTGTT CAACAACTGc   2160

TTTAAGTAGT TTTTTGCCAA CACCTTGACC ACCAAGTTCA TCAGATACGC CTGTATGATC   2220

AATGTTAATT TCATTATTAT CCACAAAACG GTATGTGATT TCAGCTAAAG CATTATTTTC   2280

ATCATCACCA ATATAGAATT TGTTCTCGCC TTGTTTGATT TCAAGGTTAC TCATACATAT   2340

CAACTCCTAT CATGATTGAT TATAGTATTT CCCTATTCTA TTTTAACTTA AACGAAGTCA   2400

AAGGTGCATG ACAGTCATGT GACGACATTG CCACATCTAT GTAGTCGTTT TTATTAAGCA   2460

CAGTTTGAAA TGAAGATGAA AACACGTATC TTGACATTAA ATCTATTCAG CTATATAATT   2520

TATCTCGAAA TCGAAATAAA ATAAAAAGT TGGTGATCAT ATGGATCGAA CGAAACAATC   2580

TCTCAATGTT TTTGTCGGAA TGAATAGGGC GTTAGACACA TTAGAGCAAA TTACAAAGA   2640

AGACGTAAAG CGATATGGCT TAAATATTAC TGAATTTGCA GTGCTCGAGT TGCTTTATAA   2700

TAAAGGTCCG CAACCAATTC AACGTATTAG AGACCGCGTA TTAATTGCAA GTAGCAGCAT   2760

TTCATATGTT GTAAGTCAAT TAGAGGACAA AGGTTGGATT ACACGTGAAA AGGATAAAGA   2820

TGATAAACGT GTATATATGG CTTGTTTAAC TGAAAAAGGT CAAAGTCAAA TGGCAGATAT   2880

TTTCĉCTAAG CATGCTGAGA CATTAACAAA AGCGTTTGAT GTGTTAACAA AGGATGAATT   2940

AACAATCTTA CAACAAGCGT TTAAGAAACT AAGTGCACAA TCTACAGAAG TGTAAGGCGT   3000

GCACTAAAAA TTTACATTAA AGTATCTCGA TTTCGAGATA AATGCACTAA AAATATAAAG   3060

AGGGTATATA AAATGATAAA TAATCATGAA TTACTAGGTA TTCACCATGT TACTGCAATG   3120

ACAGATGATG CAGAACGTAA TTATAAATTT TTTACAGAAG TACTAGGCAT GCGTTTAGTT   3180

AAAAAGACAG TCAATCAAGA TGATATTTAT ACGTATCATA CTTTTTTTGC AGATGATGTA   3240

GGTTCGGCAG GTACAGACAT GACGTTCTTT GATTTTCCAA ATATTACAAA AGGGCAGGCA   3300

GGAACAAATT CCATTACAAG ACCGTCTTTT AGAGTGCCTA ACGATGACGC ATTAACATAT   3360

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TTAAATGAAG GGGTAGCACC TGGTGTACCT TGGAAGAATG GACCGGTTCC AGTAGATAAA      3540

GCGATTTATG GATTAGGCCC CATTGAAATT AAAGTAAGTT ATTTTGACGA CTTTAAAAAT      3600

ATTTTAGAGA CTGTTTACGG TATGACAACT ATTGCGCATG AAGATAATGT CGCATTACTT      3660

GAAGTTGGCG AAGGAGGCAA TGGTGGCCAG GTAATCTTAA TAAAAGATGA TAAAGGGCCa      3720

GCaGCACGTC AAGGTTATGG tGAGGTACAT CATGTGTCAT TTCGTGTGAA AGATCATGAT      3780

GCAATAGAAG CGTGGGCAAC GAAATATAAA GAGGTAGGTA TTAATAACTC AGGCATCGTT      3840

AATCGTTTCT ATTTTGAAGC ATTATATGCA CGTGTGGGGC ATATTTTAAT AGAAATTTCA      3900

ACAGATGGAC CAGGATTTAT GGAAGATGAA CCTTATGAAA CATTAGGCGA AGGGTTATCC      3960

TTACCACCAT TTTTAGAAAA TAAAAGAGAA TATATTGAAT CGGAAGTTAG ACCTTTTAAT      4020

ACGAAGCGTC AACATGGTTA ATTGGAATGA GGAGGATTTG TGATGGAACA TATTTTTAGA      4080

GAAGGACAAA ATGGTGCGCC AACACTAATA TTATTGCATG GTACAGGTGG TGATGAGTTC      4140

GATTTATTAC CGTTAGGCGA AGcATTGAAT GAAAATTATC ACTTGTTAAG TATTAGAGGA      4200

CAAGTTTCAG AAAATGGGAT GAACCGTTAT TTCAAACGTC TTGGTGAAGG TGTTTATGAT      4260

GAAGAAGATT TGGCATTTCG TGGACAAGAA TTGTTGACGT TCATTAAAGA AGCTGCTGaA      4320

CGTTATGATT TTGaTATTGA AAAAGCAGTA CTTGTTGGAT TTTCAAATGG ATCAAATATA      4380

GCGATTAACT TAATGTTGCG TTCAGAAGCA CCATTTAAAA AAGCATTGTT ATATGCACCG      4440

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ATGGGGAAAC ATGATCCAAT TGTGCCATTA GCTGCAAGTG AACAAGTCAT TAACTTGTTT      4560

AATACACGTG GGGCACAAGT CGAAGAAGTT TGGGTGAAGG GCCATGAAAT TACAGAAACT      4620

GGATTAACGG CTGGTCAACA AATACTTGGG AAATAACAGT TCTATTAAGA AGCGGACAGA      4680

TGGAAAAGAT TTTTACTTTT CATCTGCCCG CTTTTTTGAT TTTGAAGTGC TGTACTAAAT      4740

TTTACAATAG TATAGATATT TTAATCGATA TGAGATTTGC CGGTAATACG CTTAATTAAA      4800

CCTTTATAGA GTACAGGTAT GAGTAAGATG AAACCGAACA ATCCCATAAT AGGGAATACT      4860

TTTCCAATTA ATGAAATGAa ACCGATAAAT GTACTAATAT AAGTGATGAC AGCCATTGTA      4920

ATAATAATGA TGAAGTAACG TCTGCTGAAT GGAACGCTGA AACGTGACGC AAATGCATAC      4980

ATTAATCCAA CAACAGTATT GTAGATGACA AGTATCATAA TGACAGACAT AATAATACCA      5040

ATTGACGGAG ACATTTGTGT CGCTAATTTT AATGTAGGTA GATCTACGTG TTTAATTTTA      5100

TCGAATTGAG AAATTAAACC TAGATTAATC ATCATGAGTA AAAATGTAAT GATTAAACCG      5160

CCAATCAAGC CCCCGTATAA CGTTGAGTCA CGATATTTAA CTTTACTACC CATCACTGAT      5220
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CCAGGTGATA ATGATTTCTG CTTATGAATC TGAGCATCAT TATTAGCGGC AGTAAAATCA   5340

AGATGACTTG TTGTGAAATA GTAGACCGCA ATCATAATGA CAATCGCAAT TAAAAATGGG   5400

GTAACACCGC CAAGCACAGC AATTAAACGA TCGAATTTTA GAAACAGTGT TGCTAAAATA   5460

AAGGCGACTA ATATGAGTGC GCTCAGCCAA TACGGTAAGT TGAAACTTTG ATGAATGGTT   5520

GACGCACCAC CTGCAGTCAT AATAATAGCT AAAGACAACA TAAACATTGT TAAAATAATA   5580

TCAAAACCTC TTGCAATAGA GGGGTATAAG AAATAGTTAA TTGAATCAGA ATGATTTCTG   5640

GACTTTAGAT GATGACCTGT ATGCATGACA ACCATTCCAC CTAAAGTAAT CAATAGTCCT   5700

GTTACAATAA TGCCTGAAAT GCTATATGCG CCATGACTTG TGAAAAACTG GAAAATTTCT   5760

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GACTCTTTTA AGATACGCAT GATTTAAAAA TGTCCCTTCG TAATTTTAAG TAATATAGAA   5880

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TAGAAGCGAG GGTGTCGGTC ATTTCATTAA TTTATTAGTT GATTTTGCAT TTTTTTGCTG   6000

TAAAGTTGTT ATAATACAGT TAACAGGAAT TAGCATAGAT ACACCAATCC CCTCACTACT   6060

CGCAATAGTG AGGGGATTTT TTTCGGTGTA GCTAGGTCGC CTATTTATCA TCGTGTTTGC   6120

GTAGCAATGC GTAAACACAG TACCACTAAA TAAGTGCACG ATACATGCAT CAAATGTCGT   6180

CTTTAGTCTA AGTAACGATC ATGCATTAAC ATTTTCAAAA TATCTATTTG AGCTTGAAGA   6240

TCTTTACCAA TATTGGTATC ACGAATCTTC TTACGTTGTA ATTCTTTATC TACGACGCGC   6300

TTTATAGAAA GTTCATCGAT ACCTTCGGAA AGTATTTTTn CTTTAGCGTT AAATTGTTGG   6360

TGTGCAACGA GTTGCATACC GAATGAATTA TACAATAGTG TATAGCCTGC AATGCCAGTn   6420

GTTGACTGAT AAGCTTTTGA AAAGCCACCA TCAATGACAA GCATCTTTCC ATCAGCCTTG   6480

AT   6482

(2) INFORMATION FOR SEQ ID NO: 53:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 16592 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATTTAAGGCG ATTGCTTGTG TATTTCTCTC TTTTGTAGGC AAACCTGCAC TCGTTCCAAA   60

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AATTTTTCTA ACTTTAACGT AGACATAACT ATATAAATTT TGATAATTAC GTTATACTTA          240

TCATTAATAA GTATCACATT AAACATGATA CATGAATCGA TATTTCATTT AAGACACTGC          300

ATACAGTCGA GCATATTGTA TGACCTACTG AATGGATTAT CTTATAATAA TAAATCATAT          360

ATCTAATTAA GAATTGAGGT TTTAATCTTG AGTACTAAAA ACAAACACAT CCCATGTTTA          420

ATCACAATCT TTGGTGCACT GCGTGACTTA AGCCATCGTA AGTnGTTTCC ATCAATATTC          480

CATCTCTACC AACAAGACAA TTTAGATGAA CATATTGCCA TcATCgGTAT TGGACGTCGT          540

GACATkwnTA ATGATGATTT CCGTAATCAA GTAAAATCAT CAATTCAAAA GCACGTAAAA          600

GATACAAACA AAATTGACGC GTTTATGGAA CATGTCTTCT ATCATAGACA TGATGTTAGT          660

AATGAAGAAA GCTATCAAGA ATTACTAGAT TTTAGTAATG AATTAGATAG CCAATTTGAA          720

TTAAAAGGTA ATCGACTATT CTATTTAGCA ATGGCACCAC AATTCTTTGG CGTTATTTCT          780

GATTATCTAA AATCTTCTGG TCTTACTGAT ACAAAAGGAT TTAAACGCCT TGTTATCGAA          840

AAACCATTCG GTAGTGATTT AAAATCAGCC GAAGCATTAA ACAATCAAAT TCGTAAATCA          900

TTTAAAGAAG AAGAAATTTA TCGTATTGAC CACTATTTAG GAAAAGACAT GGTTCAAAAT          960

ATCGAGGTAT TACGTTTTGC GAATGCGATG TTTGAACCAT TATGGAATAA CAAATATATT          1020

TCAAACATCC AAGTTACATC TTCTGAAATA CTAGGTGTTG AAGATCGTGG TGGTTATTAT          1080

GAATCAAGTG GCGCGCTAAA AGATATGGTG CAAAACCACA TGTTACAAAT GGTTGcATTA          1140

TTAGCTATGG AAGCACCTAT TAGTTTAAAT AGTGAAGATA TCCGTGCTGA GAAAGTAAAA          1200

GTACTTAAAT CACTGCGTCA TTTCCAATCT GAAGATGTTA AAAAGAACTT TGTTCGTGGT          1260

CAATATGGCG AAGGCTATAT CGATGGTAAA CAAGTTAAAG CATACCGTGA TGAAGATCGC          1320

GTTGCAGATG ACTCTAACAC ACCTACCTTT GTTTCAGGTA AATTAACAAT TGATAACTTT          1380

AGATGGGCTG GTGTACCATT CTATATTCGT ACTGGTAAAC GTATGAAATC TAAAACAATT          1440

CAAGTTGTCG TTGAATTTAA AGAAGTACCA ATGAACTTAT ACTATGgAAA CTGaTAAACT          1500

GTTAGATTCA AACCTATTAG TAATCAATAT CCAACCTAAT GAAGGTGgTA TCTTTtACAT          1560

CtAAATGcTA AGaAAAATAC ACAAGGTATC gAAACAGrAC CTGtCCmATT GtCTTACTCm          1620

ATGaGCGcTC aAGaTAAAAT GaATACTGTA GATGCATATG AAAATCTATT ATTTGATTGT          1680

CTTAAAGGTG ATGCCACTAA CTTCACGCAC TGGGAAGAAT TAAaATCAAC ATGGAAATTT          1740

GTTGATGCAA TTCAAGATGA ATGGAATATG GTTGaTCCAG AATTCCCTAA CTATGAATCA          1800

GGTACTAATG GTCCATTAGA AAGTGATTTA CTACTTGCTC GTGATGGTAA CCATTGGTGG          1860

GGACGATATT CAATAATTGA ATTAAAACGC ACATGTTAAA CAAAAATAAA TGAGCGAATG          1920
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TATATTATGA AATTATATTT TACAATGCCC AAAACTATTT TAATAATCAT TGAACAAATG        2040

GGTGTATAAT TTATAGAAAT AATGTAGAAT AAAAATAAAT GATTGAATTA ATTGGAGTGA        2100

AAGTTTTGGA CGTTATCAAG CAAATACAAC AGGCAATTGT TTATATTGAA GATCGTTTAT        2160

TAGAGCCTTT CAATTTGCAA GAATTAAGTG ATTACGTTGG TCTTTCGCCA TACCATCTTG        2220

ATCAATCATT TAAAATGATT GTCGGCTTAT CTCCAGAAGC TTATGCACGC GCGCGTAAAA        2280

TGACACTCGC TGCAAATGAT GTGATTAATG GTGCTACACG ACTTGTAGAT ATCGCTAAAA        2340

AATATCACTA TGCAAATTCA AATGATTTTG CAAATGATTT TAGTGATTTT CACGGCGTAT        2400

CACCTATTCA AGCCTCTACT AAAAAAGATG AATTACAAAT TCAAGAGCGA TTATATATCA        2460

AATTATCAAC TACTGAGAGA GCACCTTATC CATACAGATT AGAAGAGACA GATGATATTT        2520

CATTGGTTGG ATATGCACGA TTTATAGACA CTAAGTATTT GTCACATCCT TTTAATGTTC        2580

CGGATTTTTT AGAAGACTTG CTCATTGATG GTAAAATTAA AGAGTTACGA CGATATAATG        2640

ACGTTAGTCC ATTTGAACTA TTTGTTATTA GTTGTCCTCT TGAAAATGGT TTAGAAATAT        2700

TTGTAGGTGT ACCAAGTGAA CGTTATCCTG CACACTTAGA AAGTCGATTT TTACCTGGCA        2760

AACATTGTGC GAAATTCAAT TTACAAGGTG AAATTGATTA TGCAACTAAT GAAGCTTGGT        2820

ACTATATTGA ATCAAGTTTG CAGTTAACAT TGCCATATGA ACGAAATGAT TTATATGTTG        2880

AAGTGTACCC TCTCGATATT TCATTTAATG ACCCATTCAC TAAAATTCAG CTTTGGATTC        2940

CTGTTAAACA GAGTCCTTAT GACGAAGATT AAATAATAAA AAACAAAGAA GCCCCCTAAT        3000

ATATCTATAG GTCTACAAAT GGCCTTAGAT TCTATTAGGG GGCATATTAA TATGTTAATT        3060

TAGTTCGATA ACACATGCTT CATATGGACG TAACTGTTTT AAATTAACTT TGGCATCATA        3120

ATTAAATAGC TTTACTTCTC CATGGCTTAA ATCAAATGGT ACAGTTAATT CTGCTTCGTG        3180

GTTAGTAAGA TTACCTACAA TAAGAACTTG CTTTTCATTT AATGTTCTCG TGTACGCAAA        3240

AACTTGTGAA TTTTCAGCAT CTACTAAATC AAAATTGACCA TATACGTATA CATCATTAGA       3300

CTTTCTTAAT TGAATTAAAT CTTTATAAAA TTGTAATACT GAATGCTCAT CTTCTAATTG        3360

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AAATCCTCCA TTTAACGTAT CATCCCATTG CATTGGTGTG CGAGAATTAT CTCGGTTCTC        3480

ATCTTTATAT TTCGCAAGTA AAGCGTCTAC ATCTCCACCT TGAGCTTTCA CTATTTGATA        3540

GTCATTTTTA ACAGCAACAT CGTTAAACGT TTCAATACTT TCAAATGGAT AATTCGTCAT        3600

ACCAATTTCT TGACCTTGAT AAATGAATGG CGTACCTTGT TGCAAGAAAT AAACAGCTGC        3660
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CCATCTATTT AATACAGATT TATACGAATT TACATCAAAG TGAGAATCAC CACTATTCCA        3840

CAGTCCCAAA TGTTCAAATT GGAATATCAT ATTAAATTTA CCATTTTCTT CCCCGACCCA        3900

GTCATCAGCA TCATCAGGGC TTACACCATT CGCTTCACCA ACAGTCATAA TGTCATACTT        3960

ACTTAATGAG CGATCTTTCA TCTCTTGTAA CCAAGTTTGT ATACCTGGCT GATTCATATC        4020

TACATCAAAT GCTGGGGCAT ATGTTTTACC CTCAGGTACA GGTAAGTCAC CCGCTTCAAA        4080

CGTCTTCTTA ATATGCGTAA TTGCATCTAC TCTAAATCCA TCAATGCCTT TATCAAACCA        4140

CCAGTTCATC ATTTCAAATA CAGCATCTCT AACTTCCGGA TTACCCCAAT TCAAATCAGG        4200

TTGTTTTTTA CTGAATAAAT GGAAATAATA TTGCTCAGTA TTAGCATCAT ATTCCCATGT        4260

AGATCCATTA AATATACTTT CCCAGTTGTT AGGTTCAGAG CCATCTGGCT TTGGATCTTG        4320

CCAAATGTAC CAATCACGTT TGGGATTGTC TTTACTAGAT TTGGATTCTA TAAACCAAGG        4380

ATGTTCATCA GATGTATGAT TTACAACTAA ATCTAAAATA AGCTTCATGC CTCTATCATG        4440

AACACCTTTT AATAAACGAT CAAAGTCTTC CATCGTTCCA AATTCATCCA TAATCTCTTG        4500

GTAGTCACTA ATATCATAAC CATTGTCATC ATTAGGTGAT TTAAACATTG GACTGAGCCA        4560

AATGACATCG ATACCGAAAT CTTTTAAGTA GTCCAATTTA TCAATCATTC CAGGTAAATC        4620

CCCAATACCA TCGTGATTAC TATCATTAAA ACTTCTTGGA TATACTTGAT ATGCTACTGC        4680

TTCTTTCCAC CATTGCTTAT TCATTTTAAA ACTCCTTTGC TATCGCTGTG TTGATTTTCT        4740

TATTTTTAAT TCTGTATCTA TAATGACGAG TTCAATAACA TCCTGTGCTT TGTTTTTCAA        4800

TATATTTAAA ATTGCTGCAC CAGCCTGTTG ACCTAACATT CGAGGCTTGA TGTCAATACA        4860

GGTTTGTGGT GGTGACGCAA TTTCGGTTAA ATAAGAATCA TTGAACGTTG CTGTCATTAC        4920

ATCTTTCGGA ATTTCAATAT TAAGTTCATA TAGGACACTT AAAATCGCTA AATGTAACAT        4980

AGCATCTAAC GAAATGATTG CCTGTTTAAT ATTTGGGTCC TTCAAACGCG TATGTAGATT        5040

TTGCATGTAA TTAAAAATAA CTTCTCTTTC ATTACTAGTC TCAATAATTT GATAATTAAT        5100

TTTATTTTGA GAAGCTATCG TTTCAAATCC TTGAATTCTA TCTTTTGAAA CTTCAAAATT        5160

TCCTTTTTCT GTAATAAATA TTAATTCATC TACACCTTGT TCAATAACAT GTCGTGTCAA        5220

ATTTTCAGAA GCTAATATAT TATCATTATC TATATGTGTA AATTGATGAT CTATATCCGA        5280

TGTAGGCTTA CCAATCACAA TAAATGGCAT GCTTTCATCA ATTAACATTT GTTTAATCGG        5340

ATCATTTTCT TTTGAATAGA GCAGTATAAA CGCATCAACC ATTCGTTGTT TAATCATTTT        5400

ATAAACTTCA TCCATTAAAT CATTCATATT ATTTGAGACT GTCGTTTGTG TACCATAGCC        5460

ATGCTGGTTA CACGTTTCAG AAATTCCTAG CAATACATTG ATGTAGAATG GATTCAGTCG        5520
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      AGTTCTAGCA GCGGTATTAG GAAAATAATT CAATTCTTCC ATAACTTTCT TCACTTTTGA    5640

      AATTGTCGCT TCGCTAATAC GTTGATTTCC TTTTATAACT CTTGAAACTG TCGAAGGAGA    5700

 5    AACACCGGCT TTTAGTGCAA CATCTTTAAT CGTAACCATT TAATCACCTC CTGTTAATTT    5760

      CTGCATCGGA AAACGCTTCC AACCACTGTA TAATACCAGT TTAGTCACAC TTTCTAAAAA    5820

      AGTCAAAAGA TTTGTGCAAA CGATTGCATA AAACGATAAA AATAAAACCT TCATACTGAA    5880

 10   ATTCAATCCG AAAATCAATA TAAAGGTTTG TATAAATATT AAAATCGATT GTTTAGTCAC    5940

      TAACTGCAAA ATAGTTACCT TGGCCATCTT GAAAATTAAA TACACGTTGA CCATTCATTT    6000

      CTACTATATC ATGCCCAGTT AAACCTAAAT CATTTAATTT TGAGTATAAT GCATCAAAGT    6060

 15   TTTTCTCTTT AAACATTAAA GATGGTGTTC CTAGGTTCAC TTCCGGGCTA TGCTTTTCAA    6120

      TAAATTCTTT TGCCATAATC GTCAATGACG TTTCAGCATC TTTGGTAGGT GATACTTCAA    6180

      CTGCAACATA GTCCTCAGCT AACGGTGTTT CACTTACAAC AACAAATTCT AAAGTTTCTG    6240

 20   TCCAAAATGC TTTCGCTTTT TCGACATCAT CAACATATAA CATAACTTGA TTTAACTTTT    6300

      CCATAAAATA GTACCTCTAT TTCTCTATAG TACATGCTAT CATAACACAG TAAATATTTT    6360

 25   ATTACTTCAC AAAATGCTTA AAAATATGGC GGGATGCTTT TAAGGTCAAG GATAATACTT    6420

      GTGTAATTTT TTATAGGTTG TAGCTACTCT ATCACACTCT CTTTTATATT TATCAAAAGA    6480

      TATAAAAAAG GATAGTATCT TTCAACTATC CTTTAATCAA TATTATTCTT CAATCCATTG    6540

 30   TGTATGGAAT ACGCCtTCTT TATCTTTTCT TTCGTACGTA TGAGCACCGA AGTAGTCACG    6600

      TTGTGCTTGA ATTAAGTTTG CAGGTAAATC AGCAGCACGG TAACTATCAT AGTAATTAAT    6660

      ACTTGATGAG AAACCAGGTG TTGGTACACC ATTTTGAACA CCAGTTGCGA CAACATCACG    6720

 35   TAACGCATCT TGATATTCAG TAACGATGTT TTTAAAGTAA GGATCTAGCA ATAAGTTTTG    6780

      TAATCCTGGA TTATTATCGT AAGCATCTTT GATCTTTTGT AAGAATTGTG CACGGATAAT    6840

 40   GCAACCTTCT CTCCAAATCA TAGCTAAATC ACCAAGTTTT AAATTCCATT CATTATCTTC    6900

      ACTTGCTTTA CGCATTTGcG CGAAACCTTG TGCATAAGAA CAAATTTTAC TCATATATAA    6960

      TGCTTTACGA ATTTTTTCTA AAAAGTCTTT CTTGTCACCA TCAAATGATG CTTTTGGACC    7020

 45   ATTTAATTCT TTAGAAGCAT TTACGCGCTC TTCTTTGaTT GAAGAGATAA AACGTGCAAA    7080

      TACAGATTCA GTAATGATTG TTAATGGAAT ACCTAATTCT AATGCGTTAA TTGAAGTCCA    7140

      TTTTCCTGTA CCTTTTTGaC CTGCAGTATC AAGAATTTTT TCAACTAATG CTTCTTTATT    7200

 50   TTCATCTAAT TTCATGAAAA TATCACCAGT GATTCAATT AAATAACTTT CTAATTCACC    7260
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CATTCCCTGT CTCAGAATCG ATTTGTACAA GTTCAAAAAA CGTATTAAGT AATCTTTGCT        9120
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CAGATAATTG TATCAATAGC TACTGTCTGC CCCGCTTCAA CTAAAATTTC TGTAATTGTT    12600
CCTGATATCG TGGAAGGGAC TTCAGCTGTC ACTTATCTG TAATAACTTC ACATAATGGT    12660
TCATATTCAT CAATATGATC ACCAACAGAA ACTAACCATT GTTCAATGGT GCCTTCATGA    12720
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TCGAACAAGC AATGCTCTGC AATAATCGCT GACACTTCTG ACATAATACT ACCTTCTAAA      12960

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ATTCTTAGCT CTACTACTAA AGTGTGATGG CATTTGTTTT CCACCAGAGT TAACATCGTC      14460
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TATATATCCA TTGAAAATTT ATTAATACAT AGTTTTCATG TCCATTAATT ACCTATTTTA     16260

CATGATTGTC TATTTAGTTT GAATGCACAT AAATAAATCC ATAAATGAGT ATTCAACACA     16320
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AATTAACTCT TGAACTTGTG TTGTTGTACG ATCATCTTTT GATGATTTCG AAATTAATAA   16500

ATGATGGTCG CTCATCGATG CAACTTGTGG TAAGTGAGAG ATACAAATAA CTTGTATATA   16560

TTCTGCTaTA TCTCGCATTT TCTCTGCCAT TT   16592

(2) INFORMATION FOR SEQ ID NO: 54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13794 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CCAATACAAC GTAAAAAGAT TGCTTGTGTT ATTAATGAGT TAGATAAAAT AATTAAAGGA   60

TTTAATAAGG AAAGAGACTA CATAAAATAT CAATGGGCTC CAAAATATAG CAAAGAnTTT   120

TTTATACTTT TTATGAACAT TATGTACTCA AAAGATTTTT TAAAATATCG ATTTAATTTA   180

ACATTTCTTG ATTTATCTAT CTTATATGTA ATATCATCTC GAAAAAATGA GATACTAAAT   240

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ACAGTCATTC AATTTAGTTC ACCATTTCGT GTTCCAATTT TACTGAGTAT CATGCTTTTA   660

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CGTTAATACA TAACGTCCCA TAATAGCTAG GTTTGATGGT GCCGTACCTT GTGCTGGCTT   960

TTCAACAAAC TTTTTCACTT CATACTGACG TCCGTTTTTA GTTAATGGGT CAATAATTCC   1020

ATAACGATGA GTATCTGCTT CCGGAACTTC TTGGACACCT ATAACTGAGT GCCCTGTTTC   1080

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TAAACCTTTT TGTTCTTTCT GCCTTACATA AAAAATATTC GCAAGTTCCG TTGAATACTG    1260

AACTTTCTCT AGTAATTCAG ATTTACCTTT TTCTTTTAAC ACCATTTCTA ATTCTTTTTG    1320

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GATTCTTCAA AGTCTACATG AATAGAATCT TCTTCAGTTT CAATGGTACC TTCTGCATGA    2940
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GCGTTATTAG AGTAAAATGC AACGCCATTT TTCCaAGTTA AATTACTTGT ATAATAATAG      3180

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TACTTTATTT AAAGTATCAA TTCGACCATT AGCTGTTACT CCCCAATTAT CTCTAACTCC      3600

ACCTAAATAT TGAATATTAA ATATTTTGCT AACCGTAGTC TCACCCAATT TAACTTCAAC      3660

ATTTTGGTTA CCTTTTTGCG TCACTGTTGT AGGATCAATA AATAGATTTA AAGATAATTC      3720

AGCAGTTAAA TCTTTCTTTT CTTGTACATA TTCTTTAAAC GTATATCTAA CTTTTCTTTC      3780

TCCAATTATT TCTCCTGTCG CCATAACTTG ACCATCTGTA CTTTTTATCT CCGGAACTTT      3840

ACGCAGTGTT GAGATACCAT GAGTTTCAAC ATTATCGCTT AATGTGAAAT CAAAATAATC      3900

TCCCGCCTTA ATTCCTTCTC CAAATTTCCA TTTATATTTC AAGGTTACTC TTTCTGCGTT      3960

ATGAGGATTT ACAACATTCG TATCTTGTTT ATGTCCTACA ATTTCACTAC CTTCTTCTAC      4020

TTCCACTTTA TTTGTTACAT CTGTACCTGT CGCTTTAGTT TCTTCCACTA CTTCTTTCTC      4080

TGCAACTGCT GTAACGTCAt TGatCTTTTC ATTCTTGGTT TAATTTCTGA GACGTTACTT      4140

GGTTGAGCTA TGTCAACTTG AGTTCCTGTA GTTTCCTTAT CAGCAACTTT TTCCGATGGC      4200

AAATCAACTC GCGAAgTTTC TACTTTTGGT GCTTGCAcAG TTTTCGGTGC TTCTTCTGTT      4260

GTTACTTGTG TTGATTGTGA TGGTTGCTCA GTTGATGTCG CGCTGTATGA TTGTGTTTCA      4320

TCTATTGTAT TAACGTTATT TGTAGTTGTT TGTGTTTCGC TTGCTTTACT TTCAGTAGCT      4380

GAACTCCCAC TTTCCTCTAC TGTAGTATTG TTTTGTTCCG ATGCTGCAGC TTCTTTTTCT      4440

TGTCCCATTC CAACAACGAT CATTGTTCCT AAGAATACTG AGGCCGCTCC CAATTTGTGT      4500

TTTCTTATGC CGTATCTAAG ATTGCTTTTC ACTATAATAT TCTCCCTTAA ATGCAAAATT      4560

CATTTATTTT TAAAACTCAA TAAATGCAAT TCTATATTGT TCGGTTTTTA AAAGCAATGA      4620

AAAAAAGCGA GTTAATAAAA AGTTAAGATT GTTGTTAACT TTATGTATAA TGAGTTTTTT      4680
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TACTAAACCA TACATAATAA TCGCCTGTAC AATGCATCAT TAACAAGTCA CTGAAACGCC    4860

TTTCATTGTA TTAATAACGT CACTATAATT TTTATATCGT TCGGTTTTTG TTTGATTTTA    4920

ATGATTATTT ATACAAAAAC AGCCGTATTT CAAGCCGACA TTTTAAATTT AACTAAATTT    4980

GCATCTAGTT AATAATTGCA TTTATCAAAT TTGTCTTATT GATCCAATCT AATTTGTACT    5040

CACAAACTAG TTTAAAATTC TAACTTTATC TCTCAGTTCG TTATCAATCA TCAGACATAA    5100

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TTTGGAAGTG TATCTTCTTC AAAGTCAACA CTATTGTGTC CACCGAATTG ATAACTTGGT    5760

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GGCACACTGT CGAAGTCGAT ATCAATGATG TTACCGCCAT GTTCATACTT AGGTTTGTCT    5880

TTTTCTGTAT CTTCCTCGAA TGACTGATTA CCTTTATTTT GACCATGAAT TTGAGGTACA    5940

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GTGTCTTCCT CGAATGACTG GTTACCGCTA TTTTGGCCAC CTTCATAACC TAATTCACTC    6060

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GGTCCTTGTG CTTGACCATG CTCTTCAGGT AATTCATCCA CTAATTCAAT CAGATTACTT    6240

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CCACCTGGGT TTGTATCTTC TTCATATTCA ACAACATCAG CGTGATGTTT TGAATTTTCA    6420

TGTGTAGATT CTTCAAAGTC AATTGGATTT GATTCCTCAG AGGACTCAGT GTATCCTCCA    6480

ACGTGACCTG ctTCGCTATC CACAGCAGTA TGGTAATCGA TATCAATAGC TGATGAATCC    6540
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TGGTAATCAA TGTCAAGAGT TGATGAATCA TATTCCTCTT CAACAGTAGT TACTAAATTC      6660

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ACTTTTGGTT GATTTCCATT CTGATTACTA CCTTTCATTA AAGTTCCAGT AACAGTCACA      7140

CTTGTCGTTT TACCATTATT AGGTTTAATA AATGCAACAT GCGAAAATCT ATTATTCGCT      7200

TTATTAAATG TCTCAATCGA TCCATTTAAA TTGGCATAAT AATTCCCAAT ACCATCTTTA      7260

TATTTAACAT CTAATTCCTT TGAAGTTTGT TCTTCATTTA GTGTTGAAGT TATAGTTTGA      7320

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GTTTTATTAT CAGTAGCTGA ATTCCCATTT TCTTCTACTG TAGTTGTCTT TTGTTCTGAT      8160

GCTGCAGCTT CTTTGTCTTG TCCCATCCCA ACAACGATCA TTGTTCCTAA GAATACTGAT      8220

GCTGCTCCCA ATTTATGTTT TCTAATGCCG TACCTAAGAT TGTTTTTCAC TATAATATCT      8280
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AATCATACCA TACAGTAATA CATCTCCAAC ATTTGCCTTT AATTCTTTTG CGATGACTAC          9600

CGGTCCTGGA TGTGGTGGTA AAAAGCCATG TGTCACTGAT AAAGCTGTTA CCATAGGTAG          9660

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GTGGCCGAGC GTACTGCCCA TTCCTTTCTC AATCGTCTCC ATAATTTTAG TCAATGGTAT          9960

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AAACCCAATA ATTAATACTA ATAAAATAAC GATACCTAAA ACAACACTGA TTAACGGCCA         10080

TATTTCGTTA AACATGACAT TCCCCTCTTT CTCTTTTCAA TAGAATGTAA CACCGTCGTC         10140
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TGTTCATAAT TCTCTGTTAA AGAACGACTT AAATTGATAA AAATGGATAC GATCTCTTGG    10320

TAAACAGTGA CATTTTCTTC AATCGGCGTA TGATTGTTTG TGGCACCGAC CATCGATGAA    10380

ACGATTGAAA AATCTTCAAT GTCACCTACA GCTTTAAGTC CGAGCACGCA GGCACCTAAG    10440

CATGAACTTT CATAACTTTC AGGAACCACT AACTCTGTGT CAAATATATC TGACATCATT    10500

TGACGCCATA CTTCACTTTT CGCAAAACCA CCTGTTGCTT TTATCATCTT AGGTGTTTCA    10560

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GCAGCGCGAA TCATATGTTC TTTTTTATGA GATAAAGTTA AACCGAAGAA TGAACCTCTT    10680

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TTCATGATAA ATCCTTCTTT CTTTCATTTT AATTCAACCA AAATCCTTCA ATATCTTTAC    11820

CAACATCGTC GAAATTTAAA TGAAACGCTT CTTTCAAAAT TTGACTGTCG TATTGTTCCA    11880
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AAAATGAGTT TAAATATTGA TGATTAGATG CTTTGATTAA TGTTTCATGA AATTCAAAGT 12060

CATGCTTCGT AAATGATTCT GCATCCTCAA ATTTTACTGC CACTTTCATC ATTTCAAGTT 12120

GTTTCTTCAT TTCTTTTACG ATAGGTAGTC GCTCTTGATT TTTAACTCTT GAAAATGCAA 12180

ATGACTCTAA CATCAGTCGC AAATCATACA TTTCTTTCTT TTCTTGTTCC CCAAACGGCA 12240

ACACATGTGC ACCCATTCTT TCTAATTGGA TGAGTTGATT TTGTTGCAAT AATTTAAATG 12300

CATCTCGAAT TGGCGAACGA CTCACATTAA ATTGCTTTGC CATTTGATTT TCAGTGAGTA 12360

ACGTACCTTC AGCTATGTGA CCATTCACAA TGCCTAAGCG TAATTCTGCC GCGATACCTT 12420

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CTTCATTACA CGACATACTT GTATACAAGT ATGTTAATAT AGTTATTATG AGTTTGCAAG 12540

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ATTCGAATCG ACGTGTTGTC GCTGTATGTT TCGCTTTGAT AACTGCCCAC AAAGATGGTG 12780

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CACCAATGCC ATAACCAATC ATAAATGGTA AAGCAATTAA AAACGGCCAT TTATTTTTCA 12900

TCAAAATTGC ACTTATAATG CTAGAATATT GAATTATTCC TATAATACCA GCACTAATCC 12960

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TATᾹCACACG ACGCTTTCCT TCTGTAAATC CTTGTGGTTT CAAAATACCT TTGCGATCAT 13320

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TAAACTTGcC CACATATCCA TACCTATCGT TCTAATTTGA ATTTCAACAG GCAATACCTC 13740

(2) INFORMATION FOR SEQ ID NO: 55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1059 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

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GGATAAGTTC AGGTAAATTC ATTTCTTTTT CAATTTTGAT TTTCATTGTT TCCGCCCTTT        60
TAAAATAAAG TTAGTTGCTT CTGTTCCTCA TATTCCAAAT CACTTTGCTT TATATATGTT       120
TCAAGCTCTT CCGCTGTATC AAATGTCTTT TTCACACCTT GCCAACCTGG CACGATATGA       180
CCGTGAAAGT AATAAGTGCC ATTTACTACA TGGATATGTG CCACTCGTTC GTTATCCTGA       240
TACAGATATC TCTTAGATCC AAAGAATTGA TTTAGGTATT CTTTACGCGC GCTATCTGTC       300
ATGGTCATCA CTCCTTTTAA CAATTAGGCA GACCAAACGA CATGCATTCG TCGTATAGCT       360
CTTCATTACT TATGCTTGCC TTATAGTTTT CAATCACATT GCTAACTTCT TTATGACTCA       420
TTGCTTTAAC TTGTTCGTCT GTATATTTTT CGCAGTCTTC TAATTCCAGT TGCTCCTGTA       480
ATGACATCAC ATATTCAACT TGTCTTTGGG TTGCCATCGT TAACCCTCCC ACAAGTCAAA       540
AGCTCTTTGG ACGTAAAACT TCGCCTTTGC TAAATCCTCA TGACCATTCT TTAACGGTGC       600
TCTAGACATG TATTTGATTG CATTACCTAT TGCGAATGCT AGTTGAGGTG GATACTGTGC       660
CGTAACCTGT TCGATAAAAT CTATAATTTC AATGTCGCCG TATGTGTAGT GCGCTGGTTG       720
CTTAACATTG TCTTGCGCTT CGTTCATATC TACTTTTCTG TTACTGATTA CGCTCATTAT       780
GCTTCACTCC ATTTCTTGAA CATTTGGTTA TAAGTGACAT CGAACCAGTA CGGATCACGT       840
GAATGTTTTT GTGGCGTTCC ATCATAAAGC CATGGTCTTA ATCTTCTCTT TCTTTCCTGT       900
TCATATTCCG CTCTCACATT TCGTTGGTAT CGGTTCAAAA TCGCTTTTTT TCTGATTTTT       960
TCTCTCCCTT TTTCTTCATC TTTnATtTGA CTCTnCATAT ATTCAACTTC TTCTGTAGAT      1020
nTTGAGTCCT TTCTTCCACA CAATAATTCA nCGCCGCGC                             1059
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(2) INFORMATION FOR SEQ ID NO: 56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30246 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

GAAGTAAAAG AAGAATTAAA TTTAACATTA ACAATGGATG AAATTGAATA TGTCGGGACA   60

ATTGTAGGTC CTGCATATCC ACAACAGGAT ATGTTAACTG AGTTAAATGG ATTTCGCGCA   120

TTAACCAAAA TCGATTGGGA AAACGTAACT ATCAATAATG AAATTACGGA TATACGCTGG   180

ATTGATAAAG ATAATGATGC GTTGATTGCG CCTGCTGTCA AGTTTGGAT TGAAACTTAT   240

GGTGGTAAAC ATGACAAATA ATGACACCAT CATGTTACGA CATTATGTCC CACAAGATTA   300

TTCGATGTTA GAAGCTTTTC AATTAAGTGA AAGTGATTTG AAGTTTGTTA AAACGCCAGA   360

GGAAAATATT ACAGCTGCAA TGTCTGATAA TGAAAGGTAT CCCATCGTTG TAATGGATGG   420

CAGGCAATGT GTGGCCTTTT TTACATTACA TCGTGGAAAA GGGGTCGCAC CATTTAGCGA   480

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GACCTAGTGA ACAATTGACA TATATCCACA GGTCGCTTAA CTTAAGTTAT ATTGCTAGTT   900

GCGATTAATT GATAGACTCA TCATTTTTGC GCTGTCGAGA TGGTCTTTTT ATTAAAAATG   960

CCGTAATCCA AGCCGTAATC GGAATACTGA TTGCAACGGC AATACCGCCT AAAATAATAG   1020

AAATAAATTC TTGGGCAAAT ATTTTCGAGT TTATAATATG ACCAAATGAA TATTTAAGTT   1080

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CAGATGTCGC TAAAATTTCT CTACCAACAC GCATGCCAGA TTGGAATAAT CGTATTGCG   1200

TAACGTTgGA TTCACTTGAT GCAATTCATA AATGGGTGAA CTAATGGTAA TTGTTAAATC   1260

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GCtGgATAAA TGCaGCTTGT GTTTTAACAT TGTAACTATT GAGTACGAAT AAATTACAAG   1500

CGCCAATAAT AATGCAGAAA AAGAATGTGA CGACATAAAT CGGTACGCCA AAAATAATCA   1560

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TTTAATGCCT TTACCATCTG TCATATATAT GATTAATTCT GTTAAACCTA TACTCAAAAA   2160

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CGATTTGACG TACTGATGAT TAATCGTCGT CGTTCTCCA GCAAATTGAC CATTTAATAT   2580

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TGTCGAAGAA ACATGTTTGA CATCTATAAT TTGACCAATT GGTTTGTTGT AAAAGTTCTC   2700

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CAATTGTTTT TTTACAGTTT CGGCAAATGG TGCCAAGCAA TAAATATGAC TATGCTCAAA   3240

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AAAGAAACAT CATTTTATTG ATAAATATTT ATTGATTTTC AAGGAGGAAA TGGAATATGC    17700

GCGGTGGCGG AAACATGCAA CAAATGATGA AACAAATGCA AAAAATGCAA AAGAAAATGG    17760

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TTGCAGTTAC TGTAACTGGT CATAAAGAAG TTGTCGACGT TGAAATCAAA GAAGAAGCTG    17880

TAGACCCAGA CGATATTGAA ATGCTACAAG ACTTAGTGTT AGCAGCTACT AATGAAGCGA    17940
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AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA    19740
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AGGTGATGTA TagGGcTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGcTT    23280

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CAATTCCATT TAATAGAGCG ATAATGGCAA TGTATCCGAT TAACATTGCG CCTACAATGA        28620

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AGAAGCATTT GTTGTTAAGC AAATTTTACA ACATTTAGCT ACGAAACATG GAATTAATTT    30240

TCAAGA                                                               30246
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(2) INFORMATION FOR SEQ ID NO: 57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14333 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

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TTTTAATAAT GCTAACTTTT CAACTATGTC TGGGTACTTA CGATATAAAT CAACAACTTG       180

CTCAAAATCT TTAGAGCCGC TTCGACTACT ACCAATCAAC GTTAATCCTT TTTCAAGTAC       240

TAATCGTGTA TTCACTTCCA CGGGTAATTC ACTTACGCCT AACAAAGCAA TACTGCCTTC       300

TGGTGAAATA TGTTCAACTA TTTGTTGAAG TGCAACTTGA CTTCCTTTAC CTCCAACACA       360

TTCAAATGCA TGATCAATTT TAAGATCATC TGGTATTTGA TTTACTGTAA AGATGTCATC       420

TACAAATGAA AAATGACTTA ATTTATAGTC TGTCTTACCA AATACATAAG TTTTAGCTTC       480

TGGGTACAAC TTACGTAGCA AAATAGCAGT AATATAACCT AAGTTACCAT CACCCCAAAT       540

ACCAAAGCTG GTTTTCAAAG GTATAGATTT ACGTTCAAAT CGTTGTATAG CATGATAACT       600

TACTGACACT AACTCTGTGT ATGAAATCGT ACTCAAATCA ATGTCATTAG GCAGCGGAAC       660

GATACGATCA TGTGCCATCA CAACGTAGTC TTGCATAAAA CCATCATAAC CACTAGATCT       720

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TCGACCTGTG TAATACCTTT GATCAGCTGC ACAAATAGAC AAGTATAAAG GTCTTACGAT       960

GACATGATTA CCATAAATAT CAACATTATT ATATGTGACG TCGAACTGTC TCGGTGCAAC      1020

GAGTTGATAT ACTTGATTAA TCATCGGCAA TATCACCTTG AATAATGGCA TTTGCTACTT      1080

TTAAATCATA CGGTGTTGTC ACTTTAATGT TGTATAGTTC TCCaCGTACC AATTTAACTG      1140

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CATCATTATT AATTCCATTT ACATTGCGAA TATGGTCGAT AATGTTCATA ATTGTTTCAT      1500

TTCGATCCGT ACCACCTGCA ACTACTTTGA CACGTTGATC TGTAATGTTA TATTTTTTTA      1560

AAATATCCTG TGTATGGGAA ATCCACTGTG CTGGCGTTGC GATAATAATC TCATTAAATT      1620
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CTGCATAAAT CATGTTGTCC TCCATTCTGT CATTACATCA TTTCCATTTA TACATTACTG          1800

ACCTATGCCC GCACATAAGC CTAACCTATT GCTCACTTGC CTCTTTTATT AATCCAAAGA          1860

TAGTTGTCAC AATAGTGTGA TAATTTTTTA TAAAAATGTA TTTTTGTAAC TGACCATTCT          1920

AAGTTGTTTT GCCATGCAGT TAATCATTAA CTCTGACGAT ATTAAATTGT TAAAGGTATT          1980

AATGTTTACT CTTTTTCAAA TTCATTATTA CTGCCATCAT TTTACCATAT ATTATAATAA          2040

ATTTATCTTA TTAAGTGGCT GTACTTGATT TTCACTTTAA AAATTATCAA ATATTGCCAT          2100

CTCATTTTAA GTATACAAAA TGCAAAACAA CCGATTCACA AGCATATTTC ACACAAGTAA          2160

ACCGGCTATT TATCAACGTA TATTCGAAGA TGAATTATTT CGATAGTATC TATAGACCAG          2220

ACGGCATTCG CACTTTCATA GCTATAACTA TACCAGCGTT TTCGTCCTCA AAGGTGCATA          2280

CTAATAAATC GTAAACATGA CTTTATCAAA TCGTTCTTTC TTGTTAACTA ATTTATCAAA          2340

TGTCTCCGGG CCTTTTTCTA ACGGTAAAAA ATGAGAAATA ATAGGCTTTA CATTAATATC          2400

TTTCGTCTTC ATATAATGTA AGGTTGCCGT CCACTCTTTG CCCGGAAAAT TACTGGACAA          2460

ACAGTTCCAA GAGCCACATA CTGTCAACTC GTTACGCAGA ATTTTTTCAA AATGAACGCG          2520

ATCAATCTCA ATATCATCAT ATGGTATTCC GAGTAATACC ACCTCGCCAC CTTTTTTAGG          2580

TAGCGTCAAT ATTTGACCAA TCGTAACTTT AGCACCTGAT GATTCTATAG CTAAATCGAT          2640

TTGATTGGCG TAATGATTTT CGATGAATTT CTCAAGATTT TCTTCTTTTG AATTGATTGT          2700

TTGATGTGCG CCCAATGATG TTGCAATATC TAGTTTATGC GCATCTATAT CTATAGCGAT          2760

GATATGTGCA GCACCAAATA TTCGTGCCCA TTGAATAGCT AACAAACCTA TACTGCCACA          2820

CCCCATTACT GCAACAGTCA TACCAGGTTG TATATTCGAT TTATAAAACC CATGCGCAAC          2880

AACGGCTGAT GGCTCAACCA TTGCTGCTTC AATGTAATCA ACATTGTCTG GAACCTTTAA          2940

AACATTTTGC GCTGGCAATT TGACATATTC CGCGAACGAT CCAGGTTCAT ATGAGCCAAT          3000

GACGAATAAC TTTTCACATC GTGCATATTC ACCTTTTAAA CAATACTCGC ATTGATAACA          3060

AGGTATTGCT GGGCAACCTG TCACTTTGTC GCCCACATTA ACATGCGTAA CATCACTTCC          3120

AATGGCATCT ACTACACCTG AAAATTCATG ACCAAATGGC ATACCTTTAA TGTATGGCCC          3180

CATTTTTTTG TATCGTGACG TGTCTGAACC ACATATGCCA GTCGCTCGTA CTTTAATAAT          3240

AACGTCATTC GCACTTTCAA TGACTGGCTT TTCATTATCC TCATACCGTA AATCTTCCAC          3300

GCCATATAAT TTCAATGCTT TCACTTGTAA ATCACCTCAA ATTTGATTTA ATTCACAACT          3360

TTTTTCTTTT TAAAAATACC TGTCGCAAAA TAACCTGCAA TGACAATGGA ATTACTTACG          3420

AGTAAATGTT CCATATAAAA ATCAGTGATT TGTCTTAATG GCCCAAGCAT AAAAGTTAGC          3480
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TGCTTTAATA CCTTCGCCGG ATTTTAAATG TTGATACGCC TCGTCCCATT TCGAAATATC   3600

ATATATTTTT GTCACCAAAG CTTCAGCATT TACTAAACCA TCCGCCATAA GTTGCAATGA   3660

AGGTTCCCAA TCTGCTGGCT TTTGACTTCT ACTACCAACA ACTGTTATTT CTTTTTGAAT   3720

CACTTTTTCC ATATCAAATG GAATTTCAGC ATCCTTAAAA ATACCTATTT GACTGTAGAA   3780

ACCTTTTTTG CGTAAAATAT CCAAACCTTG TCGTGCTGCT GGAACTGCAC CTGAACATTC   3840

AACAACAACA TCTGCACCGT AACCGTCTGT AATTCCATTG ATATACGTTT TTAAGTCTGT   3900

TTGTTGTAAA TTGACTACAT AATCCATGTG CAATGCTTCT GCTTTATCTA ATCTGACTTT   3960

GTCATTGTCC AATCCAGTTA CCACAACAGT TGCGCCTTTA CTTTTTAACA CTTGTGCTAC   4020

AAGTAATCCG ATTGGCCCAG GTCCCATTAC AACTGCTACA TCGCCTGAAT TGACTTGAAT   4080

CTTAGAAACG CCATGATGTG CACATGCTAA TGGTTCTGTC ATAGCTGCAG ACTGATACGA   4140

TAtTCGTCTG GAATATGATG CAAACTTTCT TCACGTGCAA TGACATAATT AGTAAATGCG   4200

CCATCAACTT GTGTTCCAAT ACCTTTTCGA TGGTTGCATA AATTATAGTC TTTTGATTTA   4260

CAGTATTCAC ACTCATTACA AACATAGAAT GTCGTTTCAG aTGtGACACG TCACCAACT   4320

TTAAAATCTT TAACGTCTGC TCCAACTTCA ACGATTTCAC CAGAAAATTC ATGACCTAAT   4380

GTCACTGGAA AATTAACTTT ATAATGACCT TCATAAGTAT GAATATCTGT GCCACAAATT   4440

CCTGCATAAT GTACTTTAAT CTTTACTTTA TCATCTAGCG GTGTTGCAAC TTCTTTATCA   4500

AGAAGTTCTA AGTTGCCATG TCCTTCTCTT GTTTTTACTA AAGCTTTCAC CACAAACACC   4560

TCGATTTTTA ATTGAATAGA CTAAATAGTT TAAAGATAAG ATAGTTAACG ATATTACCAC   4620

CTTGATCAAT ACTTGAAATT TCAGATGAAC CTTTTGGCAT TTGTACATTC GTACCTTTCG   4680

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TCGTACCCAC AATGACAGAA TGAATAATGT TTCCTCTTGC TGCACCAACA ATAAACGCGA   4800

CAACAAATGG TATCGTTGCT AAGTCACCAA AAGGTAGTAC TTGGTTTCCT GGTAAAATAA   4860

CGGCTAATAA AACAGTGATA GGTACTAAAA TTAATGCTGT CGAAATAACT GCTGGATGAC   4920

CTAATGCTAC AGCCGCATCC AATCCAATAT AAATTTCACG TTCGCCAAAA CGTTTATTTA   4980

GCCATGTTCT TGCAGACTCT GAAACTGGCA TTAAACCTTC CATTAAGATT TTTACCATTC   5040

TAGGCATTAA TACCATTACT GCAGCCATTG ACATTCCTAA ATTAATGATG TCTCCAGGTT   5100

TGTAACCTGC TAACACACCA ATACCTAAAC CTAAAATTAA GCCGACAAAT ATAGACTCTC   5160

CAAATGCGCC AAAACGTTTT TGAATTGTTT CAGGATCAGC ATCTAACTTA TTCAGACCGG   5220

GTACTTTTTG TAACAATTTA ACTAAGTAAA TACCTGGTGC ATAAGAAATT GTACTTCCTG   5280
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CTACTTTCAA ACAGATAATT TGGAAAATAA CTGCTGCTAA TAACGCTTGC CAAATACTGC      5400

CTGATACGGC ATAAACCATT GCTGCTGTAA ACGTATAATG CCAAAAATTC CAAATATCTA      5460

CATTCATCGT CTTTGTCACT TTAGTTACTA GCAATACAAC GTTAACTATG ATTCCGAGTG      5520

GAATAATAAA TGCTGCGACA GATGATGCCC AAGCGATAGA TGATGTTGCT GGCCAACCTA      5580

CATCAATCAC ATTCAGACTG ACGCCTAAAT TTTTAACCAT CGCTTGTGCT GCTGGCCCTA      5640

AATTTTTAAC TAATAAATCG ATGACTAAGA AAATCCCTAC AAAAGCCACA CCTATTGTTA      5700

AACCAGACCT AAATGCCGCT CCAATTTTCT GCCTAAAGAA TAGGCCAAGC AAGAATATGA      5760

CAACCGGTAA AATAACAGTt GCACCTAAAT CTAAAAATCC CCTTACAAAA TCAGTGAAGT      5820

AACTCATATT TAAACCCTCC CTGTTATATA TGCATTGTCA CGATACTTTC CGATTGTGAT      5880

TACATTTGAC GTTACAGTCA TTTCAACGAC AACCCTTGCT AAATTCGACT GCAGTCCTTT      5940

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ATGCAATTTG CATATATTAA TATGTTATCG ACCCACGTTA CATATCAATT CCGTTATTTT      6060

TGTAACTCTG TTAAGATTTG TTGTTTTGTT TCTTCAATAC CAATACCAGT TAAGAAATTA      6120

CGTGCGTTGA TAACTGGGAA TTTATATTCT TTTTTTGTCA TTGCAGTTGT AACTAATAAA      6180

TCTGCAGTGT CTTCATAAGG TCCAACTTCT GTAATTTTGA TTTGTTTAAT ATCTACTTTA      6240

ATATTGTGTT CCTTTGCCAT TTCTTCAATT GCATTATTTA CTACTGTTGA CGTTGCAATA      6300

CCTGCACCAC ACGCTACTAA TACTTGTTTC ATTTTCAATT CCTCCAATTA ATTTTTAGTT      6360

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TGTTCCCATT TCAATAAACG GCACTTCTTT TTCTAGAACA GCCACACCTA TCGTTCTATG      6600

GTTAATATGT TCGACATCTG TATGCGGTAT AGCGACCGAA CATAGATGCG TTGGTAAACC      6660

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CGCTTAATTG CGTCATTGTC TTGCGCCACA TCTCTCAATT GTAGTAACGC TCTTAAGTGT      6960

GTCACTTTAT CAACAGCAGC AATAGGTACA ATAATATGGA TTGCTGTGCC ATCTGACATG      7020

TATATTGGTT CTTGTAATAT CAACATACTC ATCGCTGTTT TATGTACATG CTTTTCAGAG      7080
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TGCATCTCAT GAATATATTT AATATCAATA AAATGATTAG CAACTAACAC ATCACTTGCT    7200

TTAGCAATAG CTTCATCAAT ATTTTCAACA TGATGCATTC TTTTCACGTG CCTTGCCGGT    7260

ATCAAGTCAG CTAAATCTAA TGyCTwATTT tGTGtGACaA TCGATCCATT AATGGTTGAA    7320

ATTGAATTAT AATTGGCAAT AAAATCTTCT AAACCATCAC GTAGTcTGTA ATGTCATTAA    7380

CTGTCGTTGT GCGTTCAATT AATGCCATTA ACTTGTTTAT TTCCTTATCA ATGTCAGCCG    7440

ATTCCTTATT AATGTACTTC ATCACTTCTT TACGTAACTT TCGTTGCTCA TTTTCAGATA    7500

AAGCTACTTT TGTGATAAAT AATTTTTTAT GTGTTAGGAC AAACATTGGT GAAAAGACGA    7560

TGTCATAATC TAATGTGTAA TTTTCAAATG TTCTAAGTGA AATCGCATCT AAGAAAATAA    7620

TTTCTGGAAA TAAGTTTCGC AACTCGTATA ACATCATTTG TGATACTGAC GTGCCTTGTG    7680

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CAGTTAACGA TTGACATGAT TGTTTCACCA TATGAAATAA GGATTGATAA TTTCCTTGTA    7860

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TCGTATCCCT CAAATACTGA TAATTAATAT TTAATGGATT CATCACATGA CCACTTTGAA    8220

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GACTCTTCAA AAATTGTTCT ACCTGTTTGA TCTTGTCTTT TTGATATGCG ATATCTTCGA    8340

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CAATCAACTT AATGAAGAAA CGGCGAACTT CAAATTCATC ACCAACAATT TCATAACCAT    8460

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TATCGTGAAT GACAGTATTT TTACTGACTT GTAAATCAAT TGAAAAATGG TTTAGAGACA    8580

TTGCGTTTTC CTTACTAAAA AGCATGAGCA TTAAATAATA ACGACGTGTT CTATGCTAA     8640

AAATGACATT GTTGCCGTTT AACATTTGCT GCTCCGATAC ATCTCGCTTG AATAACGTCA    8700

TGATTTCAGA ACTTACAATA AAATTTCCTT GGCTTGTTCT TTCAAGTTTT GGATAACCCT    8760

CTTGTTCAAG CCACAAATTG ATTTTTTGAA TGCGATATCC TAGTTGTCTA CGAGACAAAC    8820

CAAATATCGA TTCAAGTTCT TTACCATGAA TAGTAGGATT CAATACAATT TCTCTCAGTA    8880
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TCAATCGTCA CACCGATGTA CACACTTTGA ACACATATTT TCAAAATGAG CATGTACATC      9000

ATTGTGATGT TTTAACAACA TTTCAATTAT ATCTATATTT TTTGTGATTT TAATCTTTTA      9060

AAATAAAGCA ATTGAAATTT TTGCATATAT TTTTGTGTTT TGTGTTTTTT TGAAGCATTT      9120

TTAACATACA TATCTCAATC ATTATCAAAT TGTCATGACC ATTGTAACCC AATACAAAAA      9180

CCCTAAGGAC GCTTATATCA GGCGCCTTAG GGTTAACTGT ATCTATTTAA TTAAGTATTA      9240

TTATTCGTAT GTACGTAACT TATGGTCTAT CAAGTTCCAC ACTTCTTCAA CATCAACTGC      9300

TGTAGCAAAA TAAGCATTGG CAGGCTTACC TGTAACATGA TTTAAATCGA CAGCCATAGT      9360

GCCATAAGTT AGTGGACTTT GATGTTCAAT GTCGATATTA ACGGGTACCA TTGTAAACAA      9420

TTCTGGTTGT AACAAATACA AAATTGTACA AGCATCATGT ATTGGACCAC CATCCATATT      9480

AAAGTGAGTC TTGTATGTCT TCTTAAAGAA TTGCAATAAT TCTACGACGA ACTGTGCAAC      9540

AGGATTATTG ATACTTTCAA AGCGTTCAAT CACGTGATCG TCGGCTAAAA CTTGATGTGT      9600

TACATCTAAA CCAAACACAT TTATAGTAAT CCCACTTTCA AAAACACGCT TCGCTGCTTC      9660

AGCATCTACC CAAATATTGA ATTCTGCTGT AGGCGTCCAA TTTCCAAATG TACCACCACC      9720

CATCAAAGTA ATAGATTCAA TATGCTCAGC GATTCTTGGC TCACGAATCA ATGCCGTTGC      9780

TACATTCGTA AGAGGACCTG TCGCTACAAT TGTTACAGGT GTATCACTCG TCATCACTTT      9840

GTTTATAATC ACATCTGATG CTGGCATTGC AACTGCTTGA CGTGATGGTG TCGACGGTAG      9900

TTTCGGACCA TCTAATCCAG ATTCCCCATG TATTTCAGAA GCAAAGGCAG CTGGTTTAAT      9960

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GTTATCGATA GCTTATGTAT ATTTATTTAT GTGGTGAATC ATGTTTATTT TGAAAAATAG     10260

TTTTAACTTT CTCATATTTT TGGATACAAA CACTATTTAT CTATTTTATG GCTTATAAAT     10320

TTATCCGATA TGCCTTATCA ACCTACCTCG CTAAAAATAG GATGTCTACA TATCTATACC     10380

GACTTTTGTC AACTCATTTT CACAACAATA TAAACAGCAA TTTATATGAT TGTTACATGA     10440

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TCAAAAGCTA TATTGAGAAT AATTAGGAGG GATGTTGATG AAATCTTTAT TTGAAAAAGC     10560

ACAGCAGTTC GGCAAGTCCT TTATGTTACC TATCGCAATC TTACCAGCTG CAGGTCTATT     10620

GTTGGGTATC GGTGGTGCAT TAAGTAATCC AAACACCGTT AAAGCATACC CTATTTTAGA     10680
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AAATTTACCG GTCATCTTTG CAATTGGTGT CGCAATCGGA TTATCTAGAA GCGATAAAGG    10800

TACTGCAGGT tTAGctGCGC TGCTCGGTTT CTTAATTATG AACGCAACTA TGAATGGCTT    10860

ATTAACTATC ACGGGCACAT TGGCAAAAGA TCAGCTTGCA CAAAATGGAC AAGGCATGGT    10920

GCTCGGTATA CAAACGGTTG AAACCGGTGT TTTTGGCGGG ATTATCACAG GTATTATGAC    10980

CGCAATACTT CACAACAAAT ATCACAAAGT GGTATTACCA CCGTATTTAG GTTTCTTTGG    11040

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CAAAGGGCAC TTAGTTCAAG GTACGCAGAA CATCTTCTTT GCTCAACTTG GTGATCCAGA    11340

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CACATATAGT TGTATCAAAT AGCCCTTTAT ACAATTTTTT GGGTAAGGTT TTACAATTTT    12360

TGGGATGGTA TAGATTTTAT AAAAAGTTAT TTAAGTTCTT CTGCTTCAGC CATAATATCT    12420

TTTAATGTTT TAGCTGAATG TGCGAACTTG CTTTGTTCTT CGTCGTTTAA TGGGATTTCT    12480
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TCCTCATATT CGCCTTCTAA TAATGCTGAT ACAGTCAATA CGGCATCTTC ATTTCTGAAA     12600
ATCGCTTCAG TAATTCTAGC TAATCCCATT GCAACACCAT AATAAGTGGC ACCTTTAGCT     12660
TGAATAATGT CATATGCTGC ATCACGTGTT TGAACAAAAA TTTGTTCAAT TTGCGCTTTG     12720
CCCTCAGGAC GTTGTTCAAG TAATGTCTTC AAAGGTTGAC CCGCAATATT AGCGTGTGAC     12780
CATACTGGTA ATTCAGTGTC ACCATGTTCA CCAATAATTT GAGCATCGAC GCTACGTGGC     12840
GCAACATCGn AcgyTcGCTT AACAATAATC TAAAGCGTGC AGAGTCTAAA ATTGTACCAG     12900
AACCTATAAC ACGTTCTTTA GGTAAACCAG AGAATTTCCA TGTTGCATAC GCTAAAATAT     12960
CAACAGGATT TGTAGCTACC AAGAAAATAC CATCAAATTT TGATGCCATT ACTTCACCAA     13020
CAATTGATTT GAATATTTTC AAGTTTTTAG ATACTAAATC TAAACGTGTT TCTCCAGGTT     13080
TTTGTGCAGC ACCAGCACAG ATGACAACTA GATCCGCATC ATGACAATCA CTGTATTCGC     13140
CAGCTTTCAC ACGAACTGTT GTTGGAGAAT ATGGTGTGGC ATGTTTTAAA TCCATAACAT     13200
CTCCTCGAAC TTTTTCAGTG TCTAAATCAA TGATGACTAA TTCATCAACA ATGCTTTGGT     13260
TCACTAATGA AAATGCGTAG CTTGAACCTA CTGCACCATT ACCTATTAAT ACAACTTTGT     13320
TCCCTTTAAA TTTGTTCATT ACAAAAACTC CCTTATGATT AATTCACTAA CATACATGTA     13380
GCTTCAAATA TGTTAGTTTA ATGCTGCTTA TTGACGATAC AAAAGCAAAT AAACATCTCT     13440
TTTATTTTCA ACGCATAACT TAAAAGGTCA TGTGTCATCC GCTTTTAAGT TTGTGATTTA     13500
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TCACATTTTA TTTTAATTTT TACACCTTTT TAATTTGTAT mCGATTACAT CTTAGATGTC     13620
TTTAGTCTTC GTACTTCGCC AGTGATTATT TACACTTTCA CATTTTTATT ATCATGTTTA     13680
CTTTTTTCTA GGAAAACAAC AATGTTTTTT GAATTAGTCA AATAAATGCG CTCAATCGTC     13740
GGTGTGCAAA CAGACAATTG TACACAATGC TTATTGATAA GTATTTAAAA AATTAAAAAT     13800
GTCATACAAT TATCAAATTT GCCATTTTAT TTATATTTTC TCAAACCAAT TAATTGAATA     13860
TCGAAATTTT TAGTAGAATA ATCAAAATAT ACAGATTAAA GGAGGAGTAT CATGCTTACA     13920
GAACAAGAGA AAGACATTAT CAAACAAACG GTGCCTTTAC TTAAAGAGAA AGGGACAGAA     13980
ATTACGTCAA TCTTTTATCC AAAAATGTTT AAAGCGCATC CTGAACTTTT AAACATGTTT     14040
AATCAAACGA ACCAAAAACG AGGCATGCAA TCTTCAGCAT TAGCACAAGC TGTAATGGCC     14100
GCAGCGGTTA ATATCGATAA CTTAAGTGTT ATTAAACCAG TCATTATGCC AGTCGCATAT     14160
AAACACTGCG CACTACAAGT TTATGCTGAA CATTATCCAA TTGTGGGGAA AAATTTATTA     14220
AAAGCCATTC AAGACGTGAC AGGATTAGAA GAAAATGACC CTGTCATTCA AGCTTGGGCA     14280
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(2) INFORMATION FOR SEQ ID NO: 58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8779 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

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GGTATTTTnG GAnGGGTACC TAAAGCAATT CCGGCAAAGG GTnAATCCAG GTACCGAAAT        60

GGACTTCCCG TTATCGATAA TACCGACATA TATTGTGACA AGTAGATTTT ATGGACATTT       120

AGGCTTACTT TTACTTGTGA TAATTGCATG TATGTTTACT GGTATTTAtC CaTCaATACA       180

TATCATTCAA TTATTGATAT ATGTACCGTT TTGTTTTTTC TTAACTGCCt CGGTGACGTT       240

ATTAACATCA ACACTCGGTG TGTTAGTTAG AGATACACAA ATGTTAATGC AAGCAATATT       300

AAGAATATTA TTTTACTTTT CACCAATTTT GTGGCTACCA AAGAACCATG GTATCAGTGG       360

TTTAATTCAT GAAATGATGA AATATAATCC AGTTTACTTT ATTGCTGAAT CATACCGTGC       420

AGCAATTTTA TATCACGAAT GGTATTTCAT GGATCATTGG AAATTAATGT TATACAATTT       480

CGGTATTGTT GCCATTTTCT TTGCAATTGG TGCGTACTTA CACATGAAAT ATAGAGATCA       540

ATTTGCAGAC TTCTTGTAAT ATATTTATAT GACGAAACCC CGCTAACCAT TAATAAATGG       600

AAGTGGGGTT CATTTTTGTT TATAATTTAA GTAAATAACA TATTAAGTTG GTGTATTATG       660

AACGTTTTAA TAAAGAAATT TTATCATTTG GTAGTTCGAA TACTTTCTAA AATGATTACG       720

CCTCAAGTGA TTGATAAACC GCATATCGTA TTTATGATGA CTTTTCCAGA AGATATTAAG       780

CCTATCATCA AAGCATTAAA TAATTCGTCG TATCAGAAAA CTGTTTTAAC AACACCAAAA       840

CAAGCGCCTT ATTTATCTGA ACTTAGCGAC GATGTTGATG TGATAGAAAT GACTAATCGA       900

ACATTGGTAA AACAAATTAA GGCTTTGAAA AGCGCGCAGA TGATTATTAT CGATAATTAT       960

TACCTATTGC TAGGTGGATA TAATAAGACT TCTAATCAAC ACATTGTTCA AACGTGGCAT      1020

GCAAGTGGTG CATTAAAAAA CTTTGGCTTA ACAGATCATC AAGTCGATGT GTCTGACAAG      1080

GCAATGGTTC AGCAGTACCG TAAAGTTTAT CAAGCGACGG ATTTTTACTT AGTGGGTTGT      1140

GAACAAATGT CACAATGTTT TAAACAGTCT TTAGGTGCAA CAGAAGAGCA AATGCTGTAT      1200

TTTGGGCTTC CGAGAATTAA TAAATATTAC ACAGCTGATA GAGCAACGGT TAAGGCAGAG      1260

TTAAAGGATA AATATGGAAT TACAAATAAG TTGGTATTAT ATGTACCAAC ATATAGAGAA      1320

GATAAAGCAG ATAATAGGGC TATTGATAAA GCTTATTTTG AAAAATGTTT ACCAGGATAT      1380
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ATCGACACGT CTACATTAAT GCTAATGTCA GATATAATTA TTAGCGACTA TAGTTCGCTG      1500

CCAATAGAAG CTAGCTTGTT AGATATTCCA ACTATATTTT ATGTGTATGA TGAAGGAACA      1560

TATGATCAGG TGAGAGGCCT GAATCAATTT TACAAAGCAA TACCGGATAG CTACAAAGTG      1620

TATACTGAAG AAGATTTAAT AATGACGATA CAAGAAAAAG AACATCTATT AAGTCCGTTA      1680

TTTAAAGATT GGCATAAGTA TAATACTGAT AAAAGTTTAC ATCAGCTCAC AGAATATATA      1740

GATAAGATGG TGACAAAATG AGGTTTACGA TAATCATACC TACATGTAAT AATGAGGCAA      1800

CAATTCGACA ATTGTTAATA TCTATTGAGA GTAAAGAACA CTATAGAATC CTTTGTATTG      1860

ATGGTGGTTC TACTGATCAA ACAATTCCTA TGATTGAACG GTTACAAAGA GAACTCAAGC      1920

ATATTTCATT AATACAATTA CAAAATGCTT CGATAGCTAC GTGTATTAAT AAAGGTTTGA      1980

TGGATATCAA AATGACAGAT CCACATGATA GTGACGCATT TATGGTCATA AAACCAACAT      2040

CAATCGTATT GCCAGGTAAA TTAGATAGGT TAACTGCTGC TTTCAAAAAT AATGATAATA      2100

TTGATATGGT AATAGGGCAG CGAGCTTACA ATTACCATGG TGAATGGAAA TTGAAAAGTG      2160

CTGATGAGTT TATTAAAGAC AATCGAATCG TTACATTAAC GGAACAACCA GATTTGTTAT      2220

CAATGATGTC TTTTGACGGA AAGTTATTCA GTGCTAAATT TGCTGAATTA CAGTGTGaCG      2280

AAACTTTAGC TAACaCATAC AATCACGCAA TACTTGTCAA GGCGATGCAA AAAGCTACGG      2340

ATATACATTT AGTTTCACAG ATGATTGTCG GAGATAACGA TATAGATACA CATGCTACAA      2400

GTAACGATGA AGATTTTAAT AGATATATCA CAGAAATTAT GAAAATAAGA CAACGAGTCA      2460

TGGAAATGTT ACTATTACCT GAACAAAGGC TATTATATAG TGATATGGTT GATCGTATTT      2520

TATTCAATAA TTCATTAAAA TATTATATGA ACGAACACCC AGCAGTAACG CACACGACAA      2580

TTCAACTCGT AAAAGACTAT ATTATGTCTA TGCAGCATTC TGATTATGTA TCGCAAAACA      2640

TGTTTGACAT TATAAATACA GTTGAATTTA TTGGTGAGAA TTGGGATAGA GAAATATACG      2700

AATTGTGGCG ACAAACATTA ATTCAAGTGG GCATTAATAG GCCGACTTAT AAAAAATTCT      2760

TGATACAACT TAAAGGGAGA AAGTTTGCAC ATCGAACAAA ATCAATGTTA AAACGATAAC      2820

GTGTACATTG ATGACCATAA ACTGCAATCC TATGATGTGA CAATATGAGG AGGATAACTT      2880

AATGAAACGT GTAATAACAT ATGGCACATA TGACTTACTT CACTATGGTC ATATCGAATT      2940

GCTTCGTCGT GCAAGAGAGA TGGGCGATTA TTTAATAGTA GCATTATCAA CAGATGAATT      3000

TAATCAAATT AAACATAAAA AATCTTATTA TGATTATGAA CAACGAAAAA TGATGCTTGa      3060

ATCAATACGC TATGTCGATT TAGTCATTCC AGAAAAGGGC TGGGGACAAA AAGAAGACGA      3120

TGTCGAAAAA TTTGATGTAG ATGTTTTTGT TATGGGACAT GACTGGGAAG GTGAATTCGA      3180
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      TAAAATCAAA CAAGAATTAT ATGGTAAAGA TGCTAAATAA ATTATATAGA ACTATCGATA    3300

      CTAAACGATA AATTAACTTA GGTTATTATA AAATAAATAT AAAACGGACA AGTTTCGCAG    3360

5     CTTTATAATG TGCAACTTGT CCGTTTTTAG TATGTTTTAT TTTCTTTTTC TAAATAAACG    3420

      ATTGATTATC ATATGAACAA TAAGTGCTAA TCCAGCGACA AGGCATGTAC CACCAATGAT    3480

      AGTGAATAAT GGATGTTCTT CCCACATACT TTTAGCAACA GTATTTGCCT TTTGAATAAT    3540

10    TGGCTGATGA ACTTCTACAG TTGGAGGTCC ATAATCTTTA TTAATAAATT CTCTTGGATA    3600

      GTCCGCGTGT ACTTTACCAT CTTCGACTAC AAGTTTATAA TCTTTTTTAC TAAAATCACT    3660

      TGGTAAAACA TCGTAAAGAT CATTTTCAAC ATAATATTTC TTACCATTTA TCCTTTGCTC    3720

15    ACCTTTAGAC AATATTTTTA CATATTTATA CTGATCAAAT GAGCGTTCCA TTAATGCATT    3780

      CCCCATCATA TTACGTTGCT TCTCGCCACC AAGGTTTTTA TAGTCTCCTG CACCCATGAT    3840

      AACTTGATTA ATTCTAAATT TACCTCGTTT GGTAGTAATC GTATGGTTGT AATTTGCTGT    3900

20    ATCACTTGAT CCAGTTTTTA AACCATCTGT ACCCGGCAAA CTCATTTTTG CACCTTCCAA    3960

      TGAAAAGTTG AATGTGTAAT ACGTAACTGC ATGCGTTGTT GGTGCTAACT GCTTTGTAAA    4020

25    GTCTAATATT TTAGGTGTCT CTTTAATCAC GTGTAAATCT AAAATGGCAT AGTCTCTAGC    4080

      AGTCGTTACA GTACGTTCTT GGTCTTTATA CTTTGTTGGT GCAAATGTAC GTAATCTTGA    4140

      ATTTTCAGCA CCCGTTGGAT TGACGAAATG TGTATTTTTC ATTCCGATAG CTTTAGCTTT    4200

30    GTTATTCATT AAATCAACGA AATCGCTGGT GTTTTTTGAA ACCTTCTTAG CTAAAATTAA    4260

      TGCCGCGGCA TTACTAGAAT TAGATACTGT AATTTGTAAT AGGTCTGCGA TTGTCCATAC    4320

      TTGTCCAGGA TATAGTTTCG TATTACTCAA CTCAGGTAGT GTAGACATAA TATATTCTTT    4380

35    GTTCGTCATT GTGACTGTGT CATCAAGTGA AAGCTGCCCC TTATTTACAG CTTCCAATGT    4440

      TAAGTACATT GTCATTAATT TAGTCATAGA CGCTGGAtTC CACTTAGTAT CGATATTGTA    4500

      TTGATACAGT AATTGTCCAG TTTGACTTAC ATTAACAGCA CTCGTCGGTT CGTATGCAGC    4560

40    CGACAAACCT GCATAACCAT ATTGATTTGC TGCTTGTACA GGGGTTACGT CACTGTTAGT    4620

      AGCTTGTGCA TATGGTGTCA TAATACTTAA TGTTAAACAT AAAATGATGA TAATAGATAT    4680

45    TAAATTTTTC ATAAAGCGTT AATCTTCCCT TTTCCAATTC TTAAATATTC CCTAAAAGCA    4740

      ATGGTTATTC CTACTTACGG AAATCATTGC TAATTCACTT CACCTTAATT AAATTGTTGA    4800

      AAATAAAGTT TTCTGCAGTT AATTTGAAAA ATAATGCAAA TATATTACGT GTGTAGCTAA    4860

50    AGGTGTTATA ATGTTTGTAC GAAGAGCAAA CTTACTCAAA AGCGATTAAT TTTCATGTTT    4920

      TAATATAAAG ACTTTGAGAA GTTATTACAA AAAATGCAAT AGAAATATTC TATCATATAA    4980
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AGAGGTAAAA CTATGAAACG AGAAAATCCA TTGTTTTTCT TATTTAAAAA ACTATCATGG   5160

CCAGTGGGTC TTATCGTTGC AGCTATCACT ATTTCATCAC TAGGGAGCTT AAGTGGACTA   5220

TTAGTGCCAC TGTTTACTGG ACGAATTGTA GATAAATTTT CCgTGAGCCA TATCAATTGG   5280

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GCAATGATAT TTATGTTAT TCAGTTATCT ATGCCTTTAA TCAATCTTTC CACGTTAGTT   6000

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CAAATCCCAC AAGGTCAAGT GAGTGCTTTT GTAGGCCCTT CTGGGTCTGG TAAAAGTACG   6240

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GAAAGTGTCT ATGATATCCC GTTATCTAAG TGGCGACGCA AAATTGGATA TGTTATGCAA   6360

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CAATTTGATG AAGGATATGA CACGCTTGTA GGTGAACGAG GATTGAAACT GTCTGGCGGA   6540

CAACGTCAAC GTATTGATAT TGCTAGAAGT TTTGTTAAAA ATCCTGATAT TTTGTTACTT   6600

GATGAAGCAA CAGCTAATCT CGATAGTGAA AGTGAATTGA AAATTCAAGA AGCTTTAGAA   6660

ACATTGATGG AAGGTAGAAC AACGATTGTC ATTGCGCATC GTTTGTCTAC AATTAAAAAA   6720

GCCGGTCAAA TTATATTCTT AGACAAAGGA CAGGTAACAG GTAAAGGTAC GCATTCAGAA   6780

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     TTTTATATAT ATAAGTAAGC TTGGAGCAAA TACACATATA CCATCGAGGA AATTAAAGTG          6900

     TGGCACATTG ATGGATATAG ATGTTAATAA ATTGCTTCAA GCTTTTGTCT ATTTTAAATC          6960

5    ATTTGAGAAG TTACGACATA ATAATTCTTA AATTAATGAA ATCGATATTT TAAGAAAAAA          7020

     ATGCTCATGG TATAATACAA GTTATAAGCA AACATACATA TATTAAATAC TGTAGCCACG          7080

     AGTCATAATT CTTCATATTT TACATAGCAA TTTAACTGAT TTTAGAGTCC ACGGTACAGA          7140

10   AGTTTGATAT TTCAATGTTT CTAAATTTTT AAAAAATTAA ATCATAGGTG GGTGCCAAAT          7200

     GTTTTTATTA ATCAACATTA TTGGTCTAAT TGTATTTCTT GGTATTGCGG TATTATTTTC          7260

     AAGAGATCGC AAAAATATCC AATGGCAATC AATTGGGATC TTAGTTGTTT TAAACCTGTT          7320

15   TTTAGCATGG TTCTTTATTT ATTTTGATTG GGGTCAAAAA GCAGTAAGAG GAGCAGCCAA          7380

     TGGTATCGCT TGGGTAGTTC AGTCAGCGCA TGCTGGTACA GGTTTTGCAT TTGCAAGTTT          7440

     GACAAATGTT AAAATGATGG ATATGGCTGT TGCAGCCTTA TTCCCAATAT TATTAATAGT          7500

20   GCCATTATTT GATATCTTAA TGTACTTTAA TATTTTACCG AAAATTATTG GAGGTATTGG          7560

     TTGGTTACTA GCTAAAGTAA CAAGACAACC TAAATTCGAG TCATTCTTTG GGATAGAAAT          7620

     GATGTTCTTA GGAAATACTG AAGCATTAGC CGTATCAAGT GAGCAACTAA AACGTATGAA          7680

25   TGAAATGCGT GTATTAACAA TCGCAATGAT GTCAATGAGC TCTGTATCGG GAGCTATTGT          7740

     AGGTGCGTAT GTACAAATGG TACCAGGAGA ACTGGTACTA ACGGCAATTC CACTAAATAT          7800

     CGTTAACGCG ATTATTGTGT CATGCTTGTT GAATCCAGTA AGTGTTGAAG AGAAAGAAGA          7860

30   TATTATTTAC AGTCTTAAAA ACAATGAAGT TGAACGTCAA CCATTCTTCT CATTCCTTGG          7920

     AGATTCTGTA TTAGCAGCAG GTAAATTAGT ATTAATCATC ATCGCATTTG TTATTAGTTT          7980

35   TGTAGCGTTA GCTGATCTAT TTGATCGTTT TATCAATTTG ATTACAGGAT TGATAGCAGG          8040

     ATGGATAGGC ATAAAAGGTA GTTTCGGTTT AAACCAAATT TTAGGTGTGT TTATGTATCC          8100

     ATTTGCGCTA TTACTCGGTT TACCTTATGA TGAAGCGTGG TTGGTAGCAC AACAAATGGC          8160

40   TAAGAAAATT GTTACAAATG AATTTGTTGT TATGGGTGAA ATTTCTAAAG ATATTGCATC          8220

     TTATACACCA CACCATCGTG CGGTTATTAC AACATTCTTA ATTTCATTTG CAAACTTCTC          8280

45   AACGATTGGT ATGATTATCG GTACATTGAA AGGCATTGTT GATAAAAAGA CATCAGACTT          8340

     TGTATCTAAA TATGTACCTA TGATGCTATT ATCAGGTATC CTAGTTTCAT TATTAACAGC          8400

     AGCTTTCGTT GGTTTATTTG CATGGTAATA TGTCGAAGAG TGACTATGAT AATACATTTT          8460

50   AACTAATAAA TATGTCCAGG CATGTCGTCT ATTGATATAG GTGAGATGCT TGGACTTTTT          8520

     TATTATTGAT ATAAAGGTAT nTAAATATTT TTAAAGTTAC CGAAATTGAA GCATTATAAA          8580
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GACAGTAAGG ACTAGGTACA GTCATAGTAC TTCGAGCAAA ATTTGTTTTG TTATTATAAA      8700

CAACACAAAG GAGATAACTT CTCTAnTGAA GAAGTTAAAA ACATTATAGC AGACAATGAA      8760

ATGAAAGTAA ATTAAAAAT                                                   8779
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(2) INFORMATION FOR SEQ ID NO: 59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31096 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

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GTTGCAGTAG TCAAAGAATT AAACAAGGTG AAGGcGTGTA GCTTGCACAC CCGAAAATGT      60

GCGTAAGTTA aCGGATGCAG GACATAAAGT AATTGTTGAA AAAAATGCTG GCATTGGTTC      120

AGGATTTTCT AACGATATGT ATGAAAAAGA AGGCGCTAAG ATCGTAACTC ACGAACAAGC      180

ATGGGAAGCT GATCTTGTTA TCAAAGTAAA AGAACCTCAT GAAAGCGAAT ATCAATATTT      240

CAAAAAGAAT CAAATTATCT GGGGATTTTT ACATCTAGCA TCTTCAAAAG AAATAGTAGA      300

AAAAATGCAA GAAGTTGGTG TAACTGCGAT TAGTGGTGAA ACCATTATAA AAAATGGAAA      360

AGCAGAATTA TTAGCGCCAA TGAGTGCTAT AGCAGGTCAA CGCTCAGCAA TTATGGGAGC      420

TTACTACTCT GAAGCACAAC ATGGTGGTCA AGGTACTTTA GTGACTGGTG TACATGAAAA      480

TGTGGATATA CCTGGTAGTA CATATGTGAT TTTCGGTGGT GGAGTAGCAG CAACAAATGC      540

AGCAAATGTT GCCTTGGGAC TAAATGCTAA AGTAATCATT ATCGAGTTAA ACGATGACCG      600

CATTAAATAT CTTGAAGATA TGTATGCAGA AAAAGATGTC ACAGTAGTCA AATCAACACC      660

AGAAAATTTA GCAGAACAAA TTAAGAAAGC AGATGTATTT ATTTCTACAA TTTTAATTTC      720

AGGTGCGAAA CCGCCAAAAT TGGTTACTCG TGAGATGGTT AAATCAATGA AAAAAGGTTC      780

AGTATTAATC GATATAGCTA TTGACCAAGG TGGAACTATT GAAACAATTA GACCAACTAC      840

AATTTCTGAT CCAGTGTATG AAGAAGAAGG TGTGATTCAT TATGGTGTAC CAAATCAACC      900

AGGAGCAGTC CCAAGAACTT CAACAATGGC ATTAGCACAA GGAAATATTG ATTATATATT      960

AGAAATTTGT GACAAAGGCT TAGAACAAGC AATTAAAGAT AATGAAGCCT TAAGTACTGG      1020

TGTAAACATT TACCAAGGAC AAGTGACAAA TCAAGGATTA GCTTCATCAC ATGACCTAGA      1080

TTATAAAGAA ATATTAAATG TTATCGAATA GATAGTAATT TAAATGAAAT TGAGTGAAAT      1140

GAATATTTTA AATATAGCAT TATAGTTTGG ACTAAAAATT TACAAAACGG AAGGATGTAA      1200
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     TCGAAGAAGC TAAAGCAAGC ATTAAACCAT TTATTCGTCG AACACCTCTA ATTAAATCAA        1320

     TGTATTTAAG CCAAAGTATA ACTAAAGGGA ATGTATTTCT AAAATTAGAA AATATGCAAT        1380

5    TCACAGGATC TTTTAAATTT AGAGGCGCTA gCAATnAAAA TTAATCACTT AACAGATGAA        1440

     CAAAAAGAAA AAGGCATTAT CGCAGCATCT GCTGGGgAAC CATGCACAAG GTGTTGCTTT        1500

     AACAGCTAAA TTATTAGGCA TTGATGCAAC GATTGTAATG CCTGAAACAG CACCACAAGC        1560

10   GAAACAACAA GCAACAAAAG GCTATGGGGC AAAGGTTATT TTAAAAGGTA AAAACTTTAA        1620

     CGAAACTAGA CTTTATATGG AAGAATTAGC GAAAGAAAAT GGCATGACAA TCGTTCATCC        1680

     ATATGACGAT AAGTTTGTAA TGGCAGGCCA AGGAACAATT GGTTTAGAAA TTTTAGATGA        1740

15   TATTTGGAAT GTGAATACAG TCATCGTACC AGTTGGCGGT GGAGGATTAA TTGCAGGTAT        1800

     TGCCACCGCA TTAAAATCAT TTAACCCTTC AATTCATATT ATCGGTGTTC AATCTGAGAA        1860

     TGTTCATGGT ATGGCTGAGT CTTTCTATAA GAGAGATTTA ACTGAACATC GAGTGGATAG        1920

20   CACAATAGCA GATGGTTGTG ATGTAAAAGT TCCTGGTGAA CAAACATATG AAGTAGTTAA        1980

     ACATTTAGTA GATGAATTTA TTCTTGTTAC TGAAGAAGAA ATTGAACATG CTATGAAAGA        2040

     TTTAATGCAG CGTGCCAAAA TTATTACTGA AGGTGCAGGC GCATTACCAA CAGCTGCAAT        2100

25   TTTAAGTGGA AAAATAAACA ATAAATGGCT TGAAGATAAA AATGTTGTTG CATTAGTTTC        2160

     AGGCGGGAAT GTTGACTTAA CTAGAGTTTC AGGTGTCATT GAACATGGAC TGAATATTGC        2220

30   AGATACAAGC AAGGGTGTGG TAGGTTAAAA CATTTAATCT TAAAAATGAG GTGTAATTAT        2280

     GTCAAATGGT AAAGAATTAC AAAAAAATAT AGGTTTCTTC TCAGCGTTTG CTATTGTTAT        2340

     GGGGACAGTT ATTGGTTCAG GAGTATTCTT TAAAATATCA AACGTAACAG AAGTAACAGG        2400

35   AACAGCAGGA ATGGCCTTGT TTGTATGGTT CCTAGGCGGC ATCATTACCA TTTGTGCGGG        2460

     GTTAĀCAGCA GCAGAACTTG CTGCTGCAAT CCCTGAAACA GGTGGCTTAA CGAAGTATAT        2520

     AGAATATACA TACGGTGATT TCTGGGGCTT CCTATCAGGT TGGGCGCAAT CATTTATTTA        2580

40   TTTTCCAGCT AACGTAGCAG CATTGTCTAT CGTATTTGCG ACACAGCTAA TTAATTTATT        2640

     CCATTTATCT ATAGGTTCGT TAATACCAAT AGCAATCGCA TCTGCGTTAT CTATTGTGTT        2700

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45   ACTGATTCCA ATCATCGTTA TTGTAATTTT TGGTATTTTT CAATCTGGAG ATATCACTTT        2820

     TTCATTAATT CCAACTACAG GTAATTCaGG AAATGGCTTC TTTACAGCAA TTGGTAGTGG        2880

50   TTTATTAGCA ACTATGTTTG CATATGATGG TTGGATTCAT GTAGGAAATG TTGCGGGGGA        2940

     ACTTAAAAAT CCTAAACGCG ATTTACCTTT AGCGATTTCA GTTGGTATCG GTTGTATTAT        3000
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TGGTAATTTA AATGCAGCTT CAGATACATC AAAAATATTA TTTGGTGAAA ATGGCGGTAA          3120

GATTATTACA ATCGGTATAT TAATTTCTGT TTATGGTACG ATCAATGGCT ATACTATGAC          3180

TGGTATGCGC GTACCATATG CAATGGCTGA AAGAAAATTA TTGCCATTTA GCCATTTATT          3240

CGCAAAATTA ACAAAATCTG GCGCACCATG GTTTGGCGCA ATTATACAAC TTATAATCGC          3300

TATCATCATG ATGTCAATGG GAGCATTTGA TACAATTACA AATATGTTAA TCTTTGTTAT          3360

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TATGGAACGA CCATATAAAG TACCGTTATA TCCGATCATA CCTTTAATTG CTATTTTGGC          3480

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AAGATTAATT CAAGGACTTT CAGCAGCATG TATTATGCCT GCAACTTTGT CTATTATTAA          4140

GTCATATTAC ATTGGGAAAG ATAGACAACG CGCTTTAAGT TATTGGTCAA TTGGCTCATG          4200

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AACCTCACTT CTTTTTATTA CTTTATTAGC TATTGCAATT GGATCTTTTA GTTTATTTAT          4500

AGTTCTTGAA AAGCGTGCTA CAAATCCTTT AATCGATTTT AAATTATTTA AAAATAAAGC          4560

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AATCACTTAT TTAGTAATGG TACTAATTAT GATTCGTGTT GGTGAAAAGT TACTTCAAAC          4740

ACTCGGATGC AAGAAACCAA TGTTAATTGG AACAGGAGTT CTTATTGTCG GAGAATGTCT          4800
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TGCACCGTTA GAAAAAGTAG GCGTTGCTGC AGGTATCTAT AAAATGGCTT CTGCATTAGG       4980

TGGAGCATTT GGCGTCGCAT TGAGTGGTGC AGTATATGCA ATCGTATCAA ATATGaCAAA       5040

CATTTATACA GGTGcAATGa TTGnCATTAT GGTTaAATGC AGGTATGGGa ATATTATCaT       5100

TCGTTATCAT TTTGtTACTT GTGcCTAAAC mAAACGACAC TCAATTATGA TAATTGAGAA       5160

TTAAATTGAA ATCATACAAG TCGCTACAAT ATTAAACAAA AATATAAACC GATTCTTATG       5220

TGTCATTATT TTAAATGAAC ATAGGGATTG GTTTTTTATT ACTCTTTTAC GCTACTTTAT       5280

TTATAATTAT TATAAATTGT CACAAATTCA ATTTACCTTA CAATATATTT TGTGTTATTA       5340

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AATTCACAAA ATGGTCAATC ATTATCTGCT ACTCATGAAA ATGAGCAACC AAATATTAGT       5820

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CGTCAACAGA CTAGCCGACG TTCAAATAGA ATTCAAACGC GTTCGGTTGA GTCAAGAGCT       6360

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GCTAATGATG GTTCGGGCTA TCCTGTTGGT ACATATATCa ATGCTTCTAG TAAAGGGGCG       6480

CCATATAATT TACCAACTAC ACCATGGAAT ACATTGAAGG CCTCTGACTC AAAGGAAATT       6540

GCTCTTATGA CAGCGAAACA AACTGGAGAC GGGTACCAAT GGGTTATTAA GTTTAATAAA       6600
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GTAGGAAGAA CTGACTTTGT AACAGTTAAT TCAGATGGAA CAAATGTACA ATGGAGTCAT        6720

GGAGCAGGAG CAGGTGCAAA TAAACCACTT CAACAAATGT GGGAATATGG AGTAAATGAT        6780

CCTCATCGTT CACATGACTT TAAAATAAGA AATAGAAGTG GCCAAGTAAT ATATGACTGG        6840

CCAACTGTCC ATATTTATTC TTTAGAAGAT TTATCTAGAG CGAGTGATTA TTTTAGTGAA        6900

GCTGGAGCGA CACCTGCTAC TAAAGCTTTT GGTAGACAAA ATTTTGAATA TATTAATGGT        6960

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15   AAATGCAGCG AAAGCAATTT TAACAAAAGC TAGTGGTCAA AATGTAGACA AAGCAGCAGT      21600

     TGAACAAGCA TTGCAAAATG TGAACAGTAC GAAGACGGCG TTGAACGGTG ATGCGAAATT      21660

     AAATGAAGCT AAAGCAGCTG CGAAACAAAC GTTAGGTACA TTAACACACA TTAATAATGC      21720

20   ACAACGTACA GCGTTAGACA ATGAAATTAC ACAAGCAACA AATGTTGAAG GTGTTAATAC      21780

     AGTTAAAGCC AAAGCGCAAC AATTAGATGG TGCTATGGGT CAATTAGAAA CATCAATTCG      21840

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25   TGCTTATTCT CAAGCAGTAA ATGCAGCAGC AACTATTTTA AATAAAACAg CTGGCGGTAA      21960

     TACACCTAAA GCAGATGTTG AAAGAGCAAT GCAAGCTGTT ACACAAGCAA ATACTGcATT      22020

30   AAACGGTATT CAmAACTTAG ATCGTGCGAA ACArGCTGCT AACACAGCGA TTACAAATGC      22080

     TTCGGACTTA AATACAAAAC mAAAAGAAGC ATTAAAAgCA CAAGTAACAA GTGCAGGACG      22140

     TGTATCTGCA GCAAATGGTG TTGAACATAC TGCGACTGAA TTAAATACTG CGATGACAGC      22200

35   TTTAAAGCGT GCCATTGCTG ATAAAGCTGA GACAAAAGCT AGTGGTAACT ATGTCAATGC      22260

     TGATGCGAAT AAACGTCAAG CATATGATGA AAAAGTTACA GCTGCCGAAA ATATCGTTAG      22320

40   TGGTACACCA ACACCAACGT TAACACCAGC AGATGTTACA AATGCAGCAA CGCAAGTAAC      22380

     GAATGCTAAG ACGCAGTTAA ACGGTAATCA TAATTTAGAA GTAGCGAAAC AAAATGCTAA      22440

     CACTGCAATT GATGGTTTAA CTTCTTTAAA TGGTCCGCAA AAAGCAAAAC TTAAAGAACA      22500

45   AGTGGGTCAA GCGACGACGT TGCCAAATGT TCAAACTGTT CGTGATAATG CACAAACATT      22560

     AAACACTGCA ATGAAAGGTC TACGAGATAG CATTGCGAAT GAAGCAACGA TTAAAGCAGG      22620

     TCAAAACTAC ACAGATGCAA GTCAAAACAA ACAAACTGAC TACAACAGTG CAGTCACTGC      22680

50   AGCAAAAGCA ATCATTGGTC AAACAACTAG TCCATCAATG AATGCGCAAG AAATTAATCA      22740

     AGCGAAAGAC CAAGTGACAG CTAAACAACA AGCGTTAAAC GGTCAAGAAA ACTTAAGAAC      22800
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AGATGCAGTG AAACGTCAAA TCGAAGGTGC AACGCATGTT AATGAAGTAA CACAAGCACA        22920

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TACAAATGCA GTGACGCAAG CTGAACAAAT TTTAAATAAA GCACAAGGTC CAAATACTTC        23100

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AGATCCGACT GTTATCAATC AAGCTGCTGG ACAAGTAAGC ACAACTAAAA ATGCATTAAA        23760

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TGATGAAGCA AATCAAATTA AGCAAAATGC GCAAAACTTA AATACAGCGA TGGGTAACTT        23940

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GAAACAAAAT GTTCAACATG CTATTGATCA ATTGCCAAAC TTAAACCAAG CGCAACGTGA        24600
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ACCAĀCACCT GTATTGACGC CTGATACAGT AACACAAGCA GTGACAACTA TGAATCAAGC      25920

GAAAGATGCA TTAAACGGTG ATGAAAAATT AGCACAAGCG AAACAAGAAG CTTTAGCAAA      25980

TCTTGATACG TTACGCGATT TAAATCAACC ACAACGTGAT GCATTACGTA ACCAAATCAA      26040

TCAAGCACAA GCGTTAGCTA CAGTTGAACA AACTAAACAA AATGCACAAA ATGTGAATAC      26100

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CTATCATGAT GCTGATGCCG ATAAGCAAAC AGCATATACA AATGCAGTGT CTCAAGCGGA      26220

AGGTATTATC AATCAAACGA CAAATCCAAC GCTTAACCCA GATGAAATAA CACGTGCATT      26280

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GCAAAATGCT AAAGATGCCG TAAGTGGGAT GACGCATTTA AACGATGCTC AAAAACAAGC      26400
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CAATAAAGGT AATGTATCAA GTGCGACTCA AGCAGTAATA TCATCTAAAA ATGCATTAGA   28200
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TGATAAAGTG GCTGAAATCA TTGCACAAGC GCAAgCATtA AATGAAGCGA TGAAAGCATT    28380

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TATGGATCAA TTACAACAAG CAGTTAATGA ACATGCTAAC GTTGAGCAAA CTGTAGATTA    29940

CACACAAGCA GATTCAGATA AACAAAATGC TTATAAACAA GCTATTGCTG ATGCTGAAAA    30000
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TGCAAAACAA GCATTAAATG GTGATGAACG TGTAGCACTT GCTAAAACAA ATGGTAAACA    30120

TGACATCGAC CAATTGAATG CATTAAACAA TGCTCAACAA GATGGATTTA AAGGTCGCAT    30180

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GAAACATTTA GTTGACAATG AAATTCCAAA TGCAGAGCAA ACTGTCAATT ACCAAAACGC    31080

TGACGATAAT GCTAAA    31096
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(2) INFORMATION FOR SEQ ID NO: 60:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 2243 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

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ATGACAGAAT GGGAGCGAGG ACTTAGAATG TTTCCTAAAT CAGGTTTATT AAATTTTGAG      60

TTAGCGATAG mAAATCGTTC ATTAAATGAT GATGAAAAAG CATTAAAATA TGTGCGTAAA     120

GCATTAAATG CAGACCCTAA AAATACAGAT TATATTAACT TAGAAAAAGA GTTGACTAAA     180

TCAAATGAGT CGAAAAATAA ATAACTTTTA TGATGTACAA CAGTTATTGA AAAGTTACGG     240

ATTTCTAATA TATTTTAAAA ATCCAGAAGA TATGTACGAA ATGATTCAAC AGGAGATTTC     300
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TAATCAGAGA AGGAATGAAC AGAAATGACA AAAATTATTT TAGCAGCTGA TGTAGGCGGG      420

ACGACTTGTA AATTAGGTAT TTTCACACCT GAATTAGAAC AATTACATAA ATGGTCTATT      480

CACACTGATA CATCTGATAG TACAGGATAT ACACTTTTGA AAGGAATTTA TGATTCGTTT      540

GTTGAAAAAG TAAATGAAAA TAATTATAAT TTTTCAAATG TACTTGGCGT AGGTATTGGT      600

GTACCAGGTC CTGTTGACTT TGAAAAAGGT ACAGTAAATG GAGCAGTAAA CTTATATTGG      660

CCAGAAAAAG TTAATGTACG TGAGATTTTT GAACAATTCG TTGATTGTCC AGTGTATGTA      720

GATAATGATG CTAACATAGC TGCTTTAGGG GaGAAACACA AAGGTGCTGG TGAAGGTGCC      780

GATGATGTTG TTGCCATCAC ACTTGGTACA GGTCTAGGTG GAGGAATTAT TTCCAAATGG      840

TGAAATCGTA CATGGTCATA ATGGCTCtGG CGCAGAAATA GGTCATTTTA GAgCAGACTT      900

CgATCAACGA TTTaAATGTA ATTGTGGTCG TTCTGGATGT ATTGAAACAG TTGCTTCaGC      960

GACAGGCGTT GTTAACTTAG TTAACTTCtA CTATCCGAAG TTGACGTTTA GATCTTCTAT      1020

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TGGTGACCAA TTCTGTATTT TCATTACTGA AAAGGTTGCA AACTATATTG GATATTTATG      1140

TAGTATTATT AGTGTTACAA GTAATCCGAA ATATATCGTT CTAGGTGGAG GAATGTCTAC      1200

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CCAATGAATA CTCTAATTGA AGGTGAATTA AGCGATGTAT TAGAAGTTGT GCAAGTGATA      1560

CATGÄATTAC CTTTTGATAA AGGTTTAAGT AGAGTTTGTA CAAATATCCG TATTGATGAC      1620

CGACGAGACA AATCTAGAAA AATGAATGAT AAACTAACAT CAGTACAAAA ACATTTAGAA      1680

AATAGTGGTG AAAACCTATG AGGATTTCAA GCTTAACTTT AGGCTTAGTT GATACTAATA      1740

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TTAAGCAATA TGGATTACCA ATTATTACAA GTAAGGTAAC TCCTGAAAAG TTAAmCGAAG      2040

GTAGCACAGA AATAGAAGGA TTTAAGTTnT nAyrTGTaCA CACACCTGGA CATTCACCAG      2100
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GAATCGGACG TACAGATTTA TATAAAGGTG ATTATGAAAC GCTAGTTGAT TCTATTCAAG   2220

ATAAAATATT TGAATTAGAA GGC   2243

(2) INFORMATION FOR SEQ ID NO: 61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8009 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TTGGnATCAT tyAcgGTAAA AAGAATAAaG CAAGATTtAT TTCATTAGTA CTAATTGTG   60

CAATGTTTGC AATTTGTTGG GTTGCATATA TTCAATGGGA GTCTACAATC GCTTCATTTA   120

CACAATCTAT TAATATTTCa ATGGCACAAT ATAGTGTTTT ATGGACAATT AACGGAATAA   180

TGATTTTAGT AGCACAACCA TTAATTAAAC CGATTCTCTA TCTGTTAAAA GGAAACTTAA   240

AGAAGCAAAT GTTTGTCGGC ATCATCATTT TTATGTTGTC GTTCTTTGTC ACGAGTTTTG   300

CCGAAAACTT TACAATATTT GTTGTCGGTA TGATTATTTT AACTTTTGGA GAAATGTTTG   360

TATGGCCAGC AGTTCCAACT ATAGCCAATC AGTTAGCGCC AGATGGTAAG CAAGGACAGT   420

ACCAAGGTTT TGTGAATTCA GCTGCTACAG TAGGAAAAGC ATTTGGTCCA TTTCTTGGTG   480

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ATGCATAATG AGTAAATAGA ATTAACGTTA TAGACTTGAA ATAAATGTCG TTATAACATA   660

ATATTAATTT GTATAATTTA ATTTCGTTTG GAGCTTTTCT ACAGAAAGCT AGTGATGCTG   720

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GTCCCTATGT AAATAGAATA GTTAGAGGTG TCTTTTTTAT TGAATAGGAG GAAATGTGTT   900

GAATTACAAC CACAATCAAA TTGAAAAGAA ATGGcAAGAC TATTGGGACG AAAATAAAAC   960

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CGGATTACCA GCAGAGCAAT ATGCTTTAGA CACTGGCAAC GACCCACGTG AATTTACAAA   1200

GAAAAATATC CAAACTTTTA AACGACAAAT TAAAGAATTA GGGTTCAGTT ATGATTGGGA   1260

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AGGCACTGTT TTATCTAACG AAGAAGTGAT TGATGGTGTC TCTGAACGTG GTGGACATCC       1440

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TGAAGAAGAG CTACCATTGT TGTTACCTGA AACAGATGAA ATCAAGCCAT CAGGGACTGG       2280

TGAGTCTCCA CTAGCTAATA TTGATTCATT TGTAAATGTT GTAGATGAAA AAACAGGTAT       2340

GAAAGGACGT CGTGAAACAA ATACAATGCC ACAATGGGCA GGTAGTTGTT GGTATTATTT       2400

ACGTTACATC GATCCTAAAA ATGAAAATAT GTTAGCAGAT CCTGAAAAAT TAAAACATTG       2460

GTTACCTGTT GATTTATATA TCGGTGGAGT AGAACATGCG GTTCTTCACT TATTATATGC       2520

AAGATTTTGG CATAAAGTCC TTTATGATTT GGCTATCGTA CCTACTAAAG AACCTTTCCA       2580

AAAATTATTT AACCAAGGTA TGATTTTAGG AGAAGGTAAT GAGAAGATGA GTAAATCTAA       2640

AGGAAATGTA ATCAATCCTG ATGATATAGT ACAGTCTCAT GGTGCAGATA CTTTGCGTCT       2700

TTACGAAATG TTTATGGGAC CTTTAGATGC TGCAATTGCA TGGAGTGAAA AAGGATTAGA       2760

TGGGTCTCGT CGATTCTTAG ATCGCGTATG GCGTTTAATG GTAAATGAAG ATGGGACATT       2820

GAGTTCAAAA ATTGTAACTA CAAATAATAA ATCTTTAGAT AAAGTTTATA ACCAAACTGT       2880

TAAAAAGGTA ACAGAAGACT TTGAAACATT AGGATTTAAT ACTGCTATTA GTCAATTAAT       2940

GGTATTTATT AATGAGTGTT ATAAAGTTGA TGAAGTTTAT AAACCTTACA TTGAAGGCTT       3000

CGTTAAAATG TTAGCACCTA TTGCACCACA TATCGGTGAA GAATTATGGT CAAAATTAGG       3060
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TGATGAAGTA GAAATCGTTG TTCAAGTGAA TGGTAAATTG AGAGCTAAAA TTAAAATTGC    3180

TAAAGATACA TCAAAGAAG AAATGCAAGA AATTGCCTTA TCTAATGACA ATGTTAAAGC    3240

GAGTATTGAA GGTAAAGACA TCATGAAAGT CATCGCTGTT CCTCAAAAAT TAGTCAATAT    3300

TGTAGCTAAA TAATGTTTTA AGGAGGACTT TGAAATGAAG TCAATTACTA CAGATGAATT    3360

AAAAAATAAA CTTTTAGAAT CTAAACCAGT TCAAATTGTT GATGTTCGTA CTGATGAAGA    3420

AACAGCAATG GGATATATTC CTAATGCAAA GTTAATTCCA ATGGATACCA TTCCGGATAA    3480

TTTAAATTCA TTTAATAAAA ATGAAATATA TTATATTGTA TGTGCTGGTG GAGTTCGAAG    3540

CGCTAAAGTT GTAGAATATT TAGAGGCAAA TGGCATTGAT GCCGTAAATG TCGAAGGCGG    3600

CATGCACGCA TGGGGCGATG AAGGTTTGGA AATAAAAAGT ATTTAAAGTA GTGACATAAT    3660

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GATGATAAAA TTGAGTGAAC TTAAAATATT GTACAAAATA ATATAGCTAT AAATATAATA    3900

TAGCTATAAA TATAATATGA GGGAGCGTAT ATTTTTAGCA TAATTCTTAA CAACACAGCA    3960

GAGAACAGAC AACCAGGAGG AAAATGAAAT GAATTTGTTA AAGAAAAATA AATATAGTAT    4020

TAGGAAGTAT AAAGTAGGCA TATTCTCTAC TTTAATCGGA ACAGTTTTAT TACTTTCAAA    4080

CCCAAATGGT GCACAAGCCT TAACTACGGA TAATAATGTA CAAAGCGATA CTAATCAAGC    4140

AACACCTGTA AATTCACAAG ATAAAGATGT TGCTAATAAT AGAGGTTTAG CAAATAGTGC    4200

GCAGAATACA CCTAATCAAT CTGCAACAAC CAATCAAGCA ACGAATCAAG CATTGGTTAA    4260

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TATTAGACCA AGTACCAACC GTTCTGTGCC AACAGTAAAC GTTGTTAATA ACTTGCCGGG    4800

CTTCACACTA ATCAATGGTG GCAAAGTAGG GGTGTTTAGT CATGCAATGG TAAGAACGAG    4860
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TCGTATACAT GGAACTGATA CGAATGACCA TGGCGATTTT AATGGTATCG AGAAAGCATT        4980

AACAGTAAAT CCGAATTCTG AATTAATCTT TGAATTTAAT ACAATGACTA CTAAAAACGG        5040

TCAAGGCGCA ACAAATGTTA TTATCAAAAA TGCTGATACT AATGATACGA TTGCTGAAAA        5100

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CAAAATTCAA TTTGTACCTA AAAATGACGC AATAACAGAT GCGCGTGGCA TTTATCAACT        5220

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TGTTTTTGTT GAAAGACGAA CAATGGATCC AACAGCAACA AATAATAAAG AGTTTACTGT        5340

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ACCGGTTGTT AAACCAAATG CTAAAAAAGC AATACGTGAT AAAGCAACGA AACAAAGGGA        6240

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AGCTACGGAT GAAACAGATG CTATTGATAA TGTTACGAAT GCTACTACAA ATGCTGACGT        6360

TGAAACAGCT AAAAATAATG GCATCAATAC TATTGGAGCA GTTGTTCCTC AAGTAACTCA        6420

TAAAAAAGCT GCAAGAGATG CAATTAACCA AGCAACAGCA ACGAAAAGAC AACAAATAAA        6480

TAGTAATAGA GAAGCAACTC AGGAAGAGAA AAATGCAGCA TTGAACGAAT TAACTCAAGC        6540

AACCAACCAT GCTTTAGAAC AAATCAATCA AGCAACAACA AATGCTAATG TTGATAACGC        6600

CAAAGGAGAT GGTCTAAATG CCATTAATCC AATTGCTCCT GTAACTGTTG TTAAGCAAGC        6660
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TGATGCGACT CAAGAAGAAA GACAAGCAGC AATTGACAAA GTGAATGCTG CTGTAACTGC        6780

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TGCGATTCAA GGAATACAAG CAATTACACC AGCTACAAAA GTAAAAACAG ATGCAAAAAA        6900

TGCCATCGAT AAAAGTGCGG AAACGCAACA TAATACGATA TTTAATAATA ATGATGCGAC        6960

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AGAAGTAGAC CAAGCTGCGA CAGTAGCAGA GAATAATATC GATGCTGTTC AAGTTGATGT        7800

AGTAAAAAAA CAAGCAGCGC GAGATAAAAT CACTGCTGAA GTGGcGAacG TATTGaAGCG        7860

GTTAAACAAA CACCTAATGC AACTGACGAA GAAAAGCAGG CTGCTGTTAA TCAAATCCAA        7920

TCAACTTTAA AGATTCAAGC AATTTAATCC AAATTTAATC CAAAACCCAA ACAAATGGAT        7980

TCAGGGTAGG ACACCACTTA CAAATCCAA                                          8009
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(2) INFORMATION FOR SEQ ID NO: 62:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10953 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

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ACCCACCCCn TGGGGATAnT TTACCTGGTG GGGCCTTCGA TTGCCTTTAG GTGAAACCaG          60
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AGATGAATGC TAACCATATT CATTCTGCTA AAGATGGTCG TGTTACTGCG ACAGCTGAAA      180

TTATTCATCG AGGTAAGTCG ACACATGTAT GGGATATAAA AATTAAGAAT GACAAAGAAC      240

AATTAATTAC AGTTATGCGT GGTACAGTTG CTATTAAACC TTTAAAATAA AAGAACTGCT      300

AGCTGAAATG TTATGAGATA TTCATAACTA CGGCTAGCAG TTTTTTTATG CGCTATATTG      360

TTGTAGTTTT AGAAATGCTT GTTCAATGCG TTCGGCAGCT TTACGGCCAC CCATAACATT      420

TCTACCAAAT GGTCCTAATT CTAAGTCTGC AAAGCATCCT GCGACAAATA GATTTGGTAT      480

CCATTCTAAT TTTTCGGAAA TAACAGGGTA ATTACATTCG TTGATAGGTG CATCATAATT      540

TTGTATTAAT TGCTTAATAA GTGGTTGTGA CATAAAATCT TGTTCAAAAC CAGTTGCAAC      600

CATAATCTGT TGATATGGAA CAGAATCATT TTCAGTGTTA ATTACACCAC CACTAATTTG      660

AGTGATAGGT GTTTTATGCa CATTTATACG ACCATTTTTA ATATGTTTTT TAAGGCGTAA      720

GTACAGTTCG TGAGGCATTG ATCCTTTATG ACGTTCGCGT TGTACAATGG CATTTCTTTC      780

AGGCATGCTT TTAGTACTTA AAAATGAAGA CATATTTTTC GGACCTAACC AACCAGGATC      840

AGCATCAAAG TCATGTATTT CAATATCTTT ATTTAGCCAT AAATGAATCT TTTTATCGTT      900

ATCATGATTT AACAATTTAA GTGCAAGATG TGCAGCAGTa ATGCCGCTAC CAACGATATG      960

ATCGGTCTTA TCATATACTA CTTGATCAAG TTCTTTCTCG AAGATATGAT TTACATTCTG     1020

TTTGTCTTTT AAAATGTCAG GCATAAACGG AATATTTGTA CTGCCTATTG CAATAACGAC     1080

GCAATCTGTA GTGATAATTT GTCCATCTTC TAACTTGATA TGCCATTTGT CTTCTTGTTT     1140

ATCTAAAGTT TGAACTAAAC CTTGAACCAA GCAATCCTCT AATTGATATT GTTTAGAAGC     1200

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TAATAGTTTT TGTGCGATTG CAGTTCCCTG TATGCCACCG CCGATAATTG TCCAATGCAT     1500

AATAAAACCT CTCTCTTTTT AAAACGTAAT AGTTACGATT TATAATTATT ATTATCATAA     1560

TACATAACGA CATGAAAGGC AATTAAATTA AAGAGATATA TGTAGATAGG CGAATCTGT      1620

AGTCAAAGAA AAAATCATTG AAAAAGAGGT AACAATGTCA AAAGAwAACA GCAGTAAAAT     1680

CATTCCTAAT TTGGAATCAT CTTACTGCTG TTTGTTGTTG ATTTATATTC ATGATTTTGT     1740

TATATAATCT ACAATTTTGT GTCTTTTAAG TCTTCCGAAA TTTCATCGAC TTTAGTCTTT     1800

TTAGTATAAG GCGTTTTAAT ATTATATGCT GCTTTCATAA TCATATGACT TGAAAGAGGA     1860
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GCAATAAAAT ATAAAAACGT ACCAAATAGT AATGACATTG CACCTAATGT TGATGCTTTT        1980

CCGGCAGCAT GTGCACGTGA ATATACATCT TCAAGTCTCA ATAATCCTAT AGCTGCTAGG        2040

GCGCTAATTA AAGCACCGAT GATAACAAAG ATAAGTGCAA GACTAATCAG TATGATTTTG        2100

ATCATGTTCA ATCACCTTAC CTTTGTCCAT AAATTTAGAG AATACTGCAG TACCTAAAAA        2160

AGCTAATATA CCAATCATCA TAATAACGAC AATCATGTAT TTAATATTTA ATAAAATACT        2220

GAATAATGCT ATAACTGCCA TTAATTGAAG ACCAATCGCA TCTAATGCGA CAACACGATC        2280

GGCAAGTGAT GGGCCTAGCA CAACGCGAAT GAGCATAGCT AACATAGAAA TGACAACTAT        2340

GATTAATGCA ATAACGATAA TAACATTATG ATTCATTATA TTTCGCCCAC CTCTCTTACA        2400

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GCATGAATAT AAATTTTTGT ACGATCGTCA CTTACACCAA GCACTACAGT ACCAGGTGTT        2520

AATGTAATTA AATTAGACAG CAAGACAATT TGCCAATCTT TTTTTAAATC TGTGTGATAA        2580

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ACAACCAAAG ATGATCGTTA ATAGTGCTAA GAATAAAATG ACATAATGTG AAAAGCTTAC        3540

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CAAAGCACCA AAGAATGCAA TGATTGGAAT TGGTGGgCAT AGTATGCACT AGGTAACCAA        3660
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GATACAACGT TAACAAGAAC ATATTTTATT GTTTCTTGTA GTTGAATTTT TGTAGAACCA   3900

ATTACTAATA AGAAATAAGA TGACATTAAA AATACTTCGA AAAATACGAA TAGGTTGAAA   3960

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AGCGTTAACA CAAGCATATT ACTTTCAATC ATCTTCTGGA ACTCCTTTCA TACTCTCAAC   4380

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ACGTGCTCTT GATAAAACTT AGATATCGAT TCAAAATGTC TATTTCCGTA TGCAATTAAA   5340

CCGATAATAA TGACGGACAA ACCAACACCA CCAGCAATTA AAGCATTAGT AAGCTGGAAT   5400

GAGCGCTTTT CATTATAACG ATTTAAATTT GGTAAGTGGT AGAAGCATAA TAAGAACAAT   5460

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CTTACTTAAG TAGCCGATTG AATATAATAC TACTAAACTG CCGATTCCTG AAATAAGCAA      7260
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TGATGGTGAA aCTACATTAG AAGATATTGC AAATACAAAA GTGGGACCAC AAGATAAACC   8640

ACTTCATGAT GTTGTAATTG AATCTATTGA TGTTGAAGAA TAATATCTAA ACATAATTAA   8700

CTACCAACAT TTTAAACTCG GATAAAGCTA ATTTATGAAT GGATTAGTAT ATATTCCAAC   8760

gAAAATAAAT AAACTAATAT GATGAGCAAT CTCAATATAT TTATCaAGAA AGCACAGTTT   8820

TTAAATAGAT GTGTATTTTA AAGATAATAG TTGAGGTTGC TTTTTATGTT TTTACAGAGA   8880

ATTGCTATTC AAATAGTAAA TAAATTGAAA ACAAAGTAGC TGGATATCAT ATTGATTTAG   8940

ATAGGAATTT GTTGCTAATT TTATTTGTAA ATCCAAGTTT GTAGAATTCT TATTCATTTA   9000

TAAAATAATA TTCGTATGAT TTGATTTTTT AATTAGTCCA CCATTTCGAT TTGTGCTATG   9060

AACATATCAA GGTGCGTGTA cTGGTATTCA ACCATACGGT GCGTTTGTTG AGACCCCTAA 9180

TCATACTGAA GGACTGATTC ATATATCAGA AATTATGGAT GACTACGTTC ATAATTTGAA 9240

GAAATTTCTA TCAGAAGGCC AAATTGTTAA AGCTAAAATT TTGTCTATAG ATGATGAAGG 9300

AAAGCTTAAT CTATCATTAA AGGATAATGA TTACTTCAAA AATTATGAGC GTAAGAAGGA 9360

AAAACAATCA GTATTAGATG AAATCAGAGA AACAGAAAAA TATGGGTTTC AAACACTTAA 9420

AGAACGCTTA CCAATCTGGA TAAAACAGTC AAAGCGAGCA ATTCGAAACG ACTAAAGGAA 9480

CAGATAAATC GTACCGAAAA TCATACAAAG GGTCTGAAAT GAAAGTTTCT TAGACTATAA 9540

AAGAGATTAG TATCTATTAA ATTTTATTAG ATACTAATCT CTTTTTGTCT ACGATAACGT 9600

AATATGaTTG ATTCTATTTA CACGTACAAA TGGTTTAAGG TGACATATCC ATTATCTTTG 9660

TTAGATAGAA TCGTTGATTT GCaATATTGT ATGTGGATTT GTTTTTTTTA TTTATTTTAG 9720

AAATGAGAAC TACAACTTAA AGTATTAAAC GAATTGCAAC TATATAAACA GATAATTGGA 9780

GAATGAAAAA ATTACATGTT ATAGTCAACT CAATAATTTT AAGGAGGAAT TAAGTAATGA 9840

AAAGTAAATA CGAACCATTG TTTGATAAAG TAGAATTACC AAATGGAGTA GAGTTGAGAA 9900

ATCGATTTGT GTTAGCCCCT TTAACACATA TTTCTTCAAA TGATGATGGT ACTATTTCAG 9960

ATGTAGAACT TCCTTATATT GAAAAGCGTT CACAAGATGT TGGTATTACA ATTAATGCTG 10020

CGAGTAATGT GAGTGATGTC GGAAAAGCAT TTCCAGGACA GCCATCAATC GCGCATGACA 10080

GTAATATTGA AGGACTAAAA CGATTAGCTA CAGCAATGAA GAAAAACGGT GCCAAAGCAC 10140

TCGTACAAAT ACATCATGGC GGTGCACAAG CATTGCCTGA ATTAACACCT GATGGAGACG 10200

TCGTAGCACC AAGTCCAATT TCTTTAAAAA GTTTTGGTCA GAAACAAGAA CATAGTGCTA 10260

GAGAAATGAC GAATGAAGAG ATTGAACAAG CAATCAAGGA TTTTGGTGAA GCAACGCGAC 10320

GTGCAATTGA AGCAGGGTTT GATGGTGTTG AAATACATGG CGCGAATCAT TACTTAATTC 10380

ATCAATTTGT ATCACCATAC TATAATAGAA GAAATGATGT ATGGGCAAAT CAATATAAAT 10440

TCCCGGTCGC TGTGATTGAA GAAGTACTTA AAGCGAAAGA AGCGTATGGC AATAAAGACT 10500

TTATAGTTGG ATACAGATTA TCTCCAGAGG AAGCGGAGTC TCCAGGAATC ACAATGGAAA 10560

TTACAGAGGA ACTCGTTAAT AAAATTAGCC ATATGCCAAT CGACTATATT CATGTTTCAA 10620

TGATGGATAC GCATGCAACG ACACGTGAAG GTAAATACGC TGGACAAGAA AGACTGCCTT 10680

TAATTCACAA ATGGATAAAT GGTCGTATGC CACTTATCGG TATTGGTTCA ATTTTCACAG 10740

CTGACGAAGC TTTAGATGCA GTTGAAAATG TTGGTGTTGA CTTAGTAGCC ATTGGTAGAG 10800

AGCTACTACT GGATTATCAA TTTGTTGAAA AAATTAAAGA TGGACGGGAA GATGAAATTA 10860

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AATTTAATGA AGGGTTTTAT CCATTACCAC GTA                                10953
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(2) INFORMATION FOR SEQ ID NO: 63:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 8155 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

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TTTGATANAA AACTGAATnA ATTAAATGTA TCGATTCAAC CTAATGAAGT GAATTTACAA      60

GTTAAAGTAG AGCCTTTTAG CAnAAAGGTT AAAGTAAATG TTAAACAGAA AGGTAGTTTA     120

GCAGATGATA AAGAGTTAAG TTCGATTGAT TTAGAAGATA AAGAAATTGA AATCTTCGGT     180

AGTCGAGATG ACTTACAAAA TATAAGCGAA GTTGATGCAG AAGTAGATTT AGATGGTATT     240

TCAGAATCAA CTGAAAAGAC TGTAAAAATC AATTTwCCAG AACATGTCAC TAAAGCACAA     300

CCAAGTGAAA CGmAGGCTTA TATAAATGTA AAATAAATAG CTAAATTAAA GGAGAGTAAA     360

CAATGGGAAA ATATTTTGGT ACAGACGGAg TAAGAGGTGT CGCAAACCAA GAACTAACAC     420

CTGAATTGGC ATTTAAATTA GGAAGATACG GTGGCTATGT TCTAGCaCAT AATAAAGGTG     480

AAAAACACCC ACGTGTACTT GTAGGTCGCG ATACTAGAGT TTCAGGTGAA ATGTTAGAAT     540

CAGCATTAAT AGCTGGTTTG ATTTCAATTG GTGCAGAAGT GATGCGATTA GGTATTATTT     600

CAACACCAGG TGTTGCATAT TTAACACGCG ATATGGGTGC AGAGTTAGGT GTAATGATTT     660

CAGCCTCTCA TAATCCAGTT GCAGATAATG GTATTAAATT CTTTGGATCA GATGGTTTTA     720

AACTATCAGA TGAACAAGAA AATGAAATTG AAGCATTATT GGATCAAGAA AACCCAGAAT     780

TACCAAGACC AGTTGGCAAT GATATTGTAC ATTATTCAGA TTACTTTGAA GGGGCACAAA     840

AATATTTGAG CTATTTAAAA TCAACAGTAG ATGTTAACTT TGAAGGTTTG AAAATTGCTT     900

TAGATGGTGC AAATGGTTCA ACATCATCAC TAGCGCCATT CTTATTTGGT GACTTAGAAG     960

CAGATACTGA AACAATTGGA TGTAGTCCTG ATGGATATAA TATCAATGAG AAATGTGGCT    1020

CTACACATCC TGAAAAATTA GCTGAAAAAG TAGTTGAAAC TGAAAGTGAT TTTGGGTTAG    1080

CATTTGACGG CGATGGAGAC AGAATCATAG CAGTAGATGA GAATGGTCAA ATCGTTGACG    1140

GTGACCAAAT TATGTTTATT ATTGGTCAAG AAATGCATAA AAATCAAGAA TTGAATAATG    1200

ACATGATTGT TTCTACTGTT ATGAGTAATT TAGGTTTTTA CAAAGCGCTT GAACAAGAAG    1260

GAATTAAATC TAATAAAACT AAAGTTGGCG ACAGATATGT AGTAGAAGAA ATGCGTCGCG    1320
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CTGGTGATGG TTTATTAACT GGTATTCAAT TAGCTTCTGT AATAAAAATG ACTGGTAAAT          1440

CACTAAGTGA ATTAGCTGGA CAAATGAAAA AATATCCACA ATCATTAATT AACGTACGCG          1500

TAACAGATAA ATATCGTGTT GAAGAAAATG TTGACGTTAA AGAAGTTATG ACTAAAGTAG          1560

AAGTAGAAAT GAATGGAGAA GGTCGAATTT TAGTAAGACC TTCTGGAACA aACCATTAGT          1620

TCGTGTCATG GTTGAAGCAG CAACTGATGA AGATGCTGAA aGATTTGCAC AACAAATAGC          1680

TGATGTGGTT CAAGATAAAA TGGGATTAGA TAAATAAATA CTGTATTACA AATGAGCCGA          1740

TGCGTATGcA nTcgtTTTTT GTGTTTGTAG AAATAATTTA TAGTACAAAC GTAAAATGAT          1800

ATAAACAAAA TAAAAACAAA GTAATCAATA TGTAATATAA AATACACTGG TACTCAATAT          1860

ATAATGATGA TAAAATTAAT TTTAATTAGA TAGAGTTGCT TTGTGTTTTT AACGCAGATG          1920

CTACTACTTA TCTTAACAGT TGATTAAGTG AAATCATTTA ACAGCGAGAA TAATCAACCA          1980

GGAGGATGAC TTAATGAATT TATTCAGACA ACAAAAATTT AGTATCAGAA AATTTAATGT          2040

CGGTATTTTT TCAGCTTTAA TTGCCACTGT TACTTTTATA TCTACTAACC CGACAACAGC          2100

GTCTGCAGCA GAGCAAAATC AGCCTGCACA AAATCAACCA GCACAACCAG CTGATGCCAA          2160

TACACAGCCT AACGCAAATG CTGGTGCTCA AGCTAATCCT ACAGCACAGC CAGCTGCACC          2220

TGCCAACCAA GGACAACCAG CAGTACAACC AGCAAACCAA GGTGGACAGG CTAATCCAGC          2280

AGGAGGAGCA GCACAACCAA ATACACAACC AGCTGGACAA GGTGATCAAG CTGATCCGAA          2340

TAACGCTGCA CAAGCACAAC CTGGAAATCA AGCAACACCG GCAAACCAAG CAGGTCAAGG          2400

AAATAACCAA GCAACACCTA ATAATAATGC AACACCGGCA AATCAAACAC AGCCAGCGAA          2460

TGCTCCAGCA GCAGCGCAAC CAGCAGCACC TGTAGCAGCA AACGCACAAA CTCAAGATCC          2520

AAATGCTAGC AATACTGGTG AAGGCAGTAT TAATACGACA TTAACATTTG ATGATCCTGC          2580

CATATCAACA GATGAGAATA GACAGGATCC AACTGTAACT GTTACAGATA AAGTAAATGG          2640

TTATTCATTA ATTAACAACG GTAAGATTGG TTTCGTTAAC TCAGAATTAA GACGAAGCGA          2700

TATGTTTGAT AAGAATAACC CTCAAAACTA TCAAGCTAAA GGAAACGTGG CTGCATTAGG          2760

TCGTGTGAAT GCAAATGATT CTACAGATCA TGGTAACTTT AACGGTATTT CAAAAACTGT          2820

AAATGTAAAA CCAGATTCAG AATTAATTAT TAACTTTACT ACTATGCAAA CGAATAGTAA          2880

GCAAGGTGCA ACAAATTTAG TTATTAAAGA TGCTAAGAAA AATACTGAAT TAGCAACTGT          2940

AAATGTTGCT AAGACTGGTA CTGCACATTT ATTTAAAGTA CCAACTGATG CTGATCGTTT          3000

AGATTTACAA TTTATTCCTG ACAATACAGC AGTTGCTGAT GCTTCAAGAA TTACAACAAA          3060

TAAAGATGGT TATAAATACT ATTCATTCAT TGATAATGTA GGTCTATTCT CAGGATCACA          3120
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TAATACTGAA ATCGGTAACA ATGGTAATTT TGGTGCTTCA TTAAAAGCAG ATCAATTTAA   3240

ATATGAAGTA ACATTACCAC AAGGTGTAAC TTACGTTAAT AATTCATTAA CTACAACATT   3300

CCCTAATGGT AATGAAGACA GTACAGTATT GAAAAATATG ACTGTTAATT ATGATCAAAA   3360

TGCAAATAAA GTTACATTTA CAAGCCAAGG TGTGACAACG GCACGTGGTA CACACACTAA   3420

AGAAGTTTTA TTCCCAGATA AATCTTTAAA ATTATCATAT AAAGTTAATG TTGCGAATAT   3480

CGATACACCT AAAAATATTG ATTTTAATGA AAAATTAACA TATCGTACTG CTTCAGATGT   3540

TGTAATTAAT AATGCGCAAC CAGAAGTaCA CTAACTGCAG ATCCATTTTC AGTAGCGGTT   3600

GAAATGAACA AAGATGCGTT GCAACAACAA GTAAACTCAC AAGTTGATAA TAGTCATTAC   3660

ACAACAGCAT CAATTGCAGA ATACAATAAA CTTAAACAAC AAGCAGATAC TATTTTAAAT   3720

GAAGATGCGA ATCATGTTAA AACTGCAAAT CGTGCATCTC AAGCGGATAT TGATGGTTTA   3780

GTAACTAAAT TACAAGCTGC ATTAATTGAT AATCAAGCAG CAATTGCTGA ATTAGATACT   3840

AAAGCTCAAG AAAAGGTTAC AGCAGCACAA CAAAGTAAAA AAGTTACGCA AGATGAAGTT   3900

GCAGCACTTG TAACTAAAAT TAACAATGAT AAAAATAATG CAATCGCAGA AATTAATAAA   3960

CAAACTACAG CACAAGGTGT CACAACTGAA AAAGATAATG GTATCGCAGT GTTAGAACAA   4020

GATGTGATTA CACCAACAGT TAAACCTCAA GCGAAACAAG ATATTATCCA AGCAGTTACA   4080

ACTCGTAAAC AACAAATTAA AAAGTCAAAT GCATCATTAC AAGATGAAAA AGATGTAGCA   4140

AATGATAAAA TTGGTAAAAT TGAAACAAAG GCAATTAAAG ATATTGATGC AGCAACAACA   4200

AATGCACAAG TAGAAGCCAT TAAAACAAAA GCAATCAATG ATATTAATCA AACTACACCT   4260

GCTACAACAG CTAAAGCAGC AGCTCTTGAA GAATTTGACG AAGTTGTTCA AGCACAAATT   4320

GATCAAGCAC CTTTAAATCC TGATACAACA AATGAAGAAG TAGCGGAAgC TATTGAACGT   4380

ATTAÃTGCAG CTAAAGTTTC TGGTGTTAAA GCAATTGAAG CGACAACGAC TGCACAAGAT   4440

TTAGAAAGAG TTAAAAACGA AGAAATCTCA AAAATTGAAA ATATTACTGA CTCTACGCAA   4500

ACAAAAATGG ATGCCTATAA TGAAGTTAAA CAAGCTGCAA CAGCTAGAAA AGCTCAAAAT   4560

GCTACAGTTT CAAATGCAAC AAATGAAGAA GTAGCAGAAG CTGATGCAGC AGTAGATGCA   4620

GCTCAAAAGC AAGGTTTACA TGACATCCAA GTTGTTAAAT CAAAACAGGA AGTTGCTGAT   4680

ACAAAATCAA AAGTATTAGA TAAAATCAAT GCAATTCAAA CACAAGCAAA AGTTAAACCT   4740

GCAGCTGATA CGGAAGTAGA AAACGCATAT AATACACGTA AACAAGAAAT TCAAAATAGC   4800

AATGCTTCAA CTACAGAAGA AAAACAAGCT GCATATACAG AATTAGATAC TAAAAAGCAA   4860

GAAGCAAGAA CAAATCTTGA TGCTGCAAAT ACAAACAGTG ATGTAACAAC AGCTAAAGAC   4920

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      GCGGAAATCG CTCAAAAAGC AAGTGAACGT AAAACAGCAA TTGAAGCAAT GAATGATTCG        5040

      ACTACTGAAG AACAACAAGC AGCGAAAGAC AAAGTGGATC AAGCAGTAGT TACTGCAAAC        5100

  5   GCTGATATAG ATAATGCTGC AGCAAACAAT GATGTGGATA ATGCAAAAAC TACAAATGAA        5160

      GCTACAATCG CAGCCATTAC ACCTGATGCA AATGTTAAAC CAGCAGCAAA ACAAGCAATT        5220

      GCAGATAAAG TACAAGCTCA AGAAACAGCA ATTGATGGAA ATAACGGCTC AACAACTGAA        5280

  10  GAAAAAGCAG CTGCTAAACA ACAAGTTCAA ACTGAAAAAA CAACAGCTGA TGCCGCAATA        5340

      GATGCAGCAC ATACAAATGC GGAAGTTGAA GCGGCTAAAA AAGCAGCAAT TGCTAAAATT        5400

      GAAGCGATTC AGCCAGCAAC AACAACTAAA GATAATGCGA AAGAAGCAAT TGCTACGAAA        5460

  15  GCGAATGAAC GTAAAACAGC AATCGCTCAA ACGCAAGACA TTACTGCTGA AGAAATTGCA        5520

      GCGGCTAATG CGGACGTAGA TAATGCTGTG ACACAAGCAA ATAGCAACAT TGAAGCTGCT        5580

      AATAGTCAAA ATGATGTAGA CCAAGCGAAA ACGACAGGTG AAAATAGTAT TGATCAAGTA        5640

  20  ACACCAACAG TTAATAAAAA AGCAACTGCA CGTAATGAAA TCACAGCAAT TTTAAATAAC        5700

      AAATTGCAAG AGATTCAAGc tACGCCAGAT GCAACAGATG AAGAAAAACA AGCAGCTGAT        5760

      GCTGAAGCAA ATACTGAAAA TGGTAAAGCA AATCAAGCCA TTTCAGCAGC AACTACTAAC        5820

  25  GCACAAGTTG ATGAAGCTAA AGCAAATGCA GAAGCAGCGA TTAATGCGGT AACACCAAAA        5880

      GTTGTGAAGA AACAAGCGGC TAAAGATGAA ATTGATCAAT TACAAGCAAC GCAAACAAAT        5940

  30  GTTATCAATA ATGATCAGAA CGCTACAACA GAAGAAAAAG AAGCAGCTAT TCAACAATTA        6000

      GCAACAGCAG TTACAGACGC GAAAAATAAT ATTACAGCTG CAACTGATGA TAATGGTGTA        6060

      GATCAGGCGA AAGACGCTGG AAAGAATTCA ATTCAAAGCA CGCAACCAGC AACAGCGGTT        6120

  35  AAATCAAATG CTAAAAATGA TGTTGATCAA GCTGTGACAA CTCAAAATCA AGCAATTGAT        6180

      AATAĒAACTG GTGCTACAAC TGAAGAGAAA AATGCAGCAA AGATTTAGT TTTAAAAGCT        6240

      AAAGAAAAAG CGTATCAAGA TATCTTAAAT GCACAAACAA CTAATGATGT TACGCAAATT        6300

  40  AAAGATCAAG CAGTTGCTGA TATTCAAGGT ATTACTGCAG ATACAACAAT TAAAGATGTT        6360

      GCGAAAGATG AATTAGCAAC AAAAGCAAAC GAACAAAAAG CGCTTATTGC ACAAACTGCA        6420

  45  GATGCGACTA CTGAAGAAAA AGAACAAGCA AATCAACAAG TAGACGCACA ATTAACACAA        6480

      GGTAATCAAA ATATTGAAAA TGCACAGTCA ATCGATGATG TAAACACTGC AAAAGATAAT        6540

      GCAATTCAAG CAATTGACCC AATTCAAGCA TCAACAGATG TTAAAACGAA TGCAAGAGCG        6600

  50  GAATTGCTAA CTGAAATGCA AAATAAAATA ACTGAAATAC TTAATAATAA TGAGACTACT        6660

      AATGAAGAAA AAGGTAACGA TATTGGACCA GTTAGAGCAG CATATGAAGA AGGTTTAAAT        6720
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AAAGTTCAAC AACTTCATGC AAATCCTGTT AAGAAACCAG CAGGTAAAAA AGAATTAGAT        6840

CAAGCTGCAG CTGATAAGAA AACACAAATA GAACAAACAC CAAATGCATC ACAACAAGAA        6900

ATTAATGATG CAAAACAAGA AGTTGATACT GAATTAAATC AAGCGAAAAC AAATGTCGAT        6960

CAATCATCAA CAAATGAATA TGTTGATAAT GCAGTTAAAG AAGGAAAAGC TAAAATTAAT        7020

GCAGTTAAAA CATTTAGTGA GTACAAAAAA GATGCTTTAG CTAAAATTGA AGATGCATAT        7080

AATGCTAAAG TAAACGAAGC GGATAACTCT AACGCATCGA CTTCAAGTGA AATTGCTGAA        7140

GCGAAACAAA AACTTGCTGA ATTAAAACAA ACTGCGGATC AAAATGTTAA TCAAGCTACT        7200

TCTAAAGATG ACATTGAAGT TCAAATTCAT AATGACTTAG ATAATATTAA CGATTACACA        7260

ATTCCAACAG GTAAAAAAGA ATCAGCTACA ACAGATTTAT ATGCTTATGC AGATCAGAAG        7320

AAAAATAATA TTTCAGCTGA CACTAATGCA ACACAAGATG AAAAGCAACA AGCAATTAAG        7380

CAAGTTGACC AAAATGTTCA AACTGCATTA GAAAGCATTA ATAATGGTGT GGATAATGGT        7440

GACGTTGATG ATGCATTAAC ACAAGGTAAA GCAGCAATTG ATGCTATTCA AGTAGATGCT        7500

ACTGTTAAAC CTAAAGCGAA CCAAGCTATT GAAGTTAAAG CAGAAGATAC GAAAGAATCT        7560

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CAAATTACAG ATCAAGCTAA ACAAGGTATT ACTGATGCAA CAACAACTGC TGAAGTTGAA        7680

AAAGCGAAAg cTCaAGGACT TGAAGCATTT GATAACATTC AAATCGACTC AACAGAAAAA        7740

CAAAAAGCTA TCGAAGAATT AGAAACTGCA CTAGACCAGA TTGAAGCAGG TGTAAATGTC        7800

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AATAGTGCGC TTGAACAACT TAAAGCACAA CGTATTAATC CTGAAGTTAA GAAAAATGCT        7980

TTGGAAGCAA TCAGAGAAGT GGTTAACAAG CAAATAGGAA tAATTAAAAA TGCAGATGCA        8040

GATGCATCGG CGGAAAGAnA TTGCACGTAC GGGATTTAGG TAGATATTTT GGACCGATTT        8100

GCTGGATAAA TTTAGGGTnA AACCCCAACC AATGCCGAAG TTGCCTGAAT TACCA          8155
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(2) INFORMATION FOR SEQ ID NO: 64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1630 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CTGTTTTATT TGCAGCACCC ATACTGGAAA TCACTTTAAT CCCTCGGTCA AGACACTCTT   120

TCATTAAGTG TACTTTGTAC ATTATTGTAT CACTTGCATC TACAAAATAA TCTATATCGT   180

AGTTATCGAA AATTTCTTCA TATGTCTCTT CTGTATAAAA CATATGTAAG GGCGTGACTT   240

TACAATCTGG ATTAATTAAT TTAATACGTT CTTCCATCAA AGAAACTTTA CTTTGTCCTA   300

CCGTTGTAGT TAAAGCGTGT AATTGTCTGT TTACATTTGT AATATCAACA TCATCTTTAT   360

CTATTAATAT AATATGACCA ATATTCGTTC TTGCTAATGC TTCAGCAGCA AATGAACCAA   420

CACCTCCAAC GCCAAGTATG ACAACAGTTT GTTGCTTCAA TAAATCTAAA CCTTGTTGTC   480

CAATCGCTAG TTCATTTCTT GAAAATTGAT GTTTCATTAT TTTACCTCTT TCACTGATTT   540

ATACATAAGT ACATAGTAAC TTAAAATTTT ATATTTAGCA TTATCACTTT GATTATTTTC   600

CCAAAATTCA ACGAGGAAAC ATTTATTAAA CGCTATAAAA CCCAACTAAT TCTTTATTAA   660

AAACTTAAAG AAACGCATAA AAATACGCAA GACAAAGTCT TGCGTATCGA TAGAGTCCGT   720

ATTGCCGTAG TTATAATAGC TTGATCATTC GGCCTGTTAT ATACAGGTGG GTGCCCTGTT   780

TCTTGTTTTG TACGTCCTTC ATATAAGGCG TGTACGCTGC AAGAAAACCC ATTGGGCTCC   840

CTTGATCAAA GAGTGTTAGG CCCAAATTAA AAAGCAAACT TACGAACAAC TCAGATGACT   900

ATCTTATGAT GTTATATTAC CACATAATTA AAATTAATGA AATTATAACA AACCAAAGTT   960

TATTGATTTT TTAAAATTTA GTGACGAATT CGCAAAGAAA GTTCTTCTAA TTGTTTATCA   1020

GAAACTTCAC TAGGCGCATT CGTTAATAAA CATGTAGCAG ATGCTGTTTT AGGGAATGCG   1080

ATTGTATCTC TCAAGTTTGT TCTATTAGTC AATAACATGA CTAATCGGTC tAATCCTAAT   1140

GCAATACCGC CATGTGGTGG TGCACCATAT TTAAATGCAT CTAGTaAGAA GCCGAACTGT   1200

TCCTgTGCTT GTTCTTTAGT AAATCCAAGA ACTTCGAACA TTTTTTCTTG TAACTCACCA   1260

TCATGAATTC TGATTGAACC GCCACCTAAT TCATAACCAT TTAATACTAT GTCATAAGCA   1320

TTTGCCTCAG CTTCtTCTGG CGCAGTGCCA AGCTTAGCAA TATCAGCTTC TTTTGGAGAT   1380

GTAAATGGAT GATGTGCTGC AACGTAACGT TTCGCATCTT CATCATATTC TAATAATGGC   1440

CAATCTGTCA CCCATAAGAA GTTTAATTTT GTTTCATCGA TTAAACCTAA TTCTTTAGCT   1500

AATTTGACAC GTAATGCACC TAAACTTTGT GCAACGACAT TTGGTttGTC TGCAACAAAC   1560

ATTACTAAGT CACCAGCTTC AGCACCAGTT AATGTAAGTA ATGTTTCAAC ATTtTCTGTT   1620

cAAAGAAACG   1630

(2) INFORMATION FOR SEQ ID NO: 65:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 732 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

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CAATTGGACA TCTTGTATGA AAAGGACAAC CTTGCGGCGG ATTACTTGGC GAAGGTAATT      60

CTCCTTTTAA TATAATTCTA TTGTTATTAT GTTTATCAAT TTGTGGTATT GATGAAATCA     120

ACGCTTTTGT ATATGGATGT TTGGGATTTT CATAAATTTC TTTATCAGAT GCGATTTCAA     180

CTATATGACC TAAATACATA ACTCCAATGA CATCACTTAT ATGTTTTACT ACACTTAAAT     240

CATGTGCGAT AAATAAATAG CTTAAGTTAA ATTGTTCTTG TAAATCTTTT AATAAATTCA     300

GTACTTGAGA TTGAACAGAT ACATCTAATG CACTTACAGG CTCATCAGCA ACAATTAAAC     360

TCGGACGCAA AGCCAATGCT CTTGCAATTC CCACTCTTTG TCTCTGTCCA CCTGAAAATT     420

CATGTGCATA TTtATAATAT GCATCTTCAC TTAGGCCAAC ACATTTTAAT AAATATAGTA     480

CTTCTTTTTT TATTTCTTCT TTTGGCAATT TTTTATAATT TAAAATAGGT TCTGAAATGA     540

TATCTCCAAC CATTTGCATC GGATTCAATG ATGCATACGG ATCTTGAAAT ATCATCTGAT     600

ATTGTTGTCG TGATTTTCTG AGTTTTTTAC CTTGTAATCT TGTTATATCT TCACCATTAA     660

CAATTATTGA GCCTGAAGTT GCATCTTCAA GCCTGATAAT CACTTTACCT AACGTTGACT     720

TACCACAACC CG                                                        732
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(2) INFORMATION FOR SEQ ID NO: 66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5838 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

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AATATATTCA TATGTTTCAT CAACAATATT AGCTGCTTTT TGAATTAAAG CAATTTCGTC      60

AGCATCTTTG ACGTCTCTAA TTTTATCTAC AGTATTAGAA ATGCTTATTA ATGATATACG     120

GCTTTTATTT AATTCAAGGT ATGTATCATA ACTTACATGA TGCCCCTCAA AACCTACATT     180

TTCAAAATTT TCTTGGTGTA GCAATTCTTT AATCTCACCA ATAATAGTAG ATTTACGATT     240

AATAATTTCA TAATTTGGCG CCTGCTTAGT TGCTTGATCA ATATATCTAA AGTCTGTTAT     300

CAAATATTGT TTATCTTTAG ATATGATAAG TGCTCCACTG GTACCAGTAA AACCTGATAA     360

ATATCTTCTA TTGTAATCCG AAAGAATGaT AATCGCATCT AAATGTTTTT GTTCTAAAAT     420
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CAACTTTATA CATTAAAATA ATATCATAAT AAGGATAAAA AATAATAGAT ATTGATTTTA      540

GGGAGATAGT AATGAAAAAA TTGGTTTCAA TTGTTGGCGC AACATTATTG TTAGCTGGAT      600

GTGGATCACA AAATTTAGCA CCATTAGAAG AnAAAACAAC AGATTTAAGA GAAGATAATC      660

ATCAACTCAA ACTAGATATT CAAGAACTTA ATCAACAAAT TAGTGATTCT AAATCTAAAA      720

TTAAAGGGCT TGAAAAGGAT AAAGAAAACA GTAAAAAAAC TGCATCTAAT AATACGAAAA      780

TTAAATTGAT GAATGTTACA TCAACATACT ACGACAAAGT TGCTAAAGCT TTGAAATCCT      840

ATAACGATAT TGAGAAAGAT GTAAGTAAAA ACAAAGGCGA TAAGAATGTT CAATCGAAAT      900

TAAATCAAAT TTCTAATGAT ATTCAAAGTG CTCACACTTC ATACAAAGAT GCTATCGATG      960

GTTTATCACT TAGTGATGAT GATAAAAAAA CGTCTAAAAA TATCGATAAA TTAAACTCTG     1020

ATTTGAATCA TGCATTTGAT GATATTAAAA ATGGCTATCA AAATAAAGAT AAAAAACAAC     1080

TTACAAAAGG ACAACAAGCG TTGTCAAAAT TAAACTTAAA TGCAAAATCA TGATAGGAGT     1140

CTTTTAATGC GTAATATAAT ATTTTATCTT GTACTTATTA TTGCTGCGAT TGGATTAGTA     1200

ATGAATCTAG ATGCCTTTAT TTTTTCAATC GTCAGAATGT TAATCAGCTT TGcgTAaTAG     1260

CTGGTATTAT TTATCTGATT TATTATTTCT TCATCTTAAC TGAAGACCAA CGCAAATATC     1320

GCAAAGCAAT GCgTrAaGTA TAAAAGAAAT CAAAGAAGAA AATAGATAAA AAAACGGAAG     1380

CACTTGTAGG TAAAATAGTC TACGTGCTTC CATTTTTTAT TCTAAAAACT ACTTTCTAAA     1440

CATCCATTCA TCTGAACGAT ATTTTTCAGT TAATTCTTCC ACTTCTGCCA ATTGAGCTTC     1500

TGtTAATTCA AGTGGCTTTA ATTCTATATT TAAACCTTTC TTAAAACCTT TCTCGAAAGC     1560

TTCTTCCATT TGACTAATAG TAATGTGTTC ATCTGAAATA TCATTGATGG CAACTGCTTT     1620

TTCAACGAAT GCCTCTTTCA TTTTTAATTT TAATCTTTCA TTTTTATAAA TrAACATATC     1680

AAACAGTTCA TCAATATCAA TATCTTGTAA AATCGAACCG TGTTGGAGGA TTACGCCCTT     1740

TTGTCTCGTT TGAGCACTCC CAGCAATCTT ACGGCCTTCA ACAACTAGCT CATACCAACT     1800

TGGTGCATCA AAACACACTG AACTTCGAGG TTGTTTTAAT TTTTGACGCT CTTCAGGCGT     1860

TTTAGGTACC GCAAAATAAG TATCAAATCC TAAGTTTTTA AATCCTTCTA ATAATCCTTG     1920

TGAAATCACT CTGTACGCTT CTGTAACTGT AGAAGGCATA TTCGGATGCG ATTCAGGCAC     1980

AATCACACTG TAAGTTAACT CTTTATCATG TAGCACCCCA CGGCCACCAG TTTGACGCCT     2040

TACGAGACCA AAACCTTTCT CTTTAACCTT ATCAATATCA ATTCTTTTT GTAGCCTTTG     2100

GAAATACCCT ATTGATAATG TTGCAGGATT CCATGTGTAA AAACGTATAA CTGGATCAAT     2160

TTCACCTCTA GAGACAAAAT TTAATAACGC TTCATCCATT GCCATATTAT AATATGGGTC     ????
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AAATGTATAA TATTTGATTC GCTAATTAAT CAATTTAACT AAATGAATAA TAATTGCAAT   2340

TCTTTAGTGA AATATTTTGA TAATTTGACC TAACAGTCTT ATAATTATAT TATCGTTTAA   2400

TTAGGGAGGA TGCAAGATGA GTGCTAGTTT GTACATCGCA ATAATTTTAG TTATAGCAAT   2460

TATTGCTTAT ATGATTGTTC AACAAATTCT TAACAAGCGA GCTGTTAAAG AATTAGATCA   2520

AAATGAATTC CATAATGGGA TTAGAAAAGC TCAAGTCATC GATGTTAGAG AGAAAGTTGA   2580

CTATGACTAC GGTCACATTA ATGGGTCTCG CAATATTCCT ATGACAATGT TCAGGCAACG   2640

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CGGCTATAAA AAATGGACTG GAAAAATAAA GTCTAAAAAA TAGTTTTTGT AAATTTAATA   2820

TACGATTTAA TAAAATCTGA GTGTTAATTG ATCATCAATA ACAATACTCA GATTTTAATT   2880

TTTTAACAAA GTCTGTTACT ATATTTCTCT AGCTTCACTG ATCATTAAAC TTAGTTTCAG   2940

CATAATAAAG AAAGTTCAGC TCATTTTCAA TACGATTCAA TTACCGCAAT CTAAAAAATG   3000

AAAAGACAAT TTCTATGAAA GAATAATACC AAACCCTAAG AGTTATTACT TCGGTTTAGT   3060

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CCACTTAACA CAAACTCGTG TTTACAATAT TGTTATAAG GTATTTCAAA GTGTTTAGAT   3540

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AATGGTTTTA CACGTCCGAT AGAATTTTTA ATGTCATTAT CATATTTAAA TTTGTCGCCA   3720

TCTTTAATAA CCATTGGCTT TGGTAAGTAA CTTGCTAGTT CTTTTACTAC ACCGACTGGA   3780

CCTGAACCAG GACCGCCACC ACCATGTGGA CCAGTAAATG TTTTATGCAA GTTTAAATGA   3840

ACAGCATCAA ATCCCATATC TCCTGGGCGA ACTTTGTCCA TAATAGCGTT TAAATTCGCA   3900

CCATCATAAT ATAATAGACC ACCAGCATTA TGGACGATTT CACGGATTTC CATAATATTT   3960

TTTTCGAAAA TACCTAAAGT GTTTGGATTA GTTAACATAA TAGCTGCTGT ATTTTCATTT   4020

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      GATTTAAATC CTGCAAATGa AGCTGAGGCT GGaTTCGTAC CATGCGCAGA ATCTGGcACA        4140

      ATGACTTCAT CACGATGACC TTCACCATTA TTCTCATGGT AAGCTTTAAA TATCATCAAT        4200

 5    GCAGTCCATT CACCATGTGC GCCAGCAGCT GGTTGTAATG TCACCTCATC CATACCAGTA        4260

      ATTTCTTTTA ATTCTTCTTG CAAACTATAA ATAATTTCTA ATGAACCTTG AACTTGATCT        4320

      TCATCTTGTA ATGGATGTGA TTCACTAAAT CCTGGTATTC TAGCAACCTT TTCATTAATT        4380

10    TTAGGGTTAT ACTTCATCGT ACATGAACCC AATGGATAAA ATCCGTTGTC TACACCGAAA        4440

      TTTTTATTTG AAAGTTCAGT ATAATGACGT ACTAAGTCTA GTTCAGCAAC TTCAGGAAAC        4500

      TCCGCTTTGT TTTTACGAAT AAATTTATCA TCTAACAATG ACTCAACAGA ATTTGTTTTA        4560

15    ATATCACTTT TTGGTAATGA ATATGCATAT CTGCCTTCAC GAGATCTTTC AAAAATTAAT        4620

      GGACTTGATT TACTAGTCAT TTAACTCACC AGCCTTTTCT ACAAATGTAT CGATTTCATC        4680

      TTTTGTTCTT AATTCAGTTA CAGCTATTAA CATGTGATTT TTAAAGTCGT CTGAAACAAC        4740

20    ACCTAAATCA AAACCACCGA TAATATTGTA CTTCACTAAT TCCTCGTTAA CTTGTTGAAT        4800

      TGGTTTGTCA AATTTGACTA CAAACTCATT GmnAAGnTGT ACCATCTAAT ACTTCAAAAC        4860

25    CTTTTTTAAT AAATTGTTGT TTAGCATAGT TAGCATGTTC TATATTTTGA ACTGCAATAT        4920

      CATAGATACC TTGTTTACCA AGTGCTGACA TTGCAATTGA TGaCGcTAAA GCATTTAATG        4980

      CTTGGTTAGA ACAAATATTA GATGTCGCTT TATCGCGTCG AATATGTTGT TCACGTGCTT        5040

30    GTAATGTTAA TACAAAGCCA CGATTACCTT CATCATCTTG TGTTTGACCG ACTAATCTAC        5100

      CTGGCACTTT ACGCATTAAC TTTTTCGTCG TTGCAAAATA TCCACAATGT GGCCCACCGA        5160

      ATTGAGCAGG AATTCCGAAT GGCTGAGTAT CACCTACAAC AATATCTGCA CCAAATGAAC        5220

35    CTGGAGGTGT AAGTAATCCC AATGCTAATG GATTTGCATA TACGATAAAT AATGCTTTTT        5280

      TATCTTCAAT AAAGCTATGA ATCTTTTCAA GATCTTCAAT TGAACCGTAA AGTTTGGAT         5340

40    ATTGTACTGC AACAGCTGCT GTTTCATCAT CCACTGCTGC TTCTAATTTT TTCAAATCTG        5400

      TAACAGTGCC ATCTAAATCG ATTTCCACTA CTTCGAATTC CTTACGCGTC TTAGCATAAG        5460

      TATGAAGTAC TTGTAATGCT TGATAATGTA AACCTTTTGA GACTACAATT TTATTTTTCT        5520

45    TTGTTTGACT AAATGCTAAG ATACATGCTT CAGCAAAGCT AGTCATCCCA TCATACATAG        5580

      AAGAATTTGC TACATCCATA TCTGTTAATT CACAAATTAA AGTTTGGAAC TCAAAAATGG        5640

      CTTGTAATTC ACCTTGAGAA ATTTCCGGTT GATATGGCGT ATATGCTGTG TAAAATTCTG        5700

50    ATCTTGAAAT CATAGCATCC ACAACTGATG GCGCGTAATG ATCATAAACA CCAGCACCCA        5760

      rAAATGATGT ATGCGTTTCT TTAGTGATAT tCTTGCTkGC AATGGGGATT TAAACnTCTA        5820
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(2) INFORMATION FOR SEQ ID NO: 67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18355 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

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ATnATAATTG GCTTTGCTAA TAATTACTTC CCTGAATTAC aAGTATTAGC AAACGAAATA      60

AAATCTGATA TGGCTAGTTC ATTAAAACAA TGATATTTTT ATTTAAATTT TTaAAGCTTT     120

GTACGAAATT GTACAAAGCT TTTTTGGTGC GTATTGTATG GGCAACAACT TGACGATGAA     180

AATCCGTTAC AGGATTGGTA ATAGGAAATG TTAGCGAAAG ACAAGGGTAT CCATTGTAGA     240

TTAACAAAAG GACGTTTCCA CAAGTGTGGG TTATTCTCAC TAAAGCAATA CGCAGAGACA     300

ACTTACGTAA AATTTTGAAC TGACTAGAAC GGAACTTCTA CTCAATTATT GATAAAAATT     360

TTCAAAAAGA CTTGAATGTG CTGAGAATAC GAAGTTTATG GAAGGATTAT CAAAATATAA     420

ATGTGCATTC ATTTACAACC TTTATTGACA ATGATTCTCA ACTAATATAG TATATAATCA     480

AATCGTAATA GTTACGATTT GTTTTCTGCA ACTTTTTTGA AGTTTTAGTT GAGGTGAAAA     540

CAATAAAAGC ATCTAAGTGA ATGTAGTTAA CGGACAACTG CATTCGCTTG TAGAGCCACA     600

AGAAGCAACT TTAAATAAGG TTTACGGTTG CATTTTGATA CAACAACCGA TTACTAAGTC     660

ATGCTTTCCA CTTTGCGGGT TAGCATGACT TACCTAATAG ATAGAGCTAT TAGGTTCAGC     720

TTCTAAAAAA TTACAGTTTT AGAGGAATAC AGTTGcTTGc tTCGCAACAA CTGCATAAGA     780

GCCATGGTTT TCGCTTTTGC GAATTAGCAT GACTTACCTA CTAGATAGAG CTATTAGGTT     840

CATCTTCTAA AAAATTACAG GTTTAGAGGA ATACAGTTGT TTGcTTCGCA ACAACTGCAT     900

AAGAGCCTCT AGTAATTAAA ATTACAGAGG CTCTAAAAAT ACATCTAAAG GAGTGTCGTA     960

TGAATCGGCA GGTTATAGAA TTTTCTAAGT ATAATCCTTC GGGGAATATG ACGATACTTG    1020

TTCATTCAAA ACATGATGCT AGTGAATATG CATCTATCGC CAATCAGTTG ATGGCCGCAA    1080

CACATGTATG CTGTGAACAG GTAGGCTTTA TAGrATCAAC ACAAAATGAT GATGGTAATG    1140

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GTTCGGATTT AGTGCAATGC GCAATTCATG ATTGCCAATA CTATGAAGTT CAAATGCCAC    1320

AAGCCCATCG TGTTGTGCCA ACAACAATTA ATATGGGTAA TCATTCATGG AAAGCAATAG    1380
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TTCAACATTT GGTTGAAGCG TTTGTGCGTG AgcAACAATG GAGTCACAAA TATAAAACAG    1500

TAGGTATGAT GCTTTTTGAT GAACAACGTC AATTTTTACA GCCATTAATC TATATACCAG    1560

AAATTCAAAG TTTAATTTGG GAAAATAGCT GTGGTTCTGG TACAgcATCA ATTGGGGTTT    1620

TTAATAATTA TCAACGTAAT GACGCATGCA AAGATTTTAC AGTACATCAG CCAGGGGGCA    1680

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TTTAATAATG AAATCAAATT GATATTACAA CAATATTTAG AAAAGTTTGA AGCGCATTAC    1860

GAGCGTGTAT TACAAGACGA TCAATATATC GAAGCATTAG AAACATTGAT GGATGACTAT    1920

AGTGAATTTA TTTTAAATCC TATTTATGAA CAACAATTTA ATGCTTGGCG TGACGTTGAA    1980

GAAAAGCAC AATTaATAAA ATCACTGCAA TATATTACAG CGCAGTGTGT TAAACAAGTG      2040

GAAGTCATTA GAGCGAGACG TCTATTAGAC GGACAGGCGT CTACCACAGG TTACTTTGAC    2100

AATATAGAAC ATTGTATTGA TGAAGAGTTT GGACAATGTA GTATAGCTAG CAATGACAAA    2160

TTATTGTTAG TTGGTTCAGG TGCATATCCA ATGACGTTAA TTCAAGTAGC AAAAGAAACA    2220

GGTGCTTCAG TTATCGGTAT TGATATTGAT CCACAAGCCG TTGACCTAGG GCGCAGAATC    2280

GTTAACGTCT TAGCACCAAA TGAAGATATA ACAATTACGG ATCAAAAGGT ATCTGAACTT    2340

AAAGATATCA AAGATGTGAC GCATATCATA TTCAGCTCGA CAATTCCTTT AAAGTACAGC    2400

ATTTTAGAAG AATTATATGA TTTAACAAAT GAAAATGTCG TAGTTGCAAT GCGCTTTGGT    2460

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AATĆCAATTA GCGAATATTT GCTATTTAAA ATCAGATTAT GAGATTGATA TGGTTGGACG    2700

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ACATGTCATT TTAATATCAC CGACATTTGG TTCGCAAATG ATTGTCGAAC AATTTATGTC    3000

TAAATTTAAT AAAGATATCG AAGTGATTTC ATTCTCAACT TATCTTGGCG ATACACGTAT    3060

TGTTGATAAA GAAGCGCCTA ATCATGTGTT GACAACAGGT GTAAAAAAGA AATTGTACAT    3120

GGGATCGACA CATTCAAACT CAACAATGTG TCAACGAATC TCTGCTTTAG CTGAGCAATT    3180
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AGATGTACCG GTTTATGTGT ATAAGTTATT TCCTGAAGGA CCGATAACGA TGACACTAAT        3360

CCGTGAAATG CGTTTAATGT GGAAGGAAAT GATGGTTATT TTACAAGCAT TTAGAGTGCC        3420

GTCAGTCAAC CTGCTTCAAT TTATGGTGAA GGAAAATTAT CCAGTACGTC CTGAAACTTT        3480

GGATGAAGGT GATATTGAGC ATTTCGAAAT CTTGCCAGAT ATCTTACAAG AATATCTGCT        3540

TTATGTAAGA TATACCGCAA TCCTCATTGA TCCATTTTCA CAGCCAGACG AAAACGGACA        3600

TTACTTTGAT TTTTCAGCTG TACCATTTAA GCAAGTCTAT AAAAATGAAC AGGATGTTGT        3660

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GAAAATGCTA GGTATCAAAA CGCCAATGAT TGATCAGTTC CTAACTCGCT ATGAAGCAAG        3780

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GTTAAGAAAA ATATTGACGC AgTTCAAGAA AACAAAAAAT TGCATTCTTG GTTAAAGATT        4440

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GCTGTGAGTG ACAAAACAGT CAGACAAGCG ATTGGTCATA TGGTAAACAG AGATAAAATT        4980
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ACAGACATTA ATTTCGATAT GCCAACACGT AAGTATGACC TTAAAAAAGC AGAATCATTA          5100

TTAGATGAAG CTGGTTGGAA GAAAGGTAAA GACAGCGATG TTCGTCAAAA AGATGGTAAA          5160

AACCTTGAAA TGGCAATGTA CTATGACAAA GGTTCTTCAA GTCAAAAGA ACAAGCAGAA           5220

TACTTACAAG CAGAATTTAA GAAAATGGGT ATTAAGTTAA ACATCAATGG CGAAACATCA         5280

GATAAAATTG CTGAACGTCG TACTTCTGGT GATTATGACT TAATGTTCAA CCAAACTTGG          5340

GGATTATTGT ACGATCCACA AAGTACTATT GCAGCATTTA AAGAGAAAAA TGGTTATGAA          5400

AGTGCAACAT CAGGCATTGA GAACAAAGAT AAAATATACA ACAGCATTGA TGACGCATTT          5460

AAAATCCAAA ACGGTAAAGA GCGTTCAGAC GCTTATAAAA ACATTTTGAA ACAAATTGAT         5520

GATGAAGGTA TCTTTATCCC TATTTCACAC GGTAGTATGA CAGTTGTTGC ACCaAAAGAT          5580

TTAGAAAAAG TATCATTCAC ACAATCACAG TATGAATTAC CATTCAATGA AATGCAGTAT          5640

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GCTGTGACAA TTTTACATGC ACAAGGGACG CCAAATGTAA CACCAGAGTT GATTGCAGAA         5820

ACGAATGAGA AGTACGGTTT CAATGATCCA TTATTAATTC AATATAAAAA TTGGTTACTT          5880

GAAGCGATGC AATTTAATTT TGGTACAAGC TACATTACAG GTGACCCAGT TGCTGAACGT         5940

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CCAGTCATTC AAGCATATGT ATTAATTGTA GCGGTATTAT TTATTGTATT TAATACATTA          6540

GCAGATATCA TTAATGCGCT ATTAAATCCA AGATTAAGGG aGGGCGCACG ATGATAATTT         6600

TAAAmCGATT ATTmCArGwT AAAGGTGCAG TAATTGCTTT AGGCATTATT GTATTATATG          6660

TCTTTTTAGG ATTAGCAGCA CCACTTGTGA CATTTTATGA TCCTAACCAT ATCGATACAG         6720

CAAACAAATT TGCTGGCATG AGTTTTCAAC ATCTACTAGG TACTGACCAT TTAGGTAGAG          6780
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TATTTGTTTC TGTACTTATT GGATCTATTT TAGGATTCTT ATCAGGATAT TTCCAAGGGT     6900

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CAGAGTGGGG CATGATGCTT AACGAaGCTA GAAAAGTGAT GTTACACAT CCTGAAATGA      7320

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CTTTACAAAT TGCTATTGAT CCCCGCATCT CTTCTAAAGA TAAACTTCGT TCTGTGAAAA     7440

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TATTTCAAGA TTATACGTCA TCATTACATC CATTTCAGAC TGTTAGAGAA ATCTTATTTG     8580
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GTGGAGAGGC GCAACGTGTT GCGATTGCGC GTGCAATATG TATTAACCCT AAATATATTT        8760

TGTTTGATGA AGCCATTAGT TCACTCGACA TGTCAATTCA AACACAAATA TTAGATTTAT        8820

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ATTGAAAAAA TGCCGTTTAA CGCTGTAACT GTTTTTGCGC AATTTTTCAA AAATAAAGAG        9660

TTGTTGAACA GTGGTATTAT CATGATTGTT GCATCGATTG TATTTGGTGC AGTTAGTACA        9720

TTTGTACCGT TATACACAGT GAGTTTAGGA TTCGCGAATG CGGGAATCTT TTTGACAATA        9780

CAGGCCATCG CAGTTGTTGC GGCAAGATTT TACTTAAGGA AATACATTCC GTCAGATGGT        9840

ATGTGGCATC CTAAATATAT GGTATCTGTA CTATCATTAT TAGTAATCGC GTCATTTGTA        9900

GTGGCATTTG GTCCGCAAGT AGGTGCAATT ATTTTCTATG GTAGTGCGAT ATTAATAGGA        9960

ATGACGCAAG CAATGGTGTA CCCAACATTA ACATCATACT TAAGCTTCGT CTTACCAAAA       10020

GTAGGTCGTA ATATGTTGTT AGGTTTATTT ATTGCCTGTG CAGACTTAGG TATATCGTTA       10080

GGTGGCGCAT TGATGGGACC TATTTCCGAT TTAGTAGGAT TTAAATGGAT GTATCTAATT       10140

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CCAGCGAGTA GTCTTTAATG AAGTGAATTA AAGCATATTA AGTTAATGAA TATTTAAATT       10260

TTAAAAGGTA TATTGaGCAT GGCGATTCAT GTGCTTCATG CTAGGACATG AAACATTCTA       10320

TATGGCTCGT TTTTAGAACG ACAtATATCT AAATAAAGCA CGCTTArAAG TGAGTTTTGA       10380
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TTACATGAAA ATATGCAAAA CGAGTATAAC TGCTAATTGA TAGAAATAGC TCACCATAAA     10500

ATTACGGTAT GATTTTAAAT ATAAGTAAGT CGCACTACCT GCTAGTATCA ATGCTGGAAT     10560

GAATTCCCAC CATGTATTAA TGTATGGATA GTAGAACAGA GTTTCAAGGA TAATGGACAA     10620

TACTATTGTA ATCTTTAAAG GTATTAATCT GCTTAATTCT TGAATTAAAA TATGACGGAA     10680

AATAAGTTGA CAAATCAAAG TATTTAATAT AATGGTTAAC GAAAATATAG CTATTAAACT     10740

GATGGAaCCA TACCCTTTAA TGAGCGGGTA AATGTCAAAG ACAGTAAAGG AATCTACATT     10800

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TATAAGAATA TGCCATTTAT ATTTAGCACT AGCAACGATT TGCGAACGTA TCATTGGAAT     10920

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GCTAATGTTC ATTGAAATAG GAAAAGAGAA ACCCCACGGA GCTTGTTGAG TGAATACAGC     11040

TACTAACCCA AAAGTTAAAA AGACGATAAT GATCGGCAAG ATGTTAACCA AAAATATGTA     11100

AAGGAAAATA AATCCAATAT CACGTTTGAA AAAACGCGAT TGTTCGGTAG CGTATTCTTC     11160

TTCTATGTAA TGTTTATTTG TATTTGACAT AGTATACCTC TTAAATAGTT GTATTATATA     11220

GATACTTTAG CACATATTAC TTTGTATTGT ATGTTTATA CATTAAAATT TAAAATGAAA      11280

AACATATCAT AAAATTGTTT TATAAAATGA AGCGCTTCCA TTGTGTTTTG TTTTGTAAGG     11340

TGTATCATAA ATATTGAATT GAAATTTTGG GGGGAGGTAT TGTAATGACG TTTCTTACAG     11400

TCATGCAATT TATAGTTAAC ATTATCGTTG TAGGATTCAT GCTTACGGTT ATTGTTATCG     11460

GGCTTATTTG GTTAATTAAA GATAAAAGAC AATCACAACA TAGTGTATTA AGGAATTATC     11520

CTTTACTAGC ACGTATTAGA TATATTTCAG AAAAAATGGG ACCGGAATTA CGTCAGTATT     11580

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TGGCTGGAAA ATATAACTCT CGTATGACCA GCTTCGGTAC TACTAAAGAT TATCAAGACG     11700

GCTTTACAT ACAGAACACA ATGTTTCCGA TGCAACGTAA TGAGATTTCA GTAGATAATA      11760

CAACATTGTT ATCAACATTC ATTTATAAAA TCGCGAATGA GCGTTTATTT AGTCGTGAAG     11820

AATATCGTGT GCCGACAAAG ATTGATCCGT ATTACTTAAG TGATGACCAT GCAATAAAAT     11880

TAGGTGAACA TTTAAAACAT CCATTTATTT TAAAACGTAT CGTAGGACAA TCTGGTATGA     11940

GTTATGGCGC TTTAGGAAAA AATGCCATTA CAGCTTTATC TAAAGGTCTA GCTAAAGCGG     12000

GCACTTGGAT GAATACAGGT GAAGGTGGCT TATCAGAATA TCATTTAAAA GGTAATGGGG     12060

ATATCATTTT CCAAATTGGT CCCGGTTTAT TTGGTGTTCG TGATAAAGAA GGTAATTTTA     12120

GTGAAGGTTT ATTTAAAGAG GTTGCACAGT TATCTAACGT ACGCGCATTT GAGCTGAAGT     12180
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TTGCTAAAAT CCGAAATGTT GAACCTTATA AAACAATCAA TTCACCTAAC CGTTACGAAT      12300

TTATTCATAA TGCTGAAGAT TTGATTCGTT TCGTCGATCA GTTGCAGCAA TTAGGTCAAA      12360

AACCAGTAGG ATTCAAAATT GTAGTAAGCA AAGTTTCAGA AATTGAAACA CTTGTACGTA      12420

CGATGGTGGA ACTAGATAAG TATCCAAGCT TTATTACGAT TGATGGTGGT GAAGGTGGTA      12480

CTGGTGCAAC ATTCCAAGAA TTACAAGATG GTGTTGGCTT ACCGCTATTT ACAGCTCTAC      12540

CTATTGTGTC TGGCATGTTA GAAAAATATG GTATTCGAGA TAAAGTGAAA TTGGCGGCAT      12600

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TGAATACGTG TCCTGTAGGT GTTGCAACGA CAGATGCGAA GAAAGAAAAA GCATTGATTG      12780

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CTTCTGTGTA ATCTATGTCT AAGTGyTCAA TTGCTTTTTT ATCTTTATAG TCTACTTTGT      13320

ATTTTACGCC TTTAAGGTCT TTGAAAATAC TTTCAGATTT GGCGAATAAC TTTTTGGCTT      13380

CGTCTTTATC CATACCTAGA TCGTCATATT TAATTGTGTT GATTGTAGAC TGTTTTAAAA      13440

CTTTATCATC TTTATATGTG ATAGAAGTTA GTACATGTTT ACCACTAACA TCACCwTCAT      13500

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CAATTAATGA ACATAATTTT TTCAAAGTCA GTCGCCTTCT TTCGATATTT GTATTATAAA      13620

GAAATTATAA CATTTACTAA AAAATGATGT TATTCAAAAA TTTAAATTTT GTCATTTTTT      13680

TTGAAGATAT GAGTTTTTTT AAGCGGATTC CTCACAAAAT TTTAAAAATA TTTAAGCCTk      13740

AAAATGATAA AGCGkTAGGG AACGTTTTTC TGAAAGTTAG TGATACAATA GTTTTAAGTT      13800

GAAATACAGG AGGATGAATA ACATGAATCA GTCAGTCAAA TTACTTAAAC ATTTAACAGA      13860

TGTAAACGGC ATTGCTGGTT ATGAAATGCA AGTTAAAGAA GCAATGCGTa ACTATATAGA      13920

GCCTGTCAGT GATCAAATTA TTGAAGATAA CTTGGGTGGC ATTTTTGGAA AGAAAAATGC      13980
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AACAAAGATT GATAAACATG GTTTTATTTC ATTTACGCCA kTgGTGGATG GTGGAATCAA    14100

GTCATGCTAT CTCAAAAAGT AACGATTACA ACAGATTCGG GCAAAGAAAT TAGAGGTATC    14160

ATCGGTTCTA AACCGCCACA TGTCTTAACG CCTGAAGAAC GTAAAAAGCC AATGGAAATC    14220

AAAAATATGT TTATAGATAT TGGTGTTAGT AGCAAGGAAG AAGCTGAAGA AGCTGGCGTT    14280

GAAGTAGGCA ATATGGTTAC GCCATATAGT GAATTTGAAG TGCTTGCAAA TGATAAATAT    14340

TTAACTGCGA ArCATTTGAT AATCGCTATG GCTGTGCATT AGCTATTGAG GTATTAAAAC    14400

GTTTAAAAGA TGAAAATATT GGCATTAACT TATACAGTGG TGCCACAGTG CAAGAAGAAG    14460

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CAGGTGGAGG TACAGATGCG GGAAGTATTC ATGTCGCAAA TGAAGGTATT CCAACGATGA    14760

CAATCGGTGT TACGCTGCGA TACATGCATT CTAATGTTTC AGTGCTCAAT GTAGATGATT    14820

ATGAAAATTC TATCCGTCTT GTTACTGAAA TTGTCCGTTC ATTGAATGAT GAAAGTTATA    14880

AAAATATCAT GTGGTAATCA AATCCATAAA TAATAAAGAA TCCTTTTAAT ATGGTAGGTT    14940

GTTAAACAAT TGTCTAATTT TAATTCTTAG TCATTAGACA GTATCCATGT TAATAGGATT    15000

TTTTGTTTTT AATTTAAATG CTGAAAATCA ATTATGCCTA AATTTTGATA TTACAAGAAA    15060

ATGATTTTTT CTTAAATGTA ATTGCACTAA AAACCAAAAA AACGGGAATA ATATACCTGA    15120

TATATTACAT GAGGAGCGGT GCAAATGTTG TTAGAAATTA AAGATTTAGT GTATAAAGCG    15180

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ATTATAGGTC CATCAGGTAG TGGTAAAAGT ACATTCAAA AGCAAATATG TAATTTGTTT    15300

AGTCCAACTA GTGGAGAACT TTATTTTAAA GGTAAACCCT ATAATGATTA TGACCCGGAA    15360

GAATTGCGTC AACGAATCAG TTATTTGATG CAGCAAAGTG ACTTGTTTGG TGAAACGATT    15420

GAAGATAACA TGATATTCCC ATCACTTGCA CGTAATGATA AATTTGATAG AAAACGTGCA    15480

AAGCAATTAA TTAAAGATGT CGGTTTGGGA CATTATCAAT TAAGTTCGGA AGTGGAAAAT    15540

ATGTCGGGTG GTGAGCGGCA AAGAATTGCT ATAGCGCGCC AACTGATGTA TACACCGGAT    15600

ATTCTTTTAT TAGATGAATC GACCAGTGCA TTAGACGTTA ATAATAAAGA AAAGATAGAA    15660

AATATCATTT TTAAATTAGC AGATCAAGGC GTGGCAATTA TGTGGATTAC CCACAGCGAT    15720

GACCAAAGTA TGCGACACTT TCAAAAGCGT ATAACAATTG TTGATGGTCA AATTTCTAAT    15780
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CATTCCGATT ATCATTTCAT ATAAAGAAGG TTTACATATT ATTAAAGATT TAATTGTTGC      15900

GACATTACGA GCAGTTGTGC AATTAATCAT TTTGGGATTT TTGCTGCATT ATATTTTTAA      15960

AATAAACGAT AAATGGCTGC TTATTTTATG TGTATTGGTC ATTATTATTA ATGCATCATG      16020

GAATACAATT AGTCGAGCAT CACCAGTGAT GCATCATGTG TTTTGGATAT CATTTCTAGC      16080

TATCTTCATT GGAACGGCAT TACCGCTTGC AGGTACTATT GCGACAGGGG CCATTCAATT      16140

TACCGCAAAT GAAGTTATAC CTATCGGCGG CATGCTTGCA AATAATGGCT TGATTGCAAT      16200

TAATTTAGCT TACCAGAATT TAGATCGTGC ATTCGTACAA GATGGTACTA ATATTGAATC      16260

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TCGTTTAGCT ATAGTGCCAA CTATTGATTC GGTTAAAACA TATGGGCTTG TGTCGATTCC      16380

TGGTATGATG ACAGGCTTAA TTATTGGTGG CGTACCACCT TTACAAGCGA TTAAATTTCA      16440

ATTGTTAGTC GTGTTTATTC ATACAACTGC GACCATTATG TCTGCTTTGA TTGCGACATA      16500

TTTAAGCTAT GGTCAATTTT TCAATGCAAG ACATCAATTA GTAGCACGAA ATACTGATGT      16560

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TGAAGTGACG CGCACATATA GTATCGCTAT TCATTAGCGC AGCGAAAATA TTCATAAAGG      16680

CACGCATACT TTGTAGTCAG TTATCTGTTC TGACATATAA AGCGTGCGTG CTTTTTTGGA      16740

GTTATTGTTG AAACTGAAGT AATTATACAT AATTATTAAA TGACATACTT GTGTTAATTT      16800

TTCAAATACT GAAAAACAAT TTCaATAATT TTCCaATTAA GCACAGAAAA TTAAAGCAAA      16860

ATATTATATA ATAGAACGGT TATATATaAA nATTngTgCA CACATTTTTT AATAAATCGT      16920

TATTCTAAGG GAAATGAATA TCGGAAATTT TGTTTGAAAG GAGTTTTAAA TTGTCAATCA      16980

TGCGACTATT TACATTCATT TTAAGTATTT TTATCGTAGG AATGGTTGAA ATGATGGTTG      17040

CAGGAATTAT GAACTTGATG AGTCAGGACT TACATGTATC AGAAGCTGTC GTTGGTCAAT      17100

TAGTGACAAT GTACGCTTTA ACATTTGCGA TATGTGGACC TATTCTGGTT AAATTAACGA      17160

ACCGTTTTTC ATCAAGGCCT GTATTATTAT GGACATTACT TATATTTATC ATTGGTAATG      17220

GCATTATTGC TGTAGCGCCA AATTTTTCaA TATTAGTAGT TGGTAGAATT ATCTCATCTG      17280

CAGCAGCAGC ACTAATTATC GTAAAAGTAT TAGCTATTAC AGCGATGTTA TCAGCACCTA      17340

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GTGTACCAAT TGGAACGGTT ATCGGCGATT TAGTAGGTTG GCGCTATACA TTTCTATTCT      17460

TAATTATTGT GAGTATTATT GTTGGCTTCT TGATGATGAT CTATTTACCG AAGGATCAGG      17520

AAATACAACG AGGCCCTGTG AATCATGAGA CACCATCTCA TGAAAATCAT GTTACTTCGA      17580
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CAAACTCAGT GACATTCGTC TTTATAAATC CACTTATTTT ATCTAATGGT CATGATATGT    17700

CATTCGTTTC ATTAGCACTT CTAGTAAATG GAATCGCTGG CGTTATTGGA ACATCATTAG    17760

GTGGTATATT CTCCGATAAA ATTACAAGTA AGCGTTGGTT AATGATTTCT GTTTCTATTT    17820

TTATCGTCAT GATGTTACTT ATGAATTTAA TCTTACCTGG TTCAGGTCTA TTGTTAGCAG    17880

GACTATTTAT TTGGAATATC ATGCAATGGA GTACTAATCC AGCAGTGCAA AGCGGTGTGA    17940

TTCAACATGT TGAAGGCGAC ACAAGCCAAG TAATGAGTTG GAACATGTCT AGTTTAAACG    18000

CTGGTATTGG TGTTGGAGGC ATTATTGGAG GCTTGGTCAT GACACATGTT TCTGTTCAAG    18060

CTATCACATA TACGAGTGCC ATCATTGGCG CATTAGGATT AATCGTTGTT TTCACATTGA    18120

AAAATAATCA TTATGCTAAA ACATTTAAAT CATCATAATT CTCATATGAm AAGCACGCCT    18180

GCTATCAAAT TCAGGTGTGC TTTTTTAGAT GCGATAACGT TATTGATATG TGCGATAATA    18240

GCGACGTTCA TTATGATACA TCGGCCAAGG CATTTTACCG CTTTTAGCAA AATTAGCTAA    18300

ATCATTTGC ATTTGTCGAC TTAAAAATTT AAGGTGaGCA GTTGTTGGaT ATgAT        18355
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(2) INFORMATION FOR SEQ ID NO: 68:

    ·(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1192 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

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CGCAAAGAAG TACAAAAAAT GTTTTTACAA GAAGGTATTA AAACACCTCA ACCAATTATG      60

ACTGCTTATA ATCATAGTGA AAACGgTGTT TAGTAGTTTA TAATACATGG AGGTCATATT     120

TAATGGCGTC AAAATATGGA ATAAATGATA TAGTAGAAAT GAAAAAACAA CATGCGTGTG     180

GAACAAACCG TTTTAAGATT ATTAGAATGG GTGCAGACAT AAGAATTAAA TGTGAAAATT     240

GTCAAAGAAG TATTATGATT CCACGTCAAA CGTTTGATAA AAAACTTAAA AAAATCATCG     300

AATCTCATGA TGATACACAA AGATAGGAGA ATGATTAATG GCTTTAACAG CAGGTATCGT     360

TGGATTGCCA AACGTTGGTA AATCAACATT ATTTAATGCA ATAACAAAAG CAGGTGCTTT     420

AGCAGCGAAC TATCCATTCG CTACGATTGA TCCTAATGTA GGGATAGTAG AAGTGCCAGA     480

TGCTAGATTA CTTAAATTAG AAGAAATGGT TCAACCTAAA AAGACATTGC CGACTACATT     540

TGAATTTACA GATATCGCTG GTATTGTGAA AGGTGCTTCA AAGGGAGAAG GGTTAGGTAA     600

TAAATTCTTA TCACATATTA GAGAAGTAGA TGCGATTTGT CAGGTCGTTC GTGCATTTGA     660
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TAATATGGAA TTAGTACTAG CGGACTTAGA ATCTGTTGAG AAACGTTTGC CTAGAATTGA      780

AAAATTAGCA CGTCAAAAAG ATAAGACTGC TGAAATGGAA GTACGTATTT TAACAACTAT      840

TAAAGAAGCT TTAGAAAATG GTAAACCCGC TCGTAGTATT GACTTTAATG AAGAAGATCA      900

AAAATGGGTG AATCAAGCGC AATTACTGAC TTCTAAAAAA ATGCTTTATA TCGCTAATGT      960

TGGTGAAGAT GAAATTGGTG ATGATGATAA TGATAAAGTA AAAGCGATTC GTGAATATGC     1020

AGCGCAAGAA GACTCTGAAG TGATTGTTAT TAGTGCAAAA ATTGAAGAAG AAATTGCTAC     1080

ATTAGATGAT GAAGATAAAG AAATGTTCTT AGAAGaTTTA GGTATCGaAG AACCAGGATT     1140

AGATCgrTTA ATTAGGAmCA ctTATGAATT ATTAGGnTTA TCCACCATAA TT            1192
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(2) INFORMATION FOR SEQ ID NO: 69:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 7494 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

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AATATAGCTG CAATAGCATC TCGTTTCATT TGTATAATCA ATTCCGGTTT AAATATCAGT       60

GTGAACGTAA GCACGACACA GATTAAAAAT AACACTGCCG GAATGAGTCG TTTCAATCGT      120

CGCTtCCAAA ACTCTAGCAA ATCGATTTTT TGCGTCCGAT AATACTCACT TATCAACAAA      180

CTTGTTATTA AATAACCTGA AATAACGAAG AATGTATCTA CTCCTAAAAA GCCCCCACTT      240

AACCATTGTG CATTCAAGTG ATAAATAATG ATTCCTATAA CTGCGAATGC CCTCAATCCA      300

TCTAATCCAG GTAAGTATCG CGGGGAATAC ATTTTTTCTA AACGTTTAAA GTCTTTTGTA      360

TCCATGTTAA TAAACGCCCC ATTTATTTTT CTCTATTTTG TAGTATATCA CAATATTTTT      420

GAAAATAAAA TATTGCACTG aTTTTCATTA ATTGATTTAA CCCTTAATTA AGATAGTTTT      480

AAATTTTTTA TTAAGTAGAA AACAATTATT ACAGTTGATT TCATTACTGC AAACCACATA      540

TAAATTTGTC GATTTTACTA CATAACATAG ATTATCATAG ATTCTTGAAT TTTTAGCAAA      600

ATAACTGTTA TTTTCATTAT ATTTTTACAA AAAAAGGTTC GTTTTATATT TTATGCATCT      660

TACTGTAACA GAATCATTAA GATATGCTAT TCGAATATAC TTTTTCAAAA TTTATATAAT      720

GAATAAATTA ACATGTATTG AAAAAAAAGC GAAATGCAGC CTATCCTCTA ATGTAAACCA      780

AACGATATAT CTCGTCAGAC TTTATATTTA AACGCTATGT GTCACTTTTA AAATGAATAT      840

TACTAAGATT GTCATATCAA TTATTATTGC ATCGAATTAA TCTTTTAAAT TTCTGTAATA      900
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ACGGAAGTCA TTATTAGAAT AAAAATACTG TGCACTAATA AATTTATCAA TTGTTCCTAA    1020

ATAAATACCA TCGATATTTT GTTCTTTACA TGTCATTATA ACTTTATCTA AAAGTTTTTT    1080

ACCTATTTTT AAATTCCTAT AACCTTTATC AACAAACATT TTTTTAAGTG CAGACATATT    1140

ATTATCTAGT CTAATCAAAC CTATAGTACC AACAATATTT TGaTGATTGT TTATTGCAAG    1200

CCAAAATgCC CTCCATTATT CAAATAGTTA TGTTCGATGT TCTCCAAATC AGGTTGATCA    1260

TCTCTATCAA TTTTTATATa AATTCATTTT TTTGAATCGA TAAAATAAAC TCGATTAGCT    1320

CTTCCTTATA AGACCTATTA TATTCAATTA TGTTTATAGC CATTTTTATC TCCTTTTTCA    1380

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ATGAAGTTTC ATTCCACTTG GCACTTAATA AAGACAAGTA TTTTAGCAGT AATACAATAA    1500

AGTCCAATAA ATTTCCCTAA CTTCAATATC CACTTTTTAA AAAATGTATT TTTAATTAAT    1560

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GAATAAACCT GAAGCACCTG ATGGGTTGTA AGCATTTACT TGACCATTTG ATTCACGAGC    1800

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CCATGTAGTA CCATTTGAAG TGAAGTTATA TTGGAAACCA TCTTTTACAA AGTGGATGTC    2160

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AACTAAGTGT GCTTGATCAA CGTTTACTTC AGCAGCGTGT GCTTGATGTC CTGTACCTGC    2280

TGCGTAACCT GTTACACCTA ATGCCACTGC TAATGATGAT GCCATAATTG TCTTTTTCAT    2340

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TTGtAATGTT GAAATATGGC TGTTTTATAC TGTAATGTGA AATATGTGCC CTTTAGAATC    2580

CAATCAACCC TTGAAATAGT CTTTAACACA TAAGATTTTT ACTATATTTA GCTCAACTAT    2640

TACAGCTTTC GTAATATTAC AGATTGTATT TTTGTTACAT AGCTGTAATA TATCTGACAT    2700
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TACACATGTA TTGATTGCTA TTATTGTTGT ATATTCAAAG TTTTAAAACA CACATCTTTT      2820

GTGAATTGTC TTATCTTTTA TTAGCGCAAA TAAACTGCAG CTCAATTATA TTGTTCAACT      2880

TCATTCTCGC AATTCACAAT AACATTAAAT AATTTTTGGT CTCATATTTT CAAAAAACAT      2940

ACTGTTATTA TCCCATGAAT TTAAAAATAT CATTAGTATA TAAACGAAAC ACTTTACGAT      3000

AAATGATATC TGCAAGCCAA GCTGTTACAA ATGGTACAAC AAAGAACGCT ACTACAATTA      3060

GTAAGACACT CAACCAAGCA GAATCAACCT CCATAAATTT AAATGCATTA ATCGGTCCTA      3120

CCATTCCTAT AAAACCAAAT CCAGCTGACT CTTTCGTTCC ATGAATACCT ACTAATGCTG      3180

ATACCAAACC TGATACAATG GCTGTCGTTA ATATTGGTAA CATAAGAATT GGATATTTCA      3240

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CCATACTACC TACGCGATGT TGAATAAGTA AAATGAATAA CACTGCAATC GCTGCTGTAA      3660

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CTGCACCGCT TCCTACATAT GCTGCACTTG CCACAACAGC AATTGCTAAT GGCGATAGGT      3780

CAAATTTCAT GGCAACCAAT GCACCAATCA AAGCAGGTAC TGTAAATTGA ATTGCAACGA      3840

CAACGCCTAA TAACGTTTTA AAAATCGGAT GATAATCCAT AAAGTATTTA AAAATTTCTC      3900

CAAGTATCGC ATTAGGAACT AAACCCGCAA CAATACCTAT GGCGACACCT GATAAAACTC      3960

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TAAATTCTAA GATGTGCATG CCGATGTTGT TATATTTAGG CTAGCAGTAT CATCTATAAC      4140

TCAAGACTAT GAAAAATAGT ATATCACAAA ATTCTGAATT TTTAGATAAA TAAATTGGCA      4200

ATTTTTCAAA CATATTGTTA CAATACACTT TTATTTTATC TTCATTTTTA AAATCCATTA      4260

ATACAATAGA AGAAAGACAT TCAAATGCTT ACCAAAAAGG TACATTATTT GTTAGGAGCG      4320

TATCAGCaCT TACATATCAT CAACACAATT GACAATATAA TAGAAGATAC TGATAATAAG      4380

TGTTAAAACA ACAGATGTTA GGTAGTGAAC AAATGATGGA AAGTAAATCC ATAGATCCAA      4440

GAATCGTTAG AACCAAACAA TTGCTTGTCG ATGCTTTTCT TAAAATTTCT AGAGAAAAGA      4500
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TTTACGCTCA TTTCGCTGAT AAAGAAGACC TCCTAGACTA CACATTATCT GTAACCATTT        4620

TAAAAGACTT GAATGATAAT TTGAGCATTT CTAATGTCAT TAATGAAAAG GTTCTGCGTA        4680

ATATTTTCAT TTCAATTGCG AGTTATATCA AAGATGCTGC AAAGTCTTGC GAATTAAATA        4740

GTGAAGCATT TTGCAACAAA GCACATCAAC GTATTAATAA TGAATTAGAA GATATTTTTG        4800

CGATTATGTT AGAAACAGC TATCCGGAGC ATCAACGAGA TATCATTGTA AATAGTGCGA        4860

GTTTTTTAGC AGCTGGTATC TCAGGCTTAG CATTACATTG GTTAACACG AGTCAAGAGA         4920

CAGCCGATGT GTTTATCGAT CGCAACCTTC CATTTTTAAT TCATCATATA GCACATTTTT        4980

AATAAAACTT GGTATTTAGT CATGCATCTT GAAATCACTA TGTGACTTAG GTTCATACTT        5040

GTACACACAA TAAAATTTAA CGTATTACGA TTGATTAGCC GTGTCTAGGA CATAAATCAA        5100

CGTCCTATAC TCTACAATGT CATATTAGCA GTCGTTAACT GAATGAAAAT AAGCTTGTCA        5160

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AGGCAATATG TTGTTTAGGC AACAAATGAT ATGTGCGTGT TTATTGGCAA ACGTACGACA        5280

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TAAGATAGGA GGGATTGACG TGAGCGAGAC AGATGAACCT CAGGGGTTTG AACGCACGCA        5400

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AAAGTCGACG TTGAAGCAAC ACATAATAAT TGCTCGTGGT AAAAAGCGAA TCGACTATCG        5520

ACTGTCGTAT AACTTTTACA TACGTATTAT GATAATGTAG AAATCAAGAA AATCGACTGT        5580

GAATATACCT ATGCTATGCC CATTGCAATT TTAATAAGAC ACACGATGTC ATTCGACAAT        5640

GCTCATTTCT TTGCTCAGTT ACGTCATCCT GTCTTATAAA ACAACATTGC AGACATGTAT        5700

ATCAAACGAC ACTTCAATAA CATCACTTTG CCcATCGTAC TACTAGTAAA ATCGTGTCTC        5760

AAATcCCTTA TTTTAATTCC AAAAAtCTGC TGGTCAAAAG ACCGAGAAAC TAAAAACATT        5820

ACTTAATGTG TTGATAAATT ACCATATAAA AATAATCTCA AAATATATCA ACACTTGATT        5880

CTAAGGAGGA TATGACAATA TGAAAATTTT AGATAGAATT AATGAACTTG CAAATAAAGA        5940

AAAAGTACAA CCACTTACTG TAGCTGAAAA ACAAGAACAA CATGCATTGC GTCAAGAcTA        6000

CTTAAGcATG ATCCGAGGAC AAGTATTAAC AACATTTTCC ACAATAAAAG TGGTTGATCC        6060

AATCGGTcAG GATGTCACAC CAGATAAAGT TTATGATCTT CGCCAACAAT ACGGTTATAT        6120

TCaAAATTAA tATTTGCTCA CGAGGTATTG CACTTAAGGT GCCAACTGAC CTCATAAACA        6180

AAGCCCATAC TGATTGAAGA CACTAATGTG tCsaCCATGG TGCACATTAC GCTTCATCTC        6240

TGTATGGGCT TTTTATTTAT TCTTTTGAGA ATTTCATTTT AGCAGACCAA AAAATTAAAA        6300
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TGAACGACTG TGCCACCCGC TTCTTTCACT TTATTCACCA ACTGGTCAAC TTCTTCATTT      6420

GTGTTCACAC CTAGAGAAAT CATCACTTCA TTTGGTTCAG TATTAAGGCT TTGCTGACTT      6480

ACATTTTGAA AATGCTTGTn TTCTATTAAA ATTACGGkTG tTTGACCTAT tTGAATGCCG      6540

ACCATTTTAT CTAACATTTG TGGGTTTCTA TTTATTTTAA ATCCTAACGC TTTATAAAAC      6600

TGTGCGCTCT TTTCTAAATC TTGCACATGC AAATTAAACC ACATTGATTG AATCATGATT      6660

GCACCCCATT CATTACTTAT TATAGTTTTG GACTTTAAGC CAATCACTTA ATGATAATCT      6720

TGTTGGATTT ATTTCAGCCA TTAATTCAAA GTCTACTTCA TAACCTTTTT CTTCCAACCA      6780

TTGCTTTTCT GCAACACCAC TAACAAATTC TCCTTCTATA ACAGTAGATT TACCTGTCAC      6840

TTCACTAAAA ATTGTTGCTG CTTCACTTAA TGTAACTTCA TCGGAACCAA TCTCTATTGA      6900

TTGATGCGTA AAGCTTTGTG GATGTGCAAA AATATACGAT GCAATTTTAG CTATATCAAT      6960

AGAAGAAATC ATTGTGAATT TTATATTCGG ATTAATAAAT TCTGGTAATG TAATACGTTC      7020

ATCTTCGACT TTAGCAATGC GTAAAAAATT ATCCATAAAG AATGATGGTT TGATAACTGT      7080

TGCATTTATA TTAGATTCCA TTAATCTATT TTCTATTTTT GCTAGTACTT CAAAGTGTGG      7140

GCCAGTTCGA TTTCGATTAA CCCCTCCCGC AGTACTATAC ACAATATGTT GAATATTTTC      7200

TTGCTCAGCT ATTTCAATTA TCTTCATACC TTGTCTTAAT TCTTCGCTAA CATCATCTTT      7260

AACGATTGGC TGAATACTGT ATAAGCCATA CTTACCTTTC ATCGCTGATT GCAAACTAAC      7320

ATTATCACTC AGATCACCTT CArCGATTGA TAAATGCGGA TGTCCTATGT CTGAAAGTTT      7380

ACGATTATnC TTATTTCTAG TTAATGCACT TACATACCAT CCATCCTCTA ACAACTGTTT      7440

TACAACTGCA TTACCTTGCT TCCCTGTTGC GCCTATTACn AAAATATCTT TCAT           7494
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(2) INFORMATION FOR SEQ ID NO: 70:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11802 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

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AATTTATTTC GCCGTCCCAC CCCAACTTGC ATTGTCTGTA GAAATTGGGA ATCCAATTTC        60

TCTTTGTTGG GGCCCcGCCC CAACTCGCAT TGCCTGTAGA ATTTCTTTTC GAAATTCTCT       120

GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTATTAC AAGCGCATTT TCGTTCAGTC       180

AATTACTGCC AATATAACTT CGTAGATCAT AGAACATTGA TTtATTtCCC AGCCTATTCT       ???
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AGCAAAGGTA ATAATGATAT TAATAATGTA CAAAAAATAT AAATCAAATC GACATCCTTA    360

TAAAACATCA GAACCACTAA AAACAAAAAA GCACAAAATA AAATTAAATT TAAAATAAAC    420

GACCACTTTT CAAAAAAATC TCtTTTCaTa TTTCCACCCC TAATTTTAAT AAGCATTATT    480

TTATATTCTC TTTTAAGTTT ATTATTCAAA AGGAAAACAG AAATATCTTT CaTATTATT     540

ATAAACATTT CAACTACTTT TAAAAACCAA CAAAAAAATA CTTATTTTAA GTAGATGAGC    600

ATAAGTGAAC ATAGTTCTTT AGTTATAATA ATTAATTCAA CCAAAAGTCG ATTTGTTTTT    660

GCAATTGGTT TTCATTTCCT CTTAAAGATA TTTTCATTAA ATCTGTCAAA TCAATAGACG    720

CTATATTTTT CAACTTATCT CTATATTTAT TTTTAGTACG TCTTTCTAAA TTTCCCCATT    780

CCTCTTCTTC GTGAGTTAAT AAATGAAGCA TTGCTCGTTC TTGTATATTT TCAATCATTT    840

TTAAATTCGG TTTTAAAATA TGCAAATCAT CAAAACAATC TTTCCAACAA TCAACCATAT    900

CTCGTTTTAA TTCAATTTCC ACACGCCATA GAAATGTTGA ATCAATTTCA ACATCTGCAT    960

TATCTTTACG TTCTTGTTTT TATTATAAAT CCGAATAAAC CTATCACTAT TACGCACACC   1020

AAAATATTTT GTTTCTGGTT TTACATTACG TCCATAAAAT ATAGTTTTCT TTACCGACTT   1080

ATCTGACAAT GCATAATAGT CATTTAAATC AAATTCAAAA TCAAAAGCCA AATCTAATCT   1140

CGTAAAACTA ACATCGTCCA AATAACTGAT GATATTTTGT TTTAACCAAA GCACTTCATC   1200

ATGCGAAAGC TTATTAGGAT TAAATTCAAC GCGCATAtAC GTCTATTCCA AAGAGTTGCT   1260

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TGTAAAATAT CCCAAAGCCG AATTTCAGGA TTAGTACTCA TAAAATGTGA AAGTCTCTCT   1380

GCGTTAGACA TGCTAAGATT CCCAACAATC GTTATAGCGT CAAAAGACAA TTTTGGAATA   1440

GCTAGTGACA TCCTATGTCG ATTTAACCGG CTATTACCGG ATATTAGAGT ATCCAGTTTT   1500

ACAAATGGAT GAAACGAAAT TCAAAACACT AAAAAATATG TTCCACTAAC AGCAAAAAAA   1560

TACCATTATG TTCCTACTAA AAAACyAAAA ATACTGGAGA ACAAATGTCA GGATATAACT   1620

TAGGATACTA TGTAATAAAA ATTTACAATA AAAAAACAGG AAAACAAATT TCAAGTAAAA   1680

GmATACCCAT ACAAAGAGGA TAAAATAAAA AACCTCGAAC TGaAATGATG ATCTTTTCAG   1740

CTCGAGGTTT AAATATTGGT GCCTTATTTA TATAGATTCG TTATATTATA TTCTCTATTT   1800

TCATTAACmT AATCCTTAAA GAGTTTTAAA TTAATACCTG CTAGATGATT CAAAAATGTT   1860

TCATCAACTT TTAAATAATT CAATAATTTT TGTGGTGTCA GTAAATnTCT ATCAAAATAC   1920

AACTTTAATA AACTATTCAT TTTGACAGGA CGTGACATTT CAATCACGTC GTCTAAAGAT   1980

AATACTTTCT CGCTTTAnAC AAAnACAAAA ACTTACCCGA TTAAAATCAA GTAAGTTTTA   2040
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TATTTGATAA AAAATCAATA AGTAATTGTG CGCCTTCAAC TTGAATATCT TTTACAACTG        2160

GCGCGTCGAT ATACATATCA TACTGACCAC CGCCTACTGC ACGATAATTA TTTACACAAA        2220

TTGTATATGT CTGCTTTAAA TCAACTGCGT GACCTTGAAT CATCATATTG CTCACACGTT        2280

GTCCCTTTGG TCTTCCAACA TGAATGGTAT AACTTACGCC ACCATATATA TCATAATTAA        2340

AGTGTTGTGG TTTGGGTTCA AGGAAGTCTG CGCTCACACT AACTTCATCA TTTTTCACGT        2400

CAAAATATTC TGCTGATCGT TCAATGGCTT CTTTAAGTTT GGCACCACTT ACAGCTAAAA        2460

CTTTAAATGT ATTTGGAAAT GGGTAATTGT TAATAACATC TCGCATCGTC ACGACTTGCT        2520

TGAAACCACT AGCAGAATCA AACAAAGCTG TACAGGCAAC ATCTGCGTCA CTTTTTTCTA        2580

ATAAAGCGTA ATTCATAAAA TTTGTAAAAG GATGCGGTGC CACACGTGCC TCAAATGCAT        2640

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GCTTTCGTAA ATGTTGGTCA TCTTCATCAA TAGTAAATGT GGAATCATCT ATAACAGGAA        2760

GTAATTCACA TGATTCAACG GATAGATTTT CATATTCATC AGTACTCAAG ACTACTCTGC        2820

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TGGCATATCC TTCATTTTCA CCCGTTAATA CTTCGGTCGG CGTACCACTT TCTAAATCCT        3000

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GCTGGCTACT GCCGCTATGC GCGATTAAGT AATTACAAAA TGGTGACCCT TGCAAAAAAT        3420

CACCATTATC TATTTTAAAA CTTTGGTCAT ACTGCCTTCT GTsTTGTTCT ATAACATGAT        3480

TCGCTAGTAA CAATCCCATA GGTTGATATT GATTCTACT CGTAAAATCT GTTGGGAAAA         3540

TATAACCATG TACGTCACTC ACGACATAAA ATGCTATGTT TGACATCCTC ACTCACTCCT        3600

TCAATCACAA ACATCTTTCT TATTTCTATT ATATATTTAT TTGAAGTCTG TTGTAATCAA        3660

GGTTTTGTCA CCGAGTTTTA AACGAATCTT TGAACCTTCC ATACTTTCAA GTACTTTAGC        3720

ATTGACCTTA ATTGTGACAT TTCCGTTTTC ATCTGCTTTA ACTGTTGGCA AAGTACTGTA        3780
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TATTGTCATT TCAAATGGCT CATTTACAGA AACATTTTGC GGGATATCAA ATGTTACTTT          3960

TTCGTTCTGA TTTGGTGGTG TATGATCATC TGGTGTGTTT GGCTGAGGAT CTGCGCCTTT          4020

TTCGCTGCCA TAACTACCTG CTTTAAATGT TGTTGGATCA TACCATTTAT AACCACTCGG          4080

CGGTTGTGAC CATGGCTCTT TTTCAGGCTC AGTTGAACGC TCTGGTCGTT CAAAATCAAG          4140

CAACTTAGTC TTTGTATCTA ATGTTAGGCT ACTCGCCTTA AGTGATTTCC CATCATTATC          4200

TTTAGACATC CAAGCCGTTA TATTATTTAA TAGCTTACCG TTGTCTTGTT CTTTAAAACC          4260

ATCATATGTT TTCTTCTTTT CTCCATTATC TTCTCTTACA TATTTGGGCG AACTATCTTC          4320

CACAAGTGAT GAATCACCGA TAAATGCTGC TTTACCTTTT CCAACTTTAG AAATTGCTAC          4380

ATAGGGGCCT TCTGCTTTAC CGCCCCCATT ATAAATACCT TGATCTACAG CATGTGACCA          4440

TTTACTTTTC GCTGGCAATT GTTCTGGTGT ATACACAATA CCTTTTGCTT TCTCTGGATT          4500

AGTAATTGCT AATGTCGATC CGGCATGCAT AGAGACAGAT TTCACACCTT CAGTAATACC          4560

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AAAACGTACG CCAAAGTTTG TAGATAACCA ATCTGAACTT TTCACACCTT GCATTGCAGT          4680

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AGCTAAAGAT TGCGGTAAAG CACTTAATGA TACCGTTGCA ACAATTGCAG AGACAGTTAA          5160

TGACTTATAT ATTTTTTTCA TTTTGTGAGG CTCCTTTTAA AATAAATTTG TTCTTGAATT          5220

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ACTCTTAAAG AAAGTTATTA AAATTCATTT TTATAAAATA CTTTTTAACA TTTAAATGTG          5340

GTACGCTATA AGTGTAATTT CATTGCATAC ATATTACACG ATTAAGAATG TGAAGGGGAC          5400

AGTTATCAAA TGAAAAATTT TAAGTGTTTA TTTGTATTAA TGTTAGCAGT CATTGTTTTT          5460

GCAGCAGCAT GTGGAAACTC AAGTTCTTTA GATAATCAAA AGAACGCTAG TAATGATTCG          5520

GATTCTAAAT CAGGAGGATA CAAACCTAAA GAATTAACCG TTCAATTTGT ACCTTCGCAA          5580

AATGCTGGAA CATTAGAAGC TAAAGCAAAA CCATTAGAAA AATTACTATC TAAAGAATTA          5640
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TCTAAAAAAG TTGATGTTGG TTTCTTACCA CCAACGGCAT ACACATTAGC ACATGATCAA   5760

AAAGCAGCTG ATTTATTATT ACAAGCACAA CGTTTCGGTG TAAAAGAAGA TGGTTCAGCA   5820

AGTAAAGAAC TTGTAGATAG TTATAAATCA GAAATTCTTG TTAAAAAAGA CTCAAAAATT   5880

AAAAGCTTGA AAGATTTAAA AGGTAAGAAA ATTGCCTTAC AAGATGTAAC ATCAACTGCT   5940

GGATATACAT TCCCACTTGC GATGTTAAAA AACGAAGCAG GTATTAATGC AACTAAAGAT   6000

ATGAAAATTG TGAATGTTAA AGGTCATGAC CAAGCAGTTA TCTCATTATT AAATGGAGAt   6060

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GGTGTCGCTG TACATTTGAA ACCATTTGTA CACAGAAACC CAATGTCTAT GATATTTCAG   6540

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TATGATGGTC CTGCATCTGA AGCAACAGAT GACGTATTTA GTGAAATATA TGGACGTACA   7320

ATTAAAGAAG ATGAAAAGCT AGGAGTGAAC TAACATGCCT TTAGAAATAC CTACAAAGTA   7380

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AATACCTCAA ATAGGTGATC TATTCAAACA AATGATTCCA CCTGATTTCG AGTATTTACA          7560

ACAAATTACA ACGCCAATGT TAGATACCAT TCGAATGGcT ATCGTAAGTA CAGTATTAGG          7620

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GATTTCAATA CCCTCGCGCT TTATTTTAAA TATAGTTCGT ACTATTCCAG ATTTGTTATT          7740

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TTTACCGAAC TCTGGTAATG TTACGTTGAA ATTATCTGCT ATAGTTGCAC CGATAGAACT          9180

GAATGTAGTA TCACTTTCTA GTGCATGACC ACCTTTAAAT TTCGGACTGT ACATAATTAC          9240
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